functions, and accordingly utilities, of VGAM1491 correlate with, and may be deduced from, the identity of the host target genes which VGAM1491 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[20840] Nucleotide sequences of the VGAM1491 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1491 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1491 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1491 are further described hereinbelow with reference to Table 1.

[20841] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1491 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[20842] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1492 (VGAM1492) viral gene, which modulates expression of respective host target genes thereof, the func-

tion and utility of which host target genes is known in the art.

[20843] VGAM1492 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1492 was detected is described hereinabove with reference to Figs. 2-8.

[20844] VGAM1492 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Johnsongrass mosaic virus. VGAM1492 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[20845] VGAM1492 gene, herein designated VGAM GENE, encodes a VGAM1492 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1492 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1492 precursor RNA is designated SEQ ID:1478, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1478 is located at position 2047 relative to the genome of Johnsongrass mosaic virus.

[20846] VGAM1492 precursor RNA, herein designated VGAM PRE-

CURSOR RNA, folds onto itself, forming VGAM1492 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[20847] An enzyme complex designated DICER COMPLEX, dices the VGAM1492 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1492 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 73%) nucleotide sequence of VGAM1492 RNA is designated SEQ ID:4203, and is provided hereinbelow with reference to the sequence listing part.

[20848] VGAM1492 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM1492 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1492 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[20849] VGAM1492 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1492 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1492 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1492 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1492 host

target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[20850] The complementary binding of VGAM1492 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1492 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1492 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1492 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[20851] It is appreciated that VGAM1492 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1492 host target genes. The mRNA of each one of this plurality of VGAM1492 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1492 RNA, herein designated VGAM RNA, and which when bound by VGAM1492 RNA, herein

designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1492 host target proteins.

[20852] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1492 gene, herein designated VGAM GENE, on one or more VGAM1492 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[20853] It is yet further appreciated that a function of VGAM1492 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1492 include diagnosis, prevention and

treatment of viral infection by Johnsongrass mosaic virus. Specific functions, and accordingly utilities, of VGAM1492 correlate with, and may be deduced from, the identity of the host target genes which VGAM1492 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[20854] Nucleotide sequences of the VGAM1492 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1492 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1492 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1492 are further described hereinbelow with reference to Table 1.

[20855] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1492 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[20856] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1493 (VGAM1493) viral gene, which modulates ex-

pression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[20857] VGAM1493 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1493 was detected is described hereinabove with reference to Figs. 2-8.

[20858] VGAM1493 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Johnsongrass mosaic virus. VGAM1493 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[20859] VGAM1493 gene, herein designated VGAM GENE, encodes a VGAM1493 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1493 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1493 precursor RNA is designated SEQ ID:1479, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1479 is located at position 7469 relative to the genome of Johnsongrass mosaic virus.

[20860] VGAM1493 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1493 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[20861] An enzyme complex designated DICER COMPLEX, dices the VGAM1493 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1493 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM1493 RNA is designated SEQ ID:4204, and is provided hereinbelow with reference to the sequence listing part.

[20862] VGAM1493 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1493 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1493 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[20863] VGAM1493 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1493 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1493 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1493 RNA, herein designated VGAM RNA, may have a different number of host target

binding sites in untranslated regions of a VGAM1493 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[20864] The complementary binding of VGAM1493 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1493 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1493 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1493 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[20865] It is appreciated that VGAM1493 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1493 host target genes. The mRNA of each one of this plurality of VGAM1493 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1493 RNA, herein designated VGAM

RNA, and which when bound by VGAM1493 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1493 host target proteins.

[20866] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1493 gene, herein designated VGAM GENE, on one or more VGAM1493 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[20867] It is yet further appreciated that a function of VGAM1493 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM1493 include diagnosis, prevention and treatment of viral infection by Johnsongrass mosaic virus. Specific functions, and accordingly utilities, of VGAM1493 correlate with, and may be deduced from, the identity of the host target genes which VGAM1493 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[20868] Nucleotide sequences of the VGAM1493 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1493 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1493 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1493 are further described hereinbelow with reference to Table 1.

[20869] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1493 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[20870] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Mes-

senger 1494 (VGAM1494) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[20871] VGAM1494 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1494 was detected is described hereinabove with reference to Figs. 2-8.

[20872] VGAM1494 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Johnsongrass mosaic virus. VGAM1494 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[20873] VGAM1494 gene, herein designated VGAM GENE, encodes a VGAM1494 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1494 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1494 precursor RNA is designated SEQ ID:1480, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1480 is located at position 656

relative to the genome of Johnsongrass mosaic virus.

[20874] VGAM1494 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1494 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[20875] An enzyme complex designated DICER COMPLEX, dices the VGAM1494 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1494 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM1494 RNA is designated SEQ ID:4205, and is provided hereinbelow with reference to the sequence listing part.

[20876] VGAM1494 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1494 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1494 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[20877] VGAM1494 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1494 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1494 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1494 RNA, herein designated

VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1494 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[20878] The complementary binding of VGAM1494 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1494 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1494 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1494 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[20879] It is appreciated that VGAM1494 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1494 host target genes. The mRNA of each one of this plurality of VGAM1494 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM1494 RNA, herein designated VGAM RNA, and which when bound by VGAM1494 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1494 host target proteins.

[20880] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1494 gene, herein designated VGAM GENE, on one or more VGAM1494 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[20881] It is yet further appreciated that a function of VGAM1494 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1494 include diagnosis, prevention and treatment of viral infection by Johnsongrass mosaic virus. Specific functions, and accordingly utilities, of VGAM1494 correlate with, and may be deduced from, the identity of the host target genes which VGAM1494 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[20882] Nucleotide sequences of the VGAM1494 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1494 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1494 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1494 are further described hereinbelow with reference to Table 1.

[20883] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1494 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[20884] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present

invention, referred to here as Viral Genomic Address Messenger 1495 (VGAM1495) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[20885] VGAM1495 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1495 was detected is described hereinabove with reference to Figs. 2-8.

[20886] VGAM1495 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Johnsongrass mosaic virus. VGAM1495 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[20887] VGAM1495 gene, herein designated VGAM GENE, encodes a VGAM1495 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1495 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1495 precursor RNA is designated SEQ ID:1481, and is provided hereinbelow with reference to the sequence listing part. Nu-

cleotide sequence SEQ ID:1481 is located at position 5140 relative to the genome of Johnsongrass mosaic virus.

[20888] VGAM1495 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1495 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[20889] An enzyme complex designated DICER COMPLEX, dices the VGAM1495 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1495 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 66%) nucleotide sequence of VGAM1495 RNA is designated SEQ ID:4206, and is provided hereinbelow with reference to the sequence

listing part.

[20890] VGAM1495 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1495 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1495 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[20891] VGAM1495 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1495 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1495 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not

meant to be limiting VGAM1495 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1495 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[20892] The complementary binding of VGAM1495 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1495 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1495 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1495 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[20893] It is appreciated that VGAM1495 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1495 host target genes. The mRNA of each one of this plurality of VGAM1495 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM1495 RNA, herein designated VGAM RNA, and which when bound by VGAM1495 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1495 host target proteins.

[20894] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1495 gene, herein designated VGAM GENE, on one or more VGAM1495 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[20895] It is yet further appreciated that a function of VGAM1495

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1495 include diagnosis, prevention and treatment of viral infection by Johnsongrass mosaic virus. Specific functions, and accordingly utilities, of VGAM1495 correlate with, and may be deduced from, the identity of the host target genes which VGAM1495 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[20896] Nucleotide sequences of the VGAM1495 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1495 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1495 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1495 are further described hereinbelow with reference to Table 1.

[20897] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1495 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[20898] Fig. 1 further provides a conceptual description of another

novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1496 (VGAM1496) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[20899] VGAM1496 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1496 was detected is described hereinabove with reference to Figs. 2-8.

[20900] VGAM1496 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Alcelaphine herpesvirus 1. VGAM1496 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[20901] VGAM1496 gene, herein designated VGAM GENE, encodes a VGAM1496 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1496 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1496 precursor RNA is designated SEQ ID:1482, and is provided here-

inbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1482 is located at position 110360 relative to the genome of Alcelaphine herpesvirus 1.

[20902] VGAM1496 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1496 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[20903] An enzyme complex designated DICER COMPLEX, dices the VGAM1496 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1496 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 81%) nucleotide se-

quence of VGAM1496 RNA is designated SEQ ID:4207, and is provided hereinbelow with reference to the sequence listing part.

[20904] VGAM1496 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1496 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1496 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[20905] VGAM1496 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1496 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1496 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is ap-

preciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1496 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1496 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[20906] The complementary binding of VGAM1496 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1496 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1496 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1496 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[20907] It is appreciated that VGAM1496 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1496 host target genes. The mRNA of

each one of this plurality of VGAM1496 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1496 RNA, herein designated VGAM RNA, and which when bound by VGAM1496 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1496 host target proteins.

[20908] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1496 gene, herein designated VGAM GENE, on one or more VGAM1496 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science

294,779 (2001)).

[20909] It is yet further appreciated that a function of VGAM1496 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1496 include diagnosis, prevention and treatment of viral infection by Alcelaphine herpesvirus 1. Specific functions, and accordingly utilities, of VGAM1496 correlate with, and may be deduced from, the identity of the host target genes which VGAM1496 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[20910] Nucleotide sequences of the VGAM1496 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1496 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1496 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1496 are further described hereinbelow with reference to Table 1.

[20911] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1496 RNA, herein designated VGAM RNA, are de-

scribed hereinbelow with reference to Table 2.

[20912] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1497 (VGAM1497) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[20913] VGAM1497 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1497 was detected is described hereinabove with reference to Figs. 2-8.

[20914] VGAM1497 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Alcelaphine herpesvirus 1. VGAM1497 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[20915] VGAM1497 gene, herein designated VGAM GENE, encodes a VGAM1497 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1497 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly

similar to the nucleotide sequence of VGAM1497 precursor RNA is designated SEQ ID:1483, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1483 is located at position 108884 relative to the genome of Alcelaphine herpesvirus 1.

[20916] VGAM1497 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1497 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[20917] An enzyme complex designated DICER COMPLEX, dices the VGAM1497 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1497 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM1497 RNA is designated SEQ ID:4208, and is provided hereinbelow with reference to the sequence listing part.

[20918] VGAM1497 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1497 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1497 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[20919] VGAM1497 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1497 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1497 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3

such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1497 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1497 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[20920] The complementary binding of VGAM1497 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1497 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1497 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1497 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[20921] It is appreciated that VGAM1497 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1497 host target genes. The mRNA of each one of this plurality of VGAM1497 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1497 RNA, herein designated VGAM RNA, and which when bound by VGAM1497 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1497 host target proteins.

[20922] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1497 gene, herein designated VGAM GENE, on one or more VGAM1497 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[20923] It is yet further appreciated that a function of VGAM1497 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1497 include diagnosis, prevention and treatment of viral infection by Alcelaphine herpesvirus 1. Specific functions, and accordingly utilities, of VGAM1497 correlate with, and may be deduced from, the identity of the host target genes which VGAM1497 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[20924] Nucleotide sequences of the VGAM1497 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1497 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1497 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1497 are further described hereinbelow with reference to Table 1.

[20925] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the

complementarity of each of these host target binding sites to VGAM1497 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[20926] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1498 (VGAM1498) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[20927] VGAM1498 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1498 was detected is described hereinabove with reference to Figs. 2-8.

[20928] VGAM1498 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Alcelaphine herpesvirus 1. VGAM1498 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[20929] VGAM1498 gene, herein designated VGAM GENE, encodes a VGAM1498 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1498 precursor RNA,

herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1498 precursor RNA is designated SEQ ID:1484, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1484 is located at position 112274 relative to the genome of Alcelaphine herpesvirus 1.

[20930] VGAM1498 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1498 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[20931] An enzyme complex designated DICER COMPLEX, dices the VGAM1498 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1498 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 52%) nucleotide sequence of VGAM1498 RNA is designated SEQ ID:4209, and is provided hereinbelow with reference to the sequence listing part.

[20932] VGAM1498 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1498 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1498 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[20933] VGAM1498 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1498 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1498 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed

sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1498 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1498 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[20934] The complementary binding of VGAM1498 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1498 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1498 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1498 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target

protein is therefore outlined by a broken line.

[20935] It is appreciated that VGAM1498 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1498 host target genes. The mRNA of each one of this plurality of VGAM1498 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1498 RNA, herein designated VGAM RNA, and which when bound by VGAM1498 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1498 host target proteins.

[20936] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1498 gene, herein designated VGAM GENE, on one or more VGAM1498 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[20937] It is yet further appreciated that a function of VGAM1498 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1498 include diagnosis, prevention and treatment of viral infection by Alcelaphine herpesvirus 1. Specific functions, and accordingly utilities, of VGAM1498 correlate with, and may be deduced from, the identity of the host target genes which VGAM1498 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[20938] Nucleotide sequences of the VGAM1498 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1498 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1498 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1498 are further described hereinbelow with reference to Table 1.

[20939] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1498 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[20940] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1499 (VGAM1499) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[20941] VGAM1499 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1499 was detected is described hereinabove with reference to Figs. 2-8.

[20942] VGAM1499 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Alcelaphine herpesvirus 1. VGAM1499 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[20943] VGAM1499 gene, herein designated VGAM GENE, encodes a VGAM1499 precursor RNA, herein designated VGAM

PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1499 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1499 precursor RNA is designated SEQ ID:1485, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1485 is located at position 110926 relative to the genome of Alcelaphine herpesvirus 1.

[20944] VGAM1499 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1499 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[20945] An enzyme complex designated DICER COMPLEX, dices the VGAM1499 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1499 RNA,

herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 60%) nucleotide sequence of VGAM1499 RNA is designated SEQ ID:4210, and is provided hereinbelow with reference to the sequence listing part.

[20946] VGAM1499 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1499 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1499 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[20947] VGAM1499 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1499 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM1499 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1499 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1499 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[20948] The complementary binding of VGAM1499 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1499 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1499 host target RNA, herein designated VGAM HOST TARGET

RNA, into VGAM1499 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[20949] It is appreciated that VGAM1499 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1499 host target genes. The mRNA of each one of this plurality of VGAM1499 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1499 RNA, herein designated VGAM RNA, and which when bound by VGAM1499 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1499 host target proteins.

[20950] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1499 gene, herein designated VGAM GENE, on one or more VGAM1499 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[20951] It is yet further appreciated that a function of VGAM1499 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1499 include diagnosis, prevention and treatment of viral infection by Alcelaphine herpesvirus 1. Specific functions, and accordingly utilities, of VGAM1499 correlate with, and may be deduced from, the identity of the host target genes which VGAM1499 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[20952] Nucleotide sequences of the VGAM1499 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1499 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1499 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1499 are further

described hereinbelow with reference to Table 1.

[20953] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1499 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[20954] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1500 (VGAM1500) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[20955] VGAM1500 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1500 was detected is described hereinabove with reference to Figs. 2-8.

[20956] VGAM1500 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Aphid lethal paralysis virus. VGAM1500 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[20957] VGAM1500 gene, herein designated VGAM GENE, encodes a VGAM1500 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1500 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1500 precursor RNA is designated SEQ ID:1486, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1486 is located at position 3755 relative to the genome of Aphid lethal paralysis virus.

[20958] VGAM1500 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1500 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[20959] An enzyme complex designated DICER COMPLEX, dices the VGAM1500 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, into VGAM1500 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 84%) nucleotide sequence of VGAM1500 RNA is designated SEQ ID:4211, and is provided hereinbelow with reference to the sequence listing part.

[20960] VGAM1500 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1500 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1500 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[20961] VGAM1500 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1500 host target RNA, herein designated VGAM HOST TARGET RNA. This

complementary binding is due to the fact that the nucleotide sequence of VGAM1500 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1500 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1500 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[20962] The complementary binding of VGAM1500 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1500 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1500

host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1500 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[20963] It is appreciated that VGAM1500 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1500 host target genes. The mRNA of each one of this plurality of VGAM1500 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1500 RNA, herein designated VGAM RNA, and which when bound by VGAM1500 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1500 host target proteins.

[20964] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1500 gene, herein designated VGAM GENE, on one or more VGAM1500 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[20965] It is yet further appreciated that a function of VGAM1500 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1500 include diagnosis, prevention and treatment of viral infection by Aphid lethal paralysis virus. Specific functions, and accordingly utilities, of VGAM1500 correlate with, and may be deduced from, the identity of the host target genes which VGAM1500 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[20966] Nucleotide sequences of the VGAM1500 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1500 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1500 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM1500 are further described hereinbelow with reference to Table 1.

[20967] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1500 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[20968] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1501 (VGAM1501) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[20969] VGAM1501 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1501 was detected is described hereinabove with reference to Figs. 2-8.

[20970] VGAM1501 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Aphid lethal paralysis virus. VGAM1501 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in

the human genome.

[20971] VGAM1501 gene, herein designated VGAM GENE, encodes a VGAM1501 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1501 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1501 precursor RNA is designated SEQ ID:1487, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1487 is located at position 1260 relative to the genome of Aphid lethal paralysis virus.

[20972] VGAM1501 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1501 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[20973] An enzyme complex designated DICER COMPLEX, dices

the VGAM1501 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1501 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 71%) nucleotide sequence of VGAM1501 RNA is designated SEQ ID:4212, and is provided hereinbelow with reference to the sequence listing part.

[20974] VGAM1501 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1501 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1501 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[20975] VGAM1501 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1501 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1501 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1501 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1501 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[20976] The complementary binding of VGAM1501 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1501 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM1501 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1501 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[20977] It is appreciated that VGAM1501 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1501 host target genes. The mRNA of each one of this plurality of VGAM1501 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1501 RNA, herein designated VGAM RNA, and which when bound by VGAM1501 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1501 host target proteins.

[20978] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1501 gene, herein designated VGAM GENE, on one or more VGAM1501 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[20979] It is yet further appreciated that a function of VGAM1501 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1501 include diagnosis, prevention and treatment of viral infection by Aphid lethal paralysis virus. Specific functions, and accordingly utilities, of VGAM1501 correlate with, and may be deduced from, the identity of the host target genes which VGAM1501 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[20980] Nucleotide sequences of the VGAM1501 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1501 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of

VGAM1501 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1501 are further described hereinbelow with reference to Table 1.

[20981] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1501 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[20982] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1502 (VGAM1502) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[20983] VGAM1502 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1502 was detected is described hereinabove with reference to Figs. 2-8.

[20984] VGAM1502 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Aphid lethal paralysis virus. VGAM1502 host target gene, herein designated

VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[20985] VGAM1502 gene, herein designated VGAM GENE, encodes a VGAM1502 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1502 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1502 precursor RNA is designated SEQ ID:1488, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1488 is located at position 1441 relative to the genome of Aphid lethal paralysis virus.

[20986] VGAM1502 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1502 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[20987] An enzyme complex designated DICER COMPLEX, dices the VGAM1502 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1502 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 60%) nucleotide sequence of VGAM1502 RNA is designated SEQ ID:4213, and is provided hereinbelow with reference to the sequence listing part.

[20988] VGAM1502 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1502 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1502 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[20989] VGAM1502 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites

located in untranslated regions of VGAM1502 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1502 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1502 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1502 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[20990] The complementary binding of VGAM1502 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1502 host target RNA, herein designated VGAM

HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1502 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1502 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[20991] It is appreciated that VGAM1502 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1502 host target genes. The mRNA of each one of this plurality of VGAM1502 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1502 RNA, herein designated VGAM RNA, and which when bound by VGAM1502 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1502 host target proteins.

[20992] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1502 gene, herein designated VGAM GENE, on one or more VGAM1502 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove

with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[20993] It is yet further appreciated that a function of VGAM1502 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1502 include diagnosis, prevention and treatment of viral infection by Aphid lethal paralysis virus. Specific functions, and accordingly utilities, of VGAM1502 correlate with, and may be deduced from, the identity of the host target genes which VGAM1502 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[20994] Nucleotide sequences of the VGAM1502 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1502 RNA, herein designated VGAM RNA, and

a schematic representation of the secondary folding of VGAM1502 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1502 are further described hereinbelow with reference to Table 1.

[20995] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1502 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[20996] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1503 (VGAM1503) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[20997] VGAM1503 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1503 was detected is described hereinabove with reference to Figs. 2-8.

[20998] VGAM1503 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Aphid lethal paralysis

virus. VGAM1503 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[20999] VGAM1503 gene, herein designated VGAM GENE, encodes a VGAM1503 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1503 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1503 precursor RNA is designated SEQ ID:1489, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1489 is located at position 9098 relative to the genome of Aphid lethal paralysis virus.

[21000] VGAM1503 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1503 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[21001] An enzyme complex designated DICER COMPLEX, dices the VGAM1503 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1503 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 59%) nucleotide sequence of VGAM1503 RNA is designated SEQ ID:4214, and is provided hereinbelow with reference to the sequence listing part.

[21002] VGAM1503 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1503 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1503 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21003] VGAM1503 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM1503 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1503 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1503 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1503 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21004] The complementary binding of VGAM1503 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM1503 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1503 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1503 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[21005] It is appreciated that VGAM1503 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1503 host target genes. The mRNA of each one of this plurality of VGAM1503 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1503 RNA, herein designated VGAM RNA, and which when bound by VGAM1503 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1503 host target proteins.

[21006] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1503 gene, herein designated VGAM GENE, on one or more VGAM1503 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21007] It is yet further appreciated that a function of VGAM1503 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1503 include diagnosis, prevention and treatment of viral infection by Aphid lethal paralysis virus. Specific functions, and accordingly utilities, of VGAM1503 correlate with, and may be deduced from, the identity of the host target genes which VGAM1503 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[21008] Nucleotide sequences of the VGAM1503 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

diced VGAM1503 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1503 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1503 are further described hereinbelow with reference to Table 1.

[21009] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1503 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[21010] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1504 (VGAM1504) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[21011] VGAM1504 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1504 was detected is described hereinabove with reference to Figs. 2-8.

[21012] VGAM1504 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of Aphid lethal paralysis virus. VGAM1504 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[21013] VGAM1504 gene, herein designated VGAM GENE, encodes a VGAM1504 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1504 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1504 precursor RNA is designated SEQ ID:1490, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1490 is located at position 8300 relative to the genome of Aphid lethal paralysis virus.

[21014] VGAM1504 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1504 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21015] An enzyme complex designated DICER COMPLEX, dices the VGAM1504 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1504 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 57%) nucleotide sequence of VGAM1504 RNA is designated SEQ ID:4215, and is provided hereinbelow with reference to the sequence listing part.

[21016] VGAM1504 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1504 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1504 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21017] VGAM1504 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1504 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1504 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1504 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1504 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21018] The complementary binding of VGAM1504 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM1504 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1504 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1504 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[21019] It is appreciated that VGAM1504 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1504 host target genes. The mRNA of each one of this plurality of VGAM1504 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1504 RNA, herein designated VGAM RNA, and which when bound by VGAM1504 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1504 host target proteins.

[21020] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1504 gene, herein designated VGAM GENE, on one or more VGAM1504 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21021] It is yet further appreciated that a function of VGAM1504 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1504 include diagnosis, prevention and treatment of viral infection by Aphid lethal paralysis virus. Specific functions, and accordingly utilities, of VGAM1504 correlate with, and may be deduced from, the identity of the host target genes which VGAM1504 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[21022] Nucleotide sequences of the VGAM1504 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the diced VGAM1504 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1504 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1504 are further described hereinbelow with reference to Table 1.

[21023] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1504 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[21024] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1505 (VGAM1505) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[21025] VGAM1505 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1505 was detected is described hereinabove with reference to Figs. 2-8.

[21026] VGAM1505 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Aphid lethal paralysis virus. VGAM1505 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[21027] VGAM1505 gene, herein designated VGAM GENE, encodes a VGAM1505 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1505 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1505 precursor RNA is designated SEQ ID:1491, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1491 is located at position 8120 relative to the genome of Aphid lethal paralysis virus.

[21028] VGAM1505 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1505 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21029] An enzyme complex designated DICER COMPLEX, dices the VGAM1505 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1505 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM1505 RNA is designated SEQ ID:4216, and is provided hereinbelow with reference to the sequence listing part.

[21030] VGAM1505 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1505 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1505 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN COD-

ING and 3UTR respectively.

[21031] VGAM1505 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1505 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1505 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1505 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1505 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21032] The complementary binding of VGAM1505 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1505 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1505 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1505 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[21033] It is appreciated that VGAM1505 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1505 host target genes. The mRNA of each one of this plurality of VGAM1505 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1505 RNA, herein designated VGAM RNA, and which when bound by VGAM1505 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1505 host target proteins.

[21034] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1505 gene, herein designated VGAM GENE, on one

or more VGAM1505 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21035] It is yet further appreciated that a function of VGAM1505 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1505 include diagnosis, prevention and treatment of viral infection by Aphid lethal paralysis virus. Specific functions, and accordingly utilities, of VGAM1505 correlate with, and may be deduced from, the identity of the host target genes which VGAM1505 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[21036] Nucleotide sequences of the VGAM1505 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1505 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1505 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1505 are further described hereinbelow with reference to Table 1.

[21037] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1505 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[21038] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1506 (VGAM1506) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[21039] VGAM1506 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1506 was detected is de-

scribed hereinabove with reference to Figs. 2-8.

[21040] VGAM1506 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Aphid lethal paralysis virus. VGAM1506 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[21041] VGAM1506 gene, herein designated VGAM GENE, encodes a VGAM1506 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1506 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1506 precursor RNA is designated SEQ ID:1492, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1492 is located at position 8885 relative to the genome of Aphid lethal paralysis virus.

[21042] VGAM1506 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1506 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21043] An enzyme complex designated DICER COMPLEX, dices the VGAM1506 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1506 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM1506 RNA is designated SEQ ID:4217, and is provided hereinbelow with reference to the sequence listing part.

[21044] VGAM1506 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1506 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1506 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and

a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21045] VGAM1506 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1506 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1506 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1506 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1506 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both

3UTR and 5UTR regions.

[21046] The complementary binding of VGAM1506 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1506 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1506 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1506 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[21047] It is appreciated that VGAM1506 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1506 host target genes. The mRNA of each one of this plurality of VGAM1506 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1506 RNA, herein designated VGAM RNA, and which when bound by VGAM1506 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1506 host target proteins.

[21048] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM1506 gene, herein designated VGAM GENE, on one or more VGAM1506 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21049] It is yet further appreciated that a function of VGAM1506 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1506 include diagnosis, prevention and treatment of viral infection by Aphid lethal paralysis virus. Specific functions, and accordingly utilities, of VGAM1506 correlate with, and may be deduced from, the identity of the host target genes which VGAM1506 binds and inhibits, and the function of these host target genes, as

elaborated hereinbelow.

[21050] Nucleotide sequences of the VGAM1506 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1506 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1506 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1506 are further described hereinbelow with reference to Table 1.

[21051] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1506 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[21052] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1507 (VGAM1507) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[21053] VGAM1507 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene.

The method by which VGAM1507 was detected is described hereinabove with reference to Figs. 2-8.

[21054] VGAM1507 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Aphid lethal paralysis virus. VGAM1507 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[21055] VGAM1507 gene, herein designated VGAM GENE, encodes a VGAM1507 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1507 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1507 precursor RNA is designated SEQ ID:1493, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1493 is located at position 4389 relative to the genome of Aphid lethal paralysis virus.

[21056] VGAM1507 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1507 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21057] An enzyme complex designated DICER COMPLEX, dices the VGAM1507 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1507 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM1507 RNA is designated SEQ ID:4218, and is provided hereinbelow with reference to the sequence listing part.

[21058] VGAM1507 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1507 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1507 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding

gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21059] VGAM1507 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1507 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1507 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1507 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1507 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be lo-

cated in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21060] The complementary binding of VGAM1507 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1507 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1507 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1507 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[21061] It is appreciated that VGAM1507 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1507 host target genes. The mRNA of each one of this plurality of VGAM1507 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1507 RNA, herein designated VGAM RNA, and which when bound by VGAM1507 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1507 host target proteins.

[21062] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM1507 gene, herein designated VGAM GENE, on one or more VGAM1507 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21063] It is yet further appreciated that a function of VGAM1507 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1507 include diagnosis, prevention and treatment of viral infection by Aphid lethal paralysis virus. Specific functions, and accordingly utilities, of VGAM1507 correlate with, and may be deduced from, the identity of the host target genes which VGAM1507 binds and in-

hibits, and the function of these host target genes, as elaborated hereinbelow.

[21064] Nucleotide sequences of the VGAM1507 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1507 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1507 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1507 are further described hereinbelow with reference to Table 1.

[21065] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1507 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[21066] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1508 (VGAM1508) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[21067] VGAM1508 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1508 was detected is described hereinabove with reference to Figs. 2-8.

[21068] VGAM1508 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Potato virus V. VGAM1508 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[21069] VGAM1508 gene, herein designated VGAM GENE, encodes a VGAM1508 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1508 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1508 precursor RNA is designated SEQ ID:1494, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1494 is located at position 7772 relative to the genome of Potato virus V.

[21070] VGAM1508 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1508 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21071] An enzyme complex designated DICER COMPLEX, dices the VGAM1508 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1508 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM1508 RNA is designated SEQ ID:4219, and is provided hereinbelow with reference to the sequence listing part.

[21072] VGAM1508 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1508 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1508 host target RNA, herein designated VGAM HOST TARGET RNA, comprises

three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21073] VGAM1508 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1508 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1508 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1508 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1508 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an

example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21074] The complementary binding of VGAM1508 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1508 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1508 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1508 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[21075] It is appreciated that VGAM1508 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1508 host target genes. The mRNA of each one of this plurality of VGAM1508 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1508 RNA, herein designated VGAM RNA, and which when bound by VGAM1508 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1508 host target proteins.

[21076] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1508 gene, herein designated VGAM GENE, on one or more VGAM1508 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21077] It is yet further appreciated that a function of VGAM1508 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1508 include diagnosis, prevention and treatment of viral infection by Potato virus V. Specific functions, and accordingly utilities, of VGAM1508 correlate with, and may be deduced from, the identity of the

host target genes which VGAM1508 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[21078] Nucleotide sequences of the VGAM1508 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1508 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1508 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1508 are further described hereinbelow with reference to Table 1.

[21079] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1508 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[21080] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1509 (VGAM1509) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[21081] VGAM1509 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1509 was detected is described hereinabove with reference to Figs. 2-8.

[21082] VGAM1509 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Potato virus V. VGAM1509 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[21083] VGAM1509 gene, herein designated VGAM GENE, encodes a VGAM1509 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1509 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1509 precursor RNA is designated SEQ ID:1495, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1495 is located at position 8444 relative to the genome of Potato virus V.

[21084] VGAM1509 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1509 folded precursor RNA, herein designated VGAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21085] An enzyme complex designated DICER COMPLEX, dices the VGAM1509 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1509 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM1509 RNA is designated SEQ ID:4220, and is provided hereinbelow with reference to the sequence listing part.

[21086] VGAM1509 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1509 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1509 host target RNA,

herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21087] VGAM1509 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1509 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1509 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1509 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1509 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host tar-

get binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21088] The complementary binding of VGAM1509 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1509 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1509 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1509 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[21089] It is appreciated that VGAM1509 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1509 host target genes. The mRNA of each one of this plurality of VGAM1509 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1509 RNA, herein designated VGAM RNA, and which when bound by VGAM1509 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1509 host target proteins.

[21090] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1509 gene, herein designated VGAM GENE, on one or more VGAM1509 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21091] It is yet further appreciated that a function of VGAM1509 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1509 include diagnosis, prevention and treatment of viral infection by Potato virus V. Specific functions, and accordingly utilities, of VGAM1509 corre-

late with, and may be deduced from, the identity of the host target genes which VGAM1509 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[21092] Nucleotide sequences of the VGAM1509 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1509 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1509 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1509 are further described hereinbelow with reference to Table 1.

[21093] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1509 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[21094] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1510 (VGAM1510) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the

art.

[21095] VGAM1510 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1510 was detected is described hereinabove with reference to Figs. 2-8.

[21096] VGAM1510 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Potato virus V. VGAM1510 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[21097] VGAM1510 gene, herein designated VGAM GENE, encodes a VGAM1510 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1510 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1510 precursor RNA is designated SEQ ID:1496, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1496 is located at position 6444 relative to the genome of Potato virus V.

[21098] VGAM1510 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1510 folded

precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21099] An enzyme complex designated DICER COMPLEX, dices the VGAM1510 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1510 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 81%) nucleotide sequence of VGAM1510 RNA is designated SEQ ID:4221, and is provided hereinbelow with reference to the sequence listing part.

[21100] VGAM1510 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1510 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM1510 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21101] VGAM1510 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1510 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1510 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1510 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1510 host target RNA, herein designated VGAM HOST TARGET RNA.

It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21102] The complementary binding of VGAM1510 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1510 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1510 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1510 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[21103] It is appreciated that VGAM1510 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1510 host target genes. The mRNA of each one of this plurality of VGAM1510 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1510 RNA, herein designated VGAM RNA, and which when bound by VGAM1510 RNA, herein designated VGAM RNA, causes inhibition of translation of

respective one or more VGAM1510 host target proteins.

[21104] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1510 gene, herein designated VGAM GENE, on one or more VGAM1510 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21105] It is yet further appreciated that a function of VGAM1510 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1510 include diagnosis, prevention and treatment of viral infection by Potato virus V. Specific

functions, and accordingly utilities, of VGAM1510 correlate with, and may be deduced from, the identity of the host target genes which VGAM1510 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[21106] Nucleotide sequences of the VGAM1510 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1510 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1510 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1510 are further described hereinbelow with reference to Table 1.

[21107] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1510 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[21108] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1511 (VGAM1511) viral gene, which modulates expression of respective host target genes thereof, the func-

tion and utility of which host target genes is known in the art.

[21109] VGAM1511 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1511 was detected is described hereinabove with reference to Figs. 2-8.

[21110] VGAM1511 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Potato virus V. VGAM1511 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[21111] VGAM1511 gene, herein designated VGAM GENE, encodes a VGAM1511 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1511 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1511 precursor RNA is designated SEQ ID:1497, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1497 is located at position 4177 relative to the genome of Potato virus V.

[21112] VGAM1511 precursor RNA, herein designated VGAM PRE-

CURSOR RNA, folds onto itself, forming VGAM1511 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21113] An enzyme complex designated DICER COMPLEX, dices the VGAM1511 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1511 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 55%) nucleotide sequence of VGAM1511 RNA is designated SEQ ID:4222, and is provided hereinbelow with reference to the sequence listing part.

[21114] VGAM1511 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM1511 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1511 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21115] VGAM1511 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1511 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1511 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1511 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1511 host

target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21116] The complementary binding of VGAM1511 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1511 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1511 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1511 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[21117] It is appreciated that VGAM1511 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1511 host target genes. The mRNA of each one of this plurality of VGAM1511 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1511 RNA, herein designated VGAM RNA, and which when bound by VGAM1511 RNA, herein

designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1511 host target proteins.

[21118] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1511 gene, herein designated VGAM GENE, on one or more VGAM1511 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21119] It is yet further appreciated that a function of VGAM1511 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1511 include diagnosis, prevention and

treatment of viral infection by Potato virus V. Specific functions, and accordingly utilities, of VGAM1511 correlate with, and may be deduced from, the identity of the host target genes which VGAM1511 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[21120] Nucleotide sequences of the VGAM1511 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1511 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1511 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1511 are further described hereinbelow with reference to Table 1.

[21121] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1511 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[21122] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1512 (VGAM1512) viral gene, which modulates ex-

pression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[21123] VGAM1512 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1512 was detected is described hereinabove with reference to Figs. 2-8.

[21124] VGAM1512 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Parsnip yellow fleck virus. VGAM1512 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[21125] VGAM1512 gene, herein designated VGAM GENE, encodes a VGAM1512 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1512 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1512 precursor RNA is designated SEQ ID:1498, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1498 is located at position 7608 relative to the genome of Parsnip yellow fleck virus.

[21126] VGAM1512 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1512 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21127] An enzyme complex designated DICER COMPLEX, dices the VGAM1512 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1512 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM1512 RNA is designated SEQ ID:4223, and is provided hereinbelow with reference to the sequence listing part.

[21128] VGAM1512 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1512 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1512 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21129] VGAM1512 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1512 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1512 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1512 RNA, herein designated VGAM RNA, may have a different number of host target

binding sites in untranslated regions of a VGAM1512 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21130] The complementary binding of VGAM1512 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1512 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1512 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1512 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[21131] It is appreciated that VGAM1512 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1512 host target genes. The mRNA of each one of this plurality of VGAM1512 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1512 RNA, herein designated VGAM

RNA, and which when bound by VGAM1512 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1512 host target proteins.

[21132] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1512 gene, herein designated VGAM GENE, on one or more VGAM1512 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21133] It is yet further appreciated that a function of VGAM1512 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM1512 include diagnosis, prevention and treatment of viral infection by Parsnip yellow fleck virus. Specific functions, and accordingly utilities, of VGAM1512 correlate with, and may be deduced from, the identity of the host target genes which VGAM1512 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[21134] Nucleotide sequences of the VGAM1512 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1512 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1512 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1512 are further described hereinbelow with reference to Table 1.

[21135] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1512 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[21136] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Mes-

senger 1513 (VGAM1513) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[21137] VGAM1513 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1513 was detected is described hereinabove with reference to Figs. 2-8.

[21138] VGAM1513 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Parsnip yellow fleck virus. VGAM1513 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[21139] VGAM1513 gene, herein designated VGAM GENE, encodes a VGAM1513 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1513 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1513 precursor RNA is designated SEQ ID:1499, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1499 is located at position 3

relative to the genome of Parsnip yellow fleck virus.

[21140] VGAM1513 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1513 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21141] An enzyme complex designated DICER COMPLEX, dices the VGAM1513 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1513 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 61%) nucleotide sequence of VGAM1513 RNA is designated SEQ ID:4224, and is provided hereinbelow with reference to the sequence listing part.

[21142] VGAM1513 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1513 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1513 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21143] VGAM1513 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1513 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1513 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1513 RNA, herein designated

VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1513 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21144] The complementary binding of VGAM1513 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1513 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1513 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1513 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[21145] It is appreciated that VGAM1513 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1513 host target genes. The mRNA of each one of this plurality of VGAM1513 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM1513 RNA, herein designated VGAM RNA, and which when bound by VGAM1513 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1513 host target proteins.

[21146] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1513 gene, herein designated VGAM GENE, on one or more VGAM1513 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21147] It is yet further appreciated that a function of VGAM1513 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1513 include diagnosis, prevention and treatment of viral infection by Parsnip yellow fleck virus. Specific functions, and accordingly utilities, of VGAM1513 correlate with, and may be deduced from, the identity of the host target genes which VGAM1513 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[21148] Nucleotide sequences of the VGAM1513 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1513 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1513 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1513 are further described hereinbelow with reference to Table 1.

[21149] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1513 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[21150] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present

invention, referred to here as Viral Genomic Address Messenger 1514 (VGAM1514) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[21151] VGAM1514 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1514 was detected is described hereinabove with reference to Figs. 2-8.

[21152] VGAM1514 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Parsnip yellow fleck virus. VGAM1514 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[21153] VGAM1514 gene, herein designated VGAM GENE, encodes a VGAM1514 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1514 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1514 precursor RNA is designated SEQ ID:1500, and is provided hereinbelow with reference to the sequence listing part. Nu-

cleotide sequence SEQ ID:1500 is located at position 9392 relative to the genome of Parsnip yellow fleck virus.

[21154] VGAM1514 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1514 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21155] An enzyme complex designated DICER COMPLEX, dices the VGAM1514 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1514 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 51%) nucleotide sequence of VGAM1514 RNA is designated SEQ ID:4225, and is provided hereinbelow with reference to the sequence

listing part.

[21156] VGAM1514 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1514 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1514 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21157] VGAM1514 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1514 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1514 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not

meant to be limiting VGAM1514 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1514 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21158] The complementary binding of VGAM1514 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1514 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1514 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1514 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[21159] It is appreciated that VGAM1514 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1514 host target genes. The mRNA of each one of this plurality of VGAM1514 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM1514 RNA, herein designated VGAM RNA, and which when bound by VGAM1514 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1514 host target proteins.

[21160] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1514 gene, herein designated VGAM GENE, on one or more VGAM1514 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21161] It is yet further appreciated that a function of VGAM1514

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1514 include diagnosis, prevention and treatment of viral infection by Parsnip yellow fleck virus. Specific functions, and accordingly utilities, of VGAM1514 correlate with, and may be deduced from, the identity of the host target genes which VGAM1514 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[21162] Nucleotide sequences of the VGAM1514 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1514 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1514 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1514 are further described hereinbelow with reference to Table 1.

[21163] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1514 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[21164] Fig. 1 further provides a conceptual description of another

novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1515 (VGAM1515) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[21165] VGAM1515 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1515 was detected is described hereinabove with reference to Figs. 2-8.

[21166] VGAM1515 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Parsnip yellow fleck virus. VGAM1515 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[21167] VGAM1515 gene, herein designated VGAM GENE, encodes a VGAM1515 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1515 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1515 precursor RNA is designated SEQ ID:1501, and is provided here-

inbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1501 is located at position 2895 relative to the genome of Parsnip yellow fleck virus.

[21168] VGAM1515 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1515 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21169] An enzyme complex designated DICER COMPLEX, dices the VGAM1515 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1515 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide sequence of VGAM1515 RNA is designated SEQ ID:4226, and

is provided hereinbelow with reference to the sequence listing part.

[21170] VGAM1515 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1515 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1515 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21171] VGAM1515 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1515 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1515 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites

shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1515 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1515 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21172] The complementary binding of VGAM1515 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1515 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1515 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1515 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[21173] It is appreciated that VGAM1515 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1515 host target genes. The mRNA of each one of this plurality of VGAM1515 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1515 RNA, herein designated VGAM RNA, and which when bound by VGAM1515 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1515 host target proteins.

[21174] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1515 gene, herein designated VGAM GENE, on one or more VGAM1515 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21175] It is yet further appreciated that a function of VGAM1515 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1515 include diagnosis, prevention and treatment of viral infection by Parsnip yellow fleck virus. Specific functions, and accordingly utilities, of VGAM1515 correlate with, and may be deduced from, the identity of the host target genes which VGAM1515 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[21176] Nucleotide sequences of the VGAM1515 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1515 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1515 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1515 are further described hereinbelow with reference to Table 1.

[21177] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1515 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[21178] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1516 (VGAM1516) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[21179] VGAM1516 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1516 was detected is described hereinabove with reference to Figs. 2-8.

[21180] VGAM1516 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Parsnip yellow fleck virus. VGAM1516 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[21181] VGAM1516 gene, herein designated VGAM GENE, encodes a VGAM1516 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1516 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1516 precur-

sor RNA is designated SEQ ID:1502, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1502 is located at position 1828 relative to the genome of Parsnip yellow fleck virus.

[21182] VGAM1516 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1516 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21183] An enzyme complex designated DICER COMPLEX, dices the VGAM1516 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1516 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 54%) nucleotide se-

quence of VGAM1516 RNA is designated SEQ ID:4227, and is provided hereinbelow with reference to the sequence listing part.

[21184] VGAM1516 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1516 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1516 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21185] VGAM1516 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1516 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1516 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is ap-

preciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1516 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1516 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21186] The complementary binding of VGAM1516 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1516 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1516 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1516 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[21187] It is appreciated that VGAM1516 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1516 host target genes. The mRNA of

each one of this plurality of VGAM1516 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1516 RNA, herein designated VGAM RNA, and which when bound by VGAM1516 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1516 host target proteins.

[21188] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1516 gene, herein designated VGAM GENE, on one or more VGAM1516 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science

294,779 (2001)).

[21189] It is yet further appreciated that a function of VGAM1516 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1516 include diagnosis, prevention and treatment of viral infection by Parsnip yellow fleck virus. Specific functions, and accordingly utilities, of VGAM1516 correlate with, and may be deduced from, the identity of the host target genes which VGAM1516 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[21190] Nucleotide sequences of the VGAM1516 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1516 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1516 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1516 are further described hereinbelow with reference to Table 1.

[21191] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1516 RNA, herein designated VGAM RNA, are de-

scribed hereinbelow with reference to Table 2.

[21192] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1517 (VGAM1517) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[21193] VGAM1517 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1517 was detected is described hereinabove with reference to Figs. 2-8.

[21194] VGAM1517 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Pea seed-borne mosaic virus. VGAM1517 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[21195] VGAM1517 gene, herein designated VGAM GENE, encodes a VGAM1517 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1517 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly

similar to the nucleotide sequence of VGAM1517 precursor RNA is designated SEQ ID:1503, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1503 is located at position 6741 relative to the genome of Pea seed-borne mosaic virus.

[21196] VGAM1517 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1517 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21197] An enzyme complex designated DICER COMPLEX, dices the VGAM1517 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1517 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 44%) nucleotide sequence of VGAM1517 RNA is designated SEQ ID:4228, and is provided hereinbelow with reference to the sequence listing part.

[21198] VGAM1517 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1517 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1517 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21199] VGAM1517 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1517 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1517 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I,

BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1517 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1517 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21200] The complementary binding of VGAM1517 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1517 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1517 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1517 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[21201] It is appreciated that VGAM1517 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM1517 host target genes. The mRNA of each one of this plurality of VGAM1517 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1517 RNA, herein designated VGAM RNA, and which when bound by VGAM1517 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1517 host target proteins.

[21202] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1517 gene, herein designated VGAM GENE, on one or more VGAM1517 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21203] It is yet further appreciated that a function of VGAM1517 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1517 include diagnosis, prevention and treatment of viral infection by Pea seed-borne mosaic virus. Specific functions, and accordingly utilities, of VGAM1517 correlate with, and may be deduced from, the identity of the host target genes which VGAM1517 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[21204] Nucleotide sequences of the VGAM1517 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1517 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1517 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1517 are further described hereinbelow with reference to Table 1.

[21205] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites

to VGAM1517 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[21206] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1518 (VGAM1518) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[21207] VGAM1518 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1518 was detected is described hereinabove with reference to Figs. 2-8.

[21208] VGAM1518 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Pea seed-borne mosaic virus. VGAM1518 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[21209] VGAM1518 gene, herein designated VGAM GENE, encodes a VGAM1518 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1518 precursor RNA, herein designated VGAM PRECURSOR RNA, does not en-

code a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1518 precursor RNA is designated SEQ ID:1504, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1504 is located at position 9398 relative to the genome of Pea seed-borne mosaic virus.

[21210] VGAM1518 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1518 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21211] An enzyme complex designated DICER COMPLEX, dices the VGAM1518 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1518 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 72%) nucleotide sequence of VGAM1518 RNA is designated SEQ ID:4229, and is provided hereinbelow with reference to the sequence listing part.

[21212] VGAM1518 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1518 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1518 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21213] VGAM1518 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1518 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1518 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3

such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1518 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1518 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21214] The complementary binding of VGAM1518 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1518 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1518 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1518 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[21215] It is appreciated that VGAM1518 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1518 host target genes. The mRNA of each one of this plurality of VGAM1518 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1518 RNA, herein designated VGAM RNA, and which when bound by VGAM1518 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1518 host target proteins.

[21216] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1518 gene, herein designated VGAM GENE, on one or more VGAM1518 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21217] It is yet further appreciated that a function of VGAM1518 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1518 include diagnosis, prevention and treatment of viral infection by Pea seed-borne mosaic virus. Specific functions, and accordingly utilities, of VGAM1518 correlate with, and may be deduced from, the identity of the host target genes which VGAM1518 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[21218] Nucleotide sequences of the VGAM1518 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1518 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1518 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1518 are further described hereinbelow with reference to Table 1.

[21219] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the

complementarity of each of these host target binding sites to VGAM1518 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[21220] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1519 (VGAM1519) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[21221] VGAM1519 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1519 was detected is described hereinabove with reference to Figs. 2-8.

[21222] VGAM1519 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Pea seed-borne mosaic virus. VGAM1519 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[21223] VGAM1519 gene, herein designated VGAM GENE, encodes a VGAM1519 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1519 precursor RNA,

herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1519 precursor RNA is designated SEQ ID:1505, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1505 is located at position 3823 relative to the genome of Pea seed-borne mosaic virus.

[21224] VGAM1519 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1519 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21225] An enzyme complex designated DICER COMPLEX, dices the VGAM1519 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1519 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM1519 RNA is designated SEQ ID:4230, and is provided hereinbelow with reference to the sequence listing part.

[21226] VGAM1519 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1519 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1519 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21227] VGAM1519 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1519 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1519 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host

target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1519 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1519 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21228] The complementary binding of VGAM1519 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1519 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1519 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1519 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[21229] It is appreciated that VGAM1519 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1519 host target genes. The mRNA of each one of this plurality of VGAM1519 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1519 RNA, herein designated VGAM RNA, and which when bound by VGAM1519 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1519 host target proteins.

[21230] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1519 gene, herein designated VGAM GENE, on one or more VGAM1519 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21231] It is yet further appreciated that a function of VGAM1519 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1519 include diagnosis, prevention and treatment of viral infection by Pea seed-borne mosaic virus. Specific functions, and accordingly utilities, of VGAM1519 correlate with, and may be deduced from, the identity of the host target genes which VGAM1519 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[21232] Nucleotide sequences of the VGAM1519 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1519 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1519 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1519 are further described hereinbelow with reference to Table 1.

[21233] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1519 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[21234] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1520 (VGAM1520) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[21235] VGAM1520 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1520 was detected is described hereinabove with reference to Figs. 2-8.

[21236] VGAM1520 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia virus. VGAM1520 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[21237] VGAM1520 gene, herein designated VGAM GENE, encodes a VGAM1520 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and un-

like most ordinary genes, VGAM1520 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1520 precursor RNA is designated SEQ ID:1506, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1506 is located at position 74844 relative to the genome of Ectromelia virus.

[21238] VGAM1520 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1520 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21239] An enzyme complex designated DICER COMPLEX, dices the VGAM1520 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1520 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM1520 RNA is designated SEQ ID:4231, and is provided hereinbelow with reference to the sequence listing part.

[21240] VGAM1520 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1520 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1520 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21241] VGAM1520 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1520 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1520 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed

sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1520 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1520 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21242] The complementary binding of VGAM1520 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1520 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1520 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1520 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target

protein is therefore outlined by a broken line.

[21243] It is appreciated that VGAM1520 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1520 host target genes. The mRNA of each one of this plurality of VGAM1520 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1520 RNA, herein designated VGAM RNA, and which when bound by VGAM1520 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1520 host target proteins.

[21244] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1520 gene, herein designated VGAM GENE, on one or more VGAM1520 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21245] It is yet further appreciated that a function of VGAM1520 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1520 include diagnosis, prevention and treatment of viral infection by Ectromelia virus. Specific functions, and accordingly utilities, of VGAM1520 correlate with, and may be deduced from, the identity of the host target genes which VGAM1520 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[21246] Nucleotide sequences of the VGAM1520 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1520 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1520 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1520 are further described hereinbelow with reference to Table 1.

[21247] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1520 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[21248] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1521 (VGAM1521) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[21249] VGAM1521 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1521 was detected is described hereinabove with reference to Figs. 2-8.

[21250] VGAM1521 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia virus. VGAM1521 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[21251] VGAM1521 gene, herein designated VGAM GENE, encodes a VGAM1521 precursor RNA, herein designated VGAM

PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1521 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1521 precursor RNA is designated SEQ ID:1507, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1507 is located at position 67798 relative to the genome of Ectromelia virus.

[21252] VGAM1521 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1521 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21253] An enzyme complex designated DICER COMPLEX, dices the VGAM1521 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1521 RNA, herein designated VGAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM1521 RNA is designated SEQ ID:4232, and is provided hereinbelow with reference to the sequence listing part.

[21254] VGAM1521 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1521 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1521 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21255] VGAM1521 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1521 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1521 RNA, herein designated

VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1521 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1521 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21256] The complementary binding of VGAM1521 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1521 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1521 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1521 host target protein, herein desig-

nated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[21257] It is appreciated that VGAM1521 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1521 host target genes. The mRNA of each one of this plurality of VGAM1521 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1521 RNA, herein designated VGAM RNA, and which when bound by VGAM1521 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1521 host target proteins.

[21258] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1521 gene, herein designated VGAM GENE, on one or more VGAM1521 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21259] It is yet further appreciated that a function of VGAM1521 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1521 include diagnosis, prevention and treatment of viral infection by Ectromelia virus. Specific functions, and accordingly utilities, of VGAM1521 correlate with, and may be deduced from, the identity of the host target genes which VGAM1521 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[21260] Nucleotide sequences of the VGAM1521 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1521 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1521 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1521 are further described hereinbelow with reference to Table 1.

[21261] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1521 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[21262] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1522 (VGAM1522) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[21263] VGAM1522 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1522 was detected is described hereinabove with reference to Figs. 2-8.

[21264] VGAM1522 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia virus. VGAM1522 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[21265] VGAM1522 gene, herein designated VGAM GENE, encodes

a VGAM1522 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1522 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1522 precursor RNA is designated SEQ ID:1508, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1508 is located at position 72179 relative to the genome of Ectromelia virus.

[21266] VGAM1522 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1522 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21267] An enzyme complex designated DICER COMPLEX, dices the VGAM1522 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1522 RNA,

herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM1522 RNA is designated SEQ ID:4233, and is provided hereinbelow with reference to the sequence listing part.

[21268] VGAM1522 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1522 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1522 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21269] VGAM1522 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1522 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM1522 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1522 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1522 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21270] The complementary binding of VGAM1522 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1522 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1522 host target RNA, herein designated VGAM HOST TARGET

RNA, into VGAM1522 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[21271] It is appreciated that VGAM1522 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1522 host target genes. The mRNA of each one of this plurality of VGAM1522 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1522 RNA, herein designated VGAM RNA, and which when bound by VGAM1522 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1522 host target proteins.

[21272] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1522 gene, herein designated VGAM GENE, on one or more VGAM1522 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21273] It is yet further appreciated that a function of VGAM1522 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1522 include diagnosis, prevention and treatment of viral infection by Ectromelia virus. Specific functions, and accordingly utilities, of VGAM1522 correlate with, and may be deduced from, the identity of the host target genes which VGAM1522 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[21274] Nucleotide sequences of the VGAM1522 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1522 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1522 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1522 are further

described hereinbelow with reference to Table 1.

[21275] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1522 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[21276] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1523 (VGAM1523) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[21277] VGAM1523 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1523 was detected is described hereinabove with reference to Figs. 2-8.

[21278] VGAM1523 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cowpox virus.
VGAM1523 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[21279] VGAM1523 gene, herein designated VGAM GENE, encodes a VGAM1523 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1523 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1523 precursor RNA is designated SEQ ID:1509, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1509 is located at position 79940 relative to the genome of Cowpox virus.

[21280] VGAM1523 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1523 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21281] An enzyme complex designated DICER COMPLEX, dices the VGAM1523 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, into VGAM1523 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 47%) nucleotide sequence of VGAM1523 RNA is designated SEQ ID:4234, and is provided hereinbelow with reference to the sequence listing part.

[21282] VGAM1523 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1523 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1523 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21283] VGAM1523 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1523 host target RNA, herein designated VGAM HOST TARGET RNA. This

complementary binding is due to the fact that the nucleotide sequence of VGAM1523 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1523 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1523 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21284] The complementary binding of VGAM1523 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1523 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1523

host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1523 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[21285] It is appreciated that VGAM1523 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1523 host target genes. The mRNA of each one of this plurality of VGAM1523 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1523 RNA, herein designated VGAM RNA, and which when bound by VGAM1523 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1523 host target proteins.

[21286] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1523 gene, herein designated VGAM GENE, on one or more VGAM1523 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21287] It is yet further appreciated that a function of VGAM1523 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1523 include diagnosis, prevention and treatment of viral infection by Cowpox virus. Specific functions, and accordingly utilities, of VGAM1523 correlate with, and may be deduced from, the identity of the host target genes which VGAM1523 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[21288] Nucleotide sequences of the VGAM1523 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1523 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1523 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM1523 are further described hereinbelow with reference to Table 1.

[21289] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1523 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[21290] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1524 (VGAM1524) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[21291] VGAM1524 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1524 was detected is described hereinabove with reference to Figs. 2-8.

[21292] VGAM1524 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cowpox virus.
VGAM1524 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the

human genome.

[21293] VGAM1524 gene, herein designated VGAM GENE, encodes a VGAM1524 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1524 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1524 precursor RNA is designated SEQ ID:1510, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1510 is located at position 76982 relative to the genome of Cowpox virus.

[21294] VGAM1524 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1524 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21295] An enzyme complex designated DICER COMPLEX, dices

the VGAM1524 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1524 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM1524 RNA is designated SEQ ID:4235, and is provided hereinbelow with reference to the sequence listing part.

[21296] VGAM1524 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1524 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1524 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21297] VGAM1524 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1524 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1524 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1524 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1524 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21298] The complementary binding of VGAM1524 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1524 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM1524 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1524 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[21299] It is appreciated that VGAM1524 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1524 host target genes. The mRNA of each one of this plurality of VGAM1524 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1524 RNA, herein designated VGAM RNA, and which when bound by VGAM1524 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1524 host target proteins.

[21300] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1524 gene, herein designated VGAM GENE, on one or more VGAM1524 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21301] It is yet further appreciated that a function of VGAM1524 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1524 include diagnosis, prevention and treatment of viral infection by Cowpox virus. Specific functions, and accordingly utilities, of VGAM1524 correlate with, and may be deduced from, the identity of the host target genes which VGAM1524 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[21302] Nucleotide sequences of the VGAM1524 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1524 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of

VGAM1524 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1524 are further described hereinbelow with reference to Table 1.

[21303] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1524 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[21304] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1525 (VGAM1525) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[21305] VGAM1525 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1525 was detected is described hereinabove with reference to Figs. 2-8.

[21306] VGAM1525 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Camelpox virus. VGAM1525 host target gene, herein designated VGAM

HOST TARGET GENE, is a human gene contained in the human genome.

[21307] VGAM1525 gene, herein designated VGAM GENE, encodes a VGAM1525 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1525 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1525 precursor RNA is designated SEQ ID:1511, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1511 is located at position 62387 relative to the genome of Camelpox virus.

[21308] VGAM1525 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1525 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21309] An enzyme complex designated DICER COMPLEX, dices the VGAM1525 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1525 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM1525 RNA is designated SEQ ID:4236, and is provided hereinbelow with reference to the sequence listing part.

[21310] VGAM1525 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1525 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1525 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21311] VGAM1525 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites

located in untranslated regions of VGAM1525 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1525 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1525 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1525 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21312] The complementary binding of VGAM1525 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1525 host target RNA, herein designated VGAM

HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1525 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1525 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[21313] It is appreciated that VGAM1525 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1525 host target genes. The mRNA of each one of this plurality of VGAM1525 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1525 RNA, herein designated VGAM RNA, and which when bound by VGAM1525 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1525 host target proteins.

[21314] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1525 gene, herein designated VGAM GENE, on one or more VGAM1525 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove

with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21315] It is yet further appreciated that a function of VGAM1525 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1525 include diagnosis, prevention and treatment of viral infection by Camelpox virus. Specific functions, and accordingly utilities, of VGAM1525 correlate with, and may be deduced from, the identity of the host target genes which VGAM1525 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[21316] Nucleotide sequences of the VGAM1525 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1525 RNA, herein designated VGAM RNA, and

a schematic representation of the secondary folding of VGAM1525 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1525 are further described hereinbelow with reference to Table 1.

[21317] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1525 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[21318] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1526 (VGAM1526) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[21319] VGAM1526 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1526 was detected is described hereinabove with reference to Figs. 2-8.

[21320] VGAM1526 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia virus.

VGAM1526 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[21321] VGAM1526 gene, herein designated VGAM GENE, encodes a VGAM1526 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1526 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1526 precursor RNA is designated SEQ ID:1512, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1512 is located at position 71872 relative to the genome of Ectromelia virus.

[21322] VGAM1526 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1526 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[21323] An enzyme complex designated DICER COMPLEX, dices the VGAM1526 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1526 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM1526 RNA is designated SEQ ID:4237, and is provided hereinbelow with reference to the sequence listing part.

[21324] VGAM1526 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1526 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1526 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21325] VGAM1526 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM1526 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1526 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1526 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1526 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21326] The complementary binding of VGAM1526 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM1526 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1526 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1526 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[21327] It is appreciated that VGAM1526 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1526 host target genes. The mRNA of each one of this plurality of VGAM1526 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1526 RNA, herein designated VGAM RNA, and which when bound by VGAM1526 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1526 host target proteins.

[21328] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1526 gene, herein designated VGAM GENE, on one or more VGAM1526 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21329] It is yet further appreciated that a function of VGAM1526 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1526 include diagnosis, prevention and treatment of viral infection by Ectromelia virus. Specific functions, and accordingly utilities, of VGAM1526 correlate with, and may be deduced from, the identity of the host target genes which VGAM1526 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[21330] Nucleotide sequences of the VGAM1526 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

diced VGAM1526 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1526 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1526 are further described hereinbelow with reference to Table 1.

[21331] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1526 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[21332] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1527 (VGAM1527) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[21333] VGAM1527 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1527 was detected is described hereinabove with reference to Figs. 2-8.

[21334] VGAM1527 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of Camelpox virus. VGAM1527 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[21335] VGAM1527 gene, herein designated VGAM GENE, encodes a VGAM1527 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1527 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1527 precursor RNA is designated SEQ ID:1513, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1513 is located at position 68087 relative to the genome of Camelpox virus.

[21336] VGAM1527 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1527 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21337] An enzyme complex designated DICER COMPLEX, dices the VGAM1527 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1527 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 88%) nucleotide sequence of VGAM1527 RNA is designated SEQ ID:4238, and is provided hereinbelow with reference to the sequence listing part.

[21338] VGAM1527 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1527 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1527 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21339] VGAM1527 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1527 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1527 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1527 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1527 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21340] The complementary binding of VGAM1527 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM1527 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1527 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1527 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[21341] It is appreciated that VGAM1527 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1527 host target genes. The mRNA of each one of this plurality of VGAM1527 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1527 RNA, herein designated VGAM RNA, and which when bound by VGAM1527 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1527 host target proteins.

[21342] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1527 gene, herein designated VGAM GENE, on one or more VGAM1527 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21343] It is yet further appreciated that a function of VGAM1527 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1527 include diagnosis, prevention and treatment of viral infection by Camelpox virus. Specific functions, and accordingly utilities, of VGAM1527 correlate with, and may be deduced from, the identity of the host target genes which VGAM1527 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[21344] Nucleotide sequences of the VGAM1527 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the diced VGAM1527 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1527 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1527 are further described hereinbelow with reference to Table 1.

[21345] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1527 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[21346] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1528 (VGAM1528) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[21347] VGAM1528 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1528 was detected is described hereinabove with reference to Figs. 2-8.

[21348] VGAM1528 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia virus. VGAM1528 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[21349] VGAM1528 gene, herein designated VGAM GENE, encodes a VGAM1528 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1528 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1528 precursor RNA is designated SEQ ID:1514, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1514 is located at position 72786 relative to the genome of Ectromelia virus.

[21350] VGAM1528 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1528 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21351] An enzyme complex designated DICER COMPLEX, dices the VGAM1528 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1528 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM1528 RNA is designated SEQ ID:4239, and is provided hereinbelow with reference to the sequence listing part.

[21352] VGAM1528 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1528 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1528 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN COD-

ING and 3UTR respectively.

[21353] VGAM1528 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1528 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1528 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1528 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1528 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21354] The complementary binding of VGAM1528 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1528 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1528 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1528 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[21355] It is appreciated that VGAM1528 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1528 host target genes. The mRNA of each one of this plurality of VGAM1528 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1528 RNA, herein designated VGAM RNA, and which when bound by VGAM1528 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1528 host target proteins.

[21356] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1528 gene, herein designated VGAM GENE, on one

or more VGAM1528 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21357] It is yet further appreciated that a function of VGAM1528 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1528 include diagnosis, prevention and treatment of viral infection by Ectromelia virus. Specific functions, and accordingly utilities, of VGAM1528 correlate with, and may be deduced from, the identity of the host target genes which VGAM1528 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[21358] Nucleotide sequences of the VGAM1528 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1528 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1528 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1528 are further described hereinbelow with reference to Table 1.

[21359] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1528 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[21360] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1529 (VGAM1529) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[21361] VGAM1529 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1529 was detected is de-

scribed hereinabove with reference to Figs. 2-8.

[21362] VGAM1529 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia virus. VGAM1529 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[21363] VGAM1529 gene, herein designated VGAM GENE, encodes a VGAM1529 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1529 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1529 precursor RNA is designated SEQ ID:1515, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1515 is located at position 69246 relative to the genome of Ectromelia virus.

[21364] VGAM1529 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1529 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21365] An enzyme complex designated DICER COMPLEX, dices the VGAM1529 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1529 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM1529 RNA is designated SEQ ID:4240, and is provided hereinbelow with reference to the sequence listing part.

[21366] VGAM1529 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1529 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1529 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and

a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21367] VGAM1529 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1529 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1529 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1529 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1529 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both

3UTR and 5UTR regions.

[21368] The complementary binding of VGAM1529 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1529 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1529 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1529 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[21369] It is appreciated that VGAM1529 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1529 host target genes. The mRNA of each one of this plurality of VGAM1529 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1529 RNA, herein designated VGAM RNA, and which when bound by VGAM1529 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1529 host target proteins.

[21370] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM1529 gene, herein designated VGAM GENE, on one or more VGAM1529 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21371] It is yet further appreciated that a function of VGAM1529 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1529 include diagnosis, prevention and treatment of viral infection by Ectromelia virus. Specific functions, and accordingly utilities, of VGAM1529 correlate with, and may be deduced from, the identity of the host target genes which VGAM1529 binds and inhibits, and the function of these host target genes, as elaborated

hereinbelow.

[21372] Nucleotide sequences of the VGAM1529 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1529 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1529 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1529 are further described hereinbelow with reference to Table 1.

[21373] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1529 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[21374] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1530 (VGAM1530) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[21375] VGAM1530 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene.

The method by which VGAM1530 was detected is described hereinabove with reference to Figs. 2-8.

[21376] VGAM1530 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia virus. VGAM1530 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[21377] VGAM1530 gene, herein designated VGAM GENE, encodes a VGAM1530 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1530 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1530 precursor RNA is designated SEQ ID:1516, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1516 is located at position 73081 relative to the genome of Ectromelia virus.

[21378] VGAM1530 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1530 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21379] An enzyme complex designated DICER COMPLEX, dices the VGAM1530 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1530 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM1530 RNA is designated SEQ ID:4241, and is provided hereinbelow with reference to the sequence listing part.

[21380] VGAM1530 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1530 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1530 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding

gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21381] VGAM1530 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1530 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1530 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1530 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1530 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be lo-

cated in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21382] The complementary binding of VGAM1530 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1530 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1530 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1530 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[21383] It is appreciated that VGAM1530 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1530 host target genes. The mRNA of each one of this plurality of VGAM1530 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1530 RNA, herein designated VGAM RNA, and which when bound by VGAM1530 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1530 host target proteins.

[21384] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM1530 gene, herein designated VGAM GENE, on one or more VGAM1530 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21385] It is yet further appreciated that a function of VGAM1530 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1530 include diagnosis, prevention and treatment of viral infection by Ectromelia virus. Specific functions, and accordingly utilities, of VGAM1530 correlate with, and may be deduced from, the identity of the host target genes which VGAM1530 binds and inhibits,

and the function of these host target genes, as elaborated hereinbelow.

[21386] Nucleotide sequences of the VGAM1530 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1530 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1530 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1530 are further described hereinbelow with reference to Table 1.

[21387] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1530 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[21388] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1531 (VGAM1531) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[21389] VGAM1531 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1531 was detected is described hereinabove with reference to Figs. 2-8.

[21390] VGAM1531 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia virus. VGAM1531 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[21391] VGAM1531 gene, herein designated VGAM GENE, encodes a VGAM1531 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1531 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1531 precursor RNA is designated SEQ ID:1517, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1517 is located at position 66901 relative to the genome of Ectromelia virus.

[21392] VGAM1531 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1531 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21393] An enzyme complex designated DICER COMPLEX, dices the VGAM1531 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1531 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 70%) nucleotide sequence of VGAM1531 RNA is designated SEQ ID:4242, and is provided hereinbelow with reference to the sequence listing part.

[21394] VGAM1531 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1531 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1531 host target RNA, herein designated VGAM HOST TARGET RNA, comprises

three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21395] VGAM1531 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1531 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1531 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1531 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1531 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an

example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21396] The complementary binding of VGAM1531 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1531 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1531 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1531 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[21397] It is appreciated that VGAM1531 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1531 host target genes. The mRNA of each one of this plurality of VGAM1531 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1531 RNA, herein designated VGAM RNA, and which when bound by VGAM1531 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1531 host target proteins.

[21398] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1531 gene, herein designated VGAM GENE, on one or more VGAM1531 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21399] It is yet further appreciated that a function of VGAM1531 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1531 include diagnosis, prevention and treatment of viral infection by Ectromelia virus. Specific functions, and accordingly utilities, of VGAM1531 correlate with, and may be deduced from, the identity of the

host target genes which VGAM1531 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[21400] Nucleotide sequences of the VGAM1531 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1531 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1531 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1531 are further described hereinbelow with reference to Table 1.

[21401] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1531 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[21402] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1532 (VGAM1532) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[21403] VGAM1532 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1532 was detected is described hereinabove with reference to Figs. 2-8.

[21404] VGAM1532 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cowpox virus. VGAM1532 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[21405] VGAM1532 gene, herein designated VGAM GENE, encodes a VGAM1532 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1532 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1532 precursor RNA is designated SEQ ID:1518, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1518 is located at position 83358 relative to the genome of Cowpox virus.

[21406] VGAM1532 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1532 folded precursor RNA, herein designated VGAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21407] An enzyme complex designated DICER COMPLEX, dices the VGAM1532 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1532 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM1532 RNA is designated SEQ ID:4243, and is provided hereinbelow with reference to the sequence listing part.

[21408] VGAM1532 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1532 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1532 host target RNA,

herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21409] VGAM1532 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1532 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1532 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1532 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1532 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host tar-

get binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21410] The complementary binding of VGAM1532 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1532 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1532 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1532 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[21411] It is appreciated that VGAM1532 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1532 host target genes. The mRNA of each one of this plurality of VGAM1532 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1532 RNA, herein designated VGAM RNA, and which when bound by VGAM1532 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1532 host target proteins.

[21412] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1532 gene, herein designated VGAM GENE, on one or more VGAM1532 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21413] It is yet further appreciated that a function of VGAM1532 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1532 include diagnosis, prevention and treatment of viral infection by Cowpox virus. Specific functions, and accordingly utilities, of VGAM1532 corre-

late with, and may be deduced from, the identity of the host target genes which VGAM1532 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[21414] Nucleotide sequences of the VGAM1532 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1532 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1532 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1532 are further described hereinbelow with reference to Table 1.

[21415] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1532 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[21416] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1533 (VGAM1533) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the

art.

[21417] VGAM1533 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1533 was detected is described hereinabove with reference to Figs. 2-8.

[21418] VGAM1533 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cowpox virus. VGAM1533 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[21419] VGAM1533 gene, herein designated VGAM GENE, encodes a VGAM1533 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1533 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1533 precursor RNA is designated SEQ ID:1519, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1519 is located at position 82024 relative to the genome of Cowpox virus.

[21420] VGAM1533 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1533 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21421] An enzyme complex designated DICER COMPLEX, dices the VGAM1533 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1533 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM1533 RNA is designated SEQ ID:4244, and is provided hereinbelow with reference to the sequence listing part.

[21422] VGAM1533 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1533 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1533 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN COD-

ING and 3UTR respectively.

[21423] VGAM1533 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1533 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1533 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1533 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1533 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21424] The complementary binding of VGAM1533 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1533 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1533 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1533 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[21425] It is appreciated that VGAM1533 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1533 host target genes. The mRNA of each one of this plurality of VGAM1533 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1533 RNA, herein designated VGAM RNA, and which when bound by VGAM1533 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1533 host target proteins.

[21426] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1533 gene, herein designated VGAM GENE, on one

or more VGAM1533 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21427] It is yet further appreciated that a function of VGAM1533 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1533 include diagnosis, prevention and treatment of viral infection by Cowpox virus. Specific functions, and accordingly utilities, of VGAM1533 correlate with, and may be deduced from, the identity of the host target genes which VGAM1533 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[21428] Nucleotide sequences of the VGAM1533 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1533 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1533 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1533 are further described hereinbelow with reference to Table 1.

[21429] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1533 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[21430] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1534 (VGAM1534) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[21431] VGAM1534 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1534 was detected is de-

scribed hereinabove with reference to Figs. 2-8.

[21432] VGAM1534 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cowpox virus. VGAM1534 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[21433] VGAM1534 gene, herein designated VGAM GENE, encodes a VGAM1534 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1534 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1534 precursor RNA is designated SEQ ID:1520, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1520 is located at position 80718 relative to the genome of Cowpox virus.

[21434] VGAM1534 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1534 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21435] An enzyme complex designated DICER COMPLEX, dices the VGAM1534 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1534 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 66%) nucleotide sequence of VGAM1534 RNA is designated SEQ ID:4245, and is provided hereinbelow with reference to the sequence listing part.

[21436] VGAM1534 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1534 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1534 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and

a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21437] VGAM1534 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1534 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1534 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1534 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1534 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both

3UTR and 5UTR regions.

[21438] The complementary binding of VGAM1534 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1534 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1534 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1534 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[21439] It is appreciated that VGAM1534 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1534 host target genes. The mRNA of each one of this plurality of VGAM1534 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1534 RNA, herein designated VGAM RNA, and which when bound by VGAM1534 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1534 host target proteins.

[21440] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM1534 gene, herein designated VGAM GENE, on one or more VGAM1534 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21441] It is yet further appreciated that a function of VGAM1534 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1534 include diagnosis, prevention and treatment of viral infection by Cowpox virus. Specific functions, and accordingly utilities, of VGAM1534 correlate with, and may be deduced from, the identity of the host target genes which VGAM1534 binds and inhibits, and the function of these host target genes, as elaborated

hereinbelow.

[21442] Nucleotide sequences of the VGAM1534 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1534 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1534 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1534 are further described hereinbelow with reference to Table 1.

[21443] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1534 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[21444] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1535 (VGAM1535) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[21445] VGAM1535 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene.

The method by which VGAM1535 was detected is described hereinabove with reference to Figs. 2-8.

[21446] VGAM1535 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cowpox virus. VGAM1535 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[21447] VGAM1535 gene, herein designated VGAM GENE, encodes a VGAM1535 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1535 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1535 precursor RNA is designated SEQ ID:1521, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1521 is located at position 80457 relative to the genome of Cowpox virus.

[21448] VGAM1535 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1535 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21449] An enzyme complex designated DICER COMPLEX, dices the VGAM1535 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1535 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 65%) nucleotide sequence of VGAM1535 RNA is designated SEQ ID:4246, and is provided hereinbelow with reference to the sequence listing part.

[21450] VGAM1535 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1535 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1535 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding

gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21451] VGAM1535 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1535 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1535 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1535 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1535 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be lo-

cated in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21452] The complementary binding of VGAM1535 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1535 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1535 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1535 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[21453] It is appreciated that VGAM1535 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1535 host target genes. The mRNA of each one of this plurality of VGAM1535 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1535 RNA, herein designated VGAM RNA, and which when bound by VGAM1535 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1535 host target proteins.

[21454] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM1535 gene, herein designated VGAM GENE, on one or more VGAM1535 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21455] It is yet further appreciated that a function of VGAM1535 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1535 include diagnosis, prevention and treatment of viral infection by Cowpox virus. Specific functions, and accordingly utilities, of VGAM1535 correlate with, and may be deduced from, the identity of the host target genes which VGAM1535 binds and inhibits,

and the function of these host target genes, as elaborated hereinbelow.

[21456] Nucleotide sequences of the VGAM1535 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1535 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1535 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1535 are further described hereinbelow with reference to Table 1.

[21457] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1535 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[21458] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1536 (VGAM1536) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[21459] VGAM1536 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1536 was detected is described hereinabove with reference to Figs. 2-8.

[21460] VGAM1536 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cowpox virus. VGAM1536 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[21461] VGAM1536 gene, herein designated VGAM GENE, encodes a VGAM1536 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1536 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1536 precursor RNA is designated SEQ ID:1522, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1522 is located at position 77166 relative to the genome of Cowpox virus.

[21462] VGAM1536 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1536 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21463] An enzyme complex designated DICER COMPLEX, dices the VGAM1536 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1536 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM1536 RNA is designated SEQ ID:4247, and is provided hereinbelow with reference to the sequence listing part.

[21464] VGAM1536 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1536 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1536 host target RNA, herein designated VGAM HOST TARGET RNA, comprises

three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21465] VGAM1536 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1536 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1536 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1536 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1536 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an

example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21466] The complementary binding of VGAM1536 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1536 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1536 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1536 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[21467] It is appreciated that VGAM1536 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1536 host target genes. The mRNA of each one of this plurality of VGAM1536 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1536 RNA, herein designated VGAM RNA, and which when bound by VGAM1536 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1536 host target proteins.

[21468] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1536 gene, herein designated VGAM GENE, on one or more VGAM1536 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21469] It is yet further appreciated that a function of VGAM1536 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1536 include diagnosis, prevention and treatment of viral infection by Cowpox virus. Specific functions, and accordingly utilities, of VGAM1536 correlate with, and may be deduced from, the identity of the

host target genes which VGAM1536 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[21470] Nucleotide sequences of the VGAM1536 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1536 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1536 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1536 are further described hereinbelow with reference to Table 1.

[21471] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1536 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[21472] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1537 (VGAM1537) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[21473] VGAM1537 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1537 was detected is described hereinabove with reference to Figs. 2-8.

[21474] VGAM1537 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cowpox virus. VGAM1537 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[21475] VGAM1537 gene, herein designated VGAM GENE, encodes a VGAM1537 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1537 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1537 precursor RNA is designated SEQ ID:1523, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1523 is located at position 78285 relative to the genome of Cowpox virus.

[21476] VGAM1537 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1537 folded precursor RNA, herein designated VGAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21477] An enzyme complex designated DICER COMPLEX, dices the VGAM1537 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1537 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 48%) nucleotide sequence of VGAM1537 RNA is designated SEQ ID:4248, and is provided hereinbelow with reference to the sequence listing part.

[21478] VGAM1537 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1537 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1537 host target RNA,

herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21479] VGAM1537 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1537 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1537 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1537 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1537 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host tar-

get binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21480] The complementary binding of VGAM1537 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1537 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1537 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1537 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[21481] It is appreciated that VGAM1537 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1537 host target genes. The mRNA of each one of this plurality of VGAM1537 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1537 RNA, herein designated VGAM RNA, and which when bound by VGAM1537 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1537 host target proteins.

[21482] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1537 gene, herein designated VGAM GENE, on one or more VGAM1537 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21483] It is yet further appreciated that a function of VGAM1537 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1537 include diagnosis, prevention and treatment of viral infection by Cowpox virus. Specific functions, and accordingly utilities, of VGAM1537 corre-

late with, and may be deduced from, the identity of the host target genes which VGAM1537 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[21484] Nucleotide sequences of the VGAM1537 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1537 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1537 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1537 are further described hereinbelow with reference to Table 1.

[21485] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1537 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[21486] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1538 (VGAM1538) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the

art.

[21487] VGAM1538 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1538 was detected is described hereinabove with reference to Figs. 2-8.

[21488] VGAM1538 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Monkeypox virus. VGAM1538 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[21489] VGAM1538 gene, herein designated VGAM GENE, encodes a VGAM1538 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1538 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1538 precursor RNA is designated SEQ ID:1524, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1524 is located at position 59766 relative to the genome of Monkeypox virus.

[21490] VGAM1538 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1538 folded

precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21491] An enzyme complex designated DICER COMPLEX, dices the VGAM1538 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1538 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM1538 RNA is designated SEQ ID:4249, and is provided hereinbelow with reference to the sequence listing part.

[21492] VGAM1538 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1538 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM1538 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21493] VGAM1538 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1538 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1538 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1538 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1538 host target RNA, herein designated VGAM HOST TARGET RNA.

It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21494] The complementary binding of VGAM1538 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1538 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1538 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1538 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[21495] It is appreciated that VGAM1538 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1538 host target genes. The mRNA of each one of this plurality of VGAM1538 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1538 RNA, herein designated VGAM RNA, and which when bound by VGAM1538 RNA, herein designated VGAM RNA, causes inhibition of translation of

respective one or more VGAM1538 host target proteins.

[21496] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1538 gene, herein designated VGAM GENE, on one or more VGAM1538 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21497] It is yet further appreciated that a function of VGAM1538 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1538 include diagnosis, prevention and treatment of viral infection by Monkeypox virus. Specific

functions, and accordingly utilities, of VGAM1538 correlate with, and may be deduced from, the identity of the host target genes which VGAM1538 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[21498] Nucleotide sequences of the VGAM1538 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1538 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1538 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1538 are further described hereinbelow with reference to Table 1.

[21499] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1538 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[21500] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1539 (VGAM1539) viral gene, which modulates expression of respective host target genes thereof, the func-

tion and utility of which host target genes is known in the art.

[21501] VGAM1539 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1539 was detected is described hereinabove with reference to Figs. 2-8.

[21502] VGAM1539 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Monkeypox virus. VGAM1539 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[21503] VGAM1539 gene, herein designated VGAM GENE, encodes a VGAM1539 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1539 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1539 precursor RNA is designated SEQ ID:1525, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1525 is located at position 60492 relative to the genome of Monkeypox virus.

[21504] VGAM1539 precursor RNA, herein designated VGAM PRE-

CURSOR RNA, folds onto itself, forming VGAM1539 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21505] An enzyme complex designated DICER COMPLEX, dices the VGAM1539 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1539 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM1539 RNA is designated SEQ ID:4250, and is provided hereinbelow with reference to the sequence listing part.

[21506] VGAM1539 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM1539 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1539 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21507] VGAM1539 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1539 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1539 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1539 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1539 host

target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21508] The complementary binding of VGAM1539 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1539 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1539 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1539 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[21509] It is appreciated that VGAM1539 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1539 host target genes. The mRNA of each one of this plurality of VGAM1539 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1539 RNA, herein designated VGAM RNA, and which when bound by VGAM1539 RNA, herein

designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1539 host target proteins.

[21510] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1539 gene, herein designated VGAM GENE, on one or more VGAM1539 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21511] It is yet further appreciated that a function of VGAM1539 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1539 include diagnosis, prevention and

treatment of viral infection by Monkeypox virus. Specific functions, and accordingly utilities, of VGAM1539 correlate with, and may be deduced from, the identity of the host target genes which VGAM1539 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[21512] Nucleotide sequences of the VGAM1539 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1539 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1539 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1539 are further described hereinbelow with reference to Table 1.

[21513] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1539 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[21514] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1540 (VGAM1540) viral gene, which modulates ex-

pression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[21515] VGAM1540 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1540 was detected is described hereinabove with reference to Figs. 2-8.

[21516] VGAM1540 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Monkeypox virus. VGAM1540 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[21517] VGAM1540 gene, herein designated VGAM GENE, encodes a VGAM1540 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1540 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1540 precursor RNA is designated SEQ ID:1526, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1526 is located at position 61618 relative to the genome of Monkeypox virus.

[21518] VGAM1540 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1540 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21519] An enzyme complex designated DICER COMPLEX, dices the VGAM1540 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1540 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 48%) nucleotide sequence of VGAM1540 RNA is designated SEQ ID:4251, and is provided hereinbelow with reference to the sequence listing part.

[21520] VGAM1540 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1540 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1540 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21521] VGAM1540 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1540 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1540 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1540 RNA, herein designated VGAM RNA, may have a different number of host target

binding sites in untranslated regions of a VGAM1540 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21522] The complementary binding of VGAM1540 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1540 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1540 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1540 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[21523] It is appreciated that VGAM1540 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1540 host target genes. The mRNA of each one of this plurality of VGAM1540 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1540 RNA, herein designated VGAM

RNA, and which when bound by VGAM1540 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1540 host target proteins.

[21524] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1540 gene, herein designated VGAM GENE, on one or more VGAM1540 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21525] It is yet further appreciated that a function of VGAM1540 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM1540 include diagnosis, prevention and treatment of viral infection by Monkeypox virus. Specific functions, and accordingly utilities, of VGAM1540 correlate with, and may be deduced from, the identity of the host target genes which VGAM1540 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[21526] Nucleotide sequences of the VGAM1540 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1540 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1540 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1540 are further described hereinbelow with reference to Table 1.

[21527] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1540 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[21528] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Mes-

senger 1541 (VGAM1541) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[21529] VGAM1541 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1541 was detected is described hereinabove with reference to Figs. 2-8.

[21530] VGAM1541 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Monkeypox virus. VGAM1541 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[21531] VGAM1541 gene, herein designated VGAM GENE, encodes a VGAM1541 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1541 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1541 precursor RNA is designated SEQ ID:1527, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1527 is located at position

63264 relative to the genome of Monkeypox virus.

[21532] VGAM1541 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1541 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21533] An enzyme complex designated DICER COMPLEX, dices the VGAM1541 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1541 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 47%) nucleotide sequence of VGAM1541 RNA is designated SEQ ID:4252, and is provided hereinbelow with reference to the sequence listing part.

[21534] VGAM1541 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1541 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1541 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21535] VGAM1541 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1541 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1541 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1541 RNA, herein designated

VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1541 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21536] The complementary binding of VGAM1541 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1541 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1541 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1541 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[21537] It is appreciated that VGAM1541 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1541 host target genes. The mRNA of each one of this plurality of VGAM1541 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM1541 RNA, herein designated VGAM RNA, and which when bound by VGAM1541 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1541 host target proteins.

[21538] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1541 gene, herein designated VGAM GENE, on one or more VGAM1541 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21539] It is yet further appreciated that a function of VGAM1541 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1541 include diagnosis, prevention and treatment of viral infection by Monkeypox virus. Specific functions, and accordingly utilities, of VGAM1541 correlate with, and may be deduced from, the identity of the host target genes which VGAM1541 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[21540] Nucleotide sequences of the VGAM1541 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1541 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1541 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1541 are further described hereinbelow with reference to Table 1.

[21541] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1541 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[21542] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present

invention, referred to here as Viral Genomic Address Messenger 1542 (VGAM1542) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[21543] VGAM1542 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1542 was detected is described hereinabove with reference to Figs. 2-8.

[21544] VGAM1542 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Variola virus. VGAM1542 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[21545] VGAM1542 gene, herein designated VGAM GENE, encodes a VGAM1542 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1542 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1542 precursor RNA is designated SEQ ID:1528, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1528 is located at position

56199 relative to the genome of Variola virus.

[21546] VGAM1542 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1542 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21547] An enzyme complex designated DICER COMPLEX, dices the VGAM1542 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1542 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM1542 RNA is designated SEQ ID:4253, and is provided hereinbelow with reference to the sequence listing part.

[21548] VGAM1542 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1542 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1542 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21549] VGAM1542 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1542 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1542 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1542 RNA, herein designated

VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1542 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21550] The complementary binding of VGAM1542 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1542 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1542 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1542 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[21551] It is appreciated that VGAM1542 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1542 host target genes. The mRNA of each one of this plurality of VGAM1542 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM1542 RNA, herein designated VGAM RNA, and which when bound by VGAM1542 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1542 host target proteins.

[21552] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1542 gene, herein designated VGAM GENE, on one or more VGAM1542 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21553] It is yet further appreciated that a function of VGAM1542 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1542 include diagnosis, prevention and treatment of viral infection by Variola virus. Specific functions, and accordingly utilities, of VGAM1542 correlate with, and may be deduced from, the identity of the host target genes which VGAM1542 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[21554] Nucleotide sequences of the VGAM1542 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1542 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1542 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1542 are further described hereinbelow with reference to Table 1.

[21555] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1542 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[21556] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present

invention, referred to here as Viral Genomic Address Messenger 1543 (VGAM1543) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[21557] VGAM1543 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1543 was detected is described hereinabove with reference to Figs. 2-8.

[21558] VGAM1543 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Vaccinia virus. VGAM1543 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[21559] VGAM1543 gene, herein designated VGAM GENE, encodes a VGAM1543 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1543 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1543 precursor RNA is designated SEQ ID:1529, and is provided hereinbelow with reference to the sequence listing part. Nu-

cleotide sequence SEQ ID:1529 is located at position 66348 relative to the genome of Vaccinia virus.

[21560] VGAM1543 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1543 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21561] An enzyme complex designated DICER COMPLEX, dices the VGAM1543 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1543 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 47%) nucleotide sequence of VGAM1543 RNA is designated SEQ ID:4254, and is provided hereinbelow with reference to the sequence

listing part.

[21562] VGAM1543 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1543 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1543 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21563] VGAM1543 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1543 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1543 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not

meant to be limiting VGAM1543 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1543 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21564] The complementary binding of VGAM1543 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1543 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1543 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1543 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[21565] It is appreciated that VGAM1543 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1543 host target genes. The mRNA of each one of this plurality of VGAM1543 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM1543 RNA, herein designated VGAM RNA, and which when bound by VGAM1543 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1543 host target proteins.

[21566] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1543 gene, herein designated VGAM GENE, on one or more VGAM1543 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21567] It is yet further appreciated that a function of VGAM1543

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1543 include diagnosis, prevention and treatment of viral infection by Vaccinia virus. Specific functions, and accordingly utilities, of VGAM1543 correlate with, and may be deduced from, the identity of the host target genes which VGAM1543 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[21568] Nucleotide sequences of the VGAM1543 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1543 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1543 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1543 are further described hereinbelow with reference to Table 1.

[21569] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1543 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[21570] Fig. 1 further provides a conceptual description of another

novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1544 (VGAM1544) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[21571] VGAM1544 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1544 was detected is described hereinabove with reference to Figs. 2-8.

[21572] VGAM1544 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Variola virus. VGAM1544 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[21573] VGAM1544 gene, herein designated VGAM GENE, encodes a VGAM1544 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1544 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1544 precursor RNA is designated SEQ ID:1530, and is provided hereinbelow with reference to the sequence listing part. Nu-

cleotide sequence SEQ ID:1530 is located at position 50463 relative to the genome of Variola virus.

[21574] VGAM1544 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1544 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21575] An enzyme complex designated DICER COMPLEX, dices the VGAM1544 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1544 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 55%) nucleotide sequence of VGAM1544 RNA is designated SEQ ID:4255, and is provided hereinbelow with reference to the sequence

listing part.

[21576] VGAM1544 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1544 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1544 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21577] VGAM1544 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1544 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1544 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not

meant to be limiting VGAM1544 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1544 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21578] The complementary binding of VGAM1544 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1544 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1544 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1544 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[21579] It is appreciated that VGAM1544 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1544 host target genes. The mRNA of each one of this plurality of VGAM1544 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM1544 RNA, herein designated VGAM RNA, and which when bound by VGAM1544 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1544 host target proteins.

[21580] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1544 gene, herein designated VGAM GENE, on one or more VGAM1544 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21581] It is yet further appreciated that a function of VGAM1544

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1544 include diagnosis, prevention and treatment of viral infection by Variola virus. Specific functions, and accordingly utilities, of VGAM1544 correlate with, and may be deduced from, the identity of the host target genes which VGAM1544 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[21582] Nucleotide sequences of the VGAM1544 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1544 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1544 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1544 are further described hereinbelow with reference to Table 1.

[21583] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1544 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[21584] Fig. 1 further provides a conceptual description of another

novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1545 (VGAM1545) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[21585] VGAM1545 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1545 was detected is described hereinabove with reference to Figs. 2-8.

[21586] VGAM1545 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Variola virus. VGAM1545 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[21587] VGAM1545 gene, herein designated VGAM GENE, encodes a VGAM1545 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1545 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1545 precursor RNA is designated SEQ ID:1531, and is provided hereinbelow with reference to the sequence listing part. Nu-

cleotide sequence SEQ ID:1531 is located at position 53558 relative to the genome of Variola virus.

[21588] VGAM1545 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1545 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21589] An enzyme complex designated DICER COMPLEX, dices the VGAM1545 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1545 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM1545 RNA is designated SEQ ID:4256, and is provided hereinbelow with reference to the sequence

listing part.

[21590] VGAM1545 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1545 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1545 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21591] VGAM1545 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1545 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1545 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not

meant to be limiting VGAM1545 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1545 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21592] The complementary binding of VGAM1545 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1545 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1545 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1545 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[21593] It is appreciated that VGAM1545 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1545 host target genes. The mRNA of each one of this plurality of VGAM1545 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM1545 RNA, herein designated VGAM RNA, and which when bound by VGAM1545 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1545 host target proteins.

[21594] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1545 gene, herein designated VGAM GENE, on one or more VGAM1545 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21595] It is yet further appreciated that a function of VGAM1545

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1545 include diagnosis, prevention and treatment of viral infection by Variola virus. Specific functions, and accordingly utilities, of VGAM1545 correlate with, and may be deduced from, the identity of the host target genes which VGAM1545 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[21596] Nucleotide sequences of the VGAM1545 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1545 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1545 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1545 are further described hereinbelow with reference to Table 1.

[21597] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1545 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[21598] Fig. 1 further provides a conceptual description of another

novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1546 (VGAM1546) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[21599] VGAM1546 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1546 was detected is described hereinabove with reference to Figs. 2-8.

[21600] VGAM1546 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Variola virus. VGAM1546 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[21601] VGAM1546 gene, herein designated VGAM GENE, encodes a VGAM1546 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1546 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1546 precursor RNA is designated SEQ ID:1532, and is provided hereinbelow with reference to the sequence listing part. Nu-

cleotide sequence SEQ ID:1532 is located at position 51253 relative to the genome of Variola virus.

[21602] VGAM1546 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1546 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21603] An enzyme complex designated DICER COMPLEX, dices the VGAM1546 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1546 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM1546 RNA is designated SEQ ID:4257, and is provided hereinbelow with reference to the sequence

listing part.

[21604] VGAM1546 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1546 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1546 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21605] VGAM1546 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1546 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1546 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not

meant to be limiting VGAM1546 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1546 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21606] The complementary binding of VGAM1546 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1546 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1546 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1546 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[21607] It is appreciated that VGAM1546 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1546 host target genes. The mRNA of each one of this plurality of VGAM1546 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM1546 RNA, herein designated VGAM RNA, and which when bound by VGAM1546 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1546 host target proteins.

[21608] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1546 gene, herein designated VGAM GENE, on one or more VGAM1546 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21609] It is yet further appreciated that a function of VGAM1546

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1546 include diagnosis, prevention and treatment of viral infection by Variola virus. Specific functions, and accordingly utilities, of VGAM1546 correlate with, and may be deduced from, the identity of the host target genes which VGAM1546 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[21610] Nucleotide sequences of the VGAM1546 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1546 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1546 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1546 are further described hereinbelow with reference to Table 1.

[21611] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1546 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[21612] Fig. 1 further provides a conceptual description of another

novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1547 (VGAM1547) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[21613] VGAM1547 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1547 was detected is described hereinabove with reference to Figs. 2-8.

[21614] VGAM1547 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Vaccinia virus. VGAM1547 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[21615] VGAM1547 gene, herein designated VGAM GENE, encodes a VGAM1547 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1547 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1547 precursor RNA is designated SEQ ID:1533, and is provided here-

inbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1533 is located at position 64695 relative to the genome of Vaccinia virus.

[21616] VGAM1547 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1547 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21617] An enzyme complex designated DICER COMPLEX, dices the VGAM1547 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1547 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM1547 RNA is designated SEQ ID:4258, and

is provided hereinbelow with reference to the sequence listing part.

[21618] VGAM1547 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1547 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1547 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21619] VGAM1547 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1547 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1547 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites

shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1547 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1547 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21620] The complementary binding of VGAM1547 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1547 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1547 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1547 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[21621] It is appreciated that VGAM1547 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1547 host target genes. The mRNA of each one of this plurality of VGAM1547 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1547 RNA, herein designated VGAM RNA, and which when bound by VGAM1547 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1547 host target proteins.

[21622] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1547 gene, herein designated VGAM GENE, on one or more VGAM1547 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21623] It is yet further appreciated that a function of VGAM1547 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1547 include diagnosis, prevention and treatment of viral infection by Vaccinia virus. Specific functions, and accordingly utilities, of VGAM1547 correlate with, and may be deduced from, the identity of the host target genes which VGAM1547 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[21624] Nucleotide sequences of the VGAM1547 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1547 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1547 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1547 are further described hereinbelow with reference to Table 1.

[21625] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1547 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[21626] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1548 (VGAM1548) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[21627] VGAM1548 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1548 was detected is described hereinabove with reference to Figs. 2-8.

[21628] VGAM1548 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Macaca mulatta rhadinovirus. VGAM1548 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[21629] VGAM1548 gene, herein designated VGAM GENE, encodes a VGAM1548 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1548 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1548 precur-

sor RNA is designated SEQ ID:1534, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1534 is located at position 113488 relative to the genome of Macaca mulatta rhadinovirus.

[21630] VGAM1548 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1548 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21631] An enzyme complex designated DICER COMPLEX, dices the VGAM1548 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1548 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 43%) nucleotide sequence of VGAM1548 RNA is designated SEQ ID:4259, and is provided hereinbelow with reference to the sequence listing part.

[21632] VGAM1548 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1548 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1548 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21633] VGAM1548 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1548 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1548 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I,

BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1548 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1548 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21634] The complementary binding of VGAM1548 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1548 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1548 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1548 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[21635] It is appreciated that VGAM1548 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM1548 host target genes. The mRNA of each one of this plurality of VGAM1548 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1548 RNA, herein designated VGAM RNA, and which when bound by VGAM1548 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1548 host target proteins.

[21636] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1548 gene, herein designated VGAM GENE, on one or more VGAM1548 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21637] It is yet further appreciated that a function of VGAM1548 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1548 include diagnosis, prevention and treatment of viral infection by Macaca mulatta rhadinovirus. Specific functions, and accordingly utilities, of VGAM1548 correlate with, and may be deduced from, the identity of the host target genes which VGAM1548 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[21638] Nucleotide sequences of the VGAM1548 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1548 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1548 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1548 are further described hereinbelow with reference to Table 1.

[21639] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites

to VGAM1548 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[21640] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1549 (VGAM1549) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[21641] VGAM1549 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1549 was detected is described hereinabove with reference to Figs. 2-8.

[21642] VGAM1549 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Macaca mulatta rhadinovirus. VGAM1549 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[21643] VGAM1549 gene, herein designated VGAM GENE, encodes a VGAM1549 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1549 precursor RNA, herein designated VGAM PRECURSOR RNA, does not en-

code a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1549 precursor RNA is designated SEQ ID:1535, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1535 is located at position 117267 relative to the genome of Macaca mulatta rhadinovirus.

[21644] VGAM1549 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1549 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21645] An enzyme complex designated DICER COMPLEX, dices the VGAM1549 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1549 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 58%) nucleotide sequence of VGAM1549 RNA is designated SEQ ID:4260, and is provided hereinbelow with reference to the sequence listing part.

[21646] VGAM1549 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1549 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1549 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21647] VGAM1549 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1549 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1549 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host

target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1549 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1549 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21648] The complementary binding of VGAM1549 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1549 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1549 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1549 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[21649] It is appreciated that VGAM1549 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1549 host target genes. The mRNA of each one of this plurality of VGAM1549 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1549 RNA, herein designated VGAM RNA, and which when bound by VGAM1549 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1549 host target proteins.

[21650] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1549 gene, herein designated VGAM GENE, on one or more VGAM1549 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21651] It is yet further appreciated that a function of VGAM1549 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1549 include diagnosis, prevention and treatment of viral infection by Macaca mulatta rhadinovirus. Specific functions, and accordingly utilities, of VGAM1549 correlate with, and may be deduced from, the identity of the host target genes which VGAM1549 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[21652] Nucleotide sequences of the VGAM1549 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1549 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1549 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1549 are further described hereinbelow with reference to Table 1.

[21653] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1549 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[21654] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1550 (VGAM1550) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[21655] VGAM1550 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1550 was detected is described hereinabove with reference to Figs. 2-8.

[21656] VGAM1550 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Macaca mulatta rhadinovirus. VGAM1550 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[21657] VGAM1550 gene, herein designated VGAM GENE, encodes a VGAM1550 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and un-

like most ordinary genes, VGAM1550 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1550 precursor RNA is designated SEQ ID:1536, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1536 is located at position 114505 relative to the genome of Macaca mulatta rhadinovirus.

[21658] VGAM1550 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1550 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21659] An enzyme complex designated DICER COMPLEX, dices the VGAM1550 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1550 RNA, herein designated VGAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM1550 RNA is designated SEQ ID:4261, and is provided hereinbelow with reference to the sequence listing part.

[21660] VGAM1550 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1550 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1550 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21661] VGAM1550 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1550 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1550 RNA, herein designated

VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1550 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1550 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21662] The complementary binding of VGAM1550 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1550 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1550 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1550 host target protein, herein desig-

nated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[21663] It is appreciated that VGAM1550 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1550 host target genes. The mRNA of each one of this plurality of VGAM1550 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1550 RNA, herein designated VGAM RNA, and which when bound by VGAM1550 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1550 host target proteins.

[21664] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1550 gene, herein designated VGAM GENE, on one or more VGAM1550 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21665] It is yet further appreciated that a function of VGAM1550 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1550 include diagnosis, prevention and treatment of viral infection by Macaca mulatta rhadinovirus. Specific functions, and accordingly utilities, of VGAM1550 correlate with, and may be deduced from, the identity of the host target genes which VGAM1550 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[21666] Nucleotide sequences of the VGAM1550 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1550 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1550 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1550 are further described hereinbelow with reference to Table 1.

[21667] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1550 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[21668] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1551 (VGAM1551) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[21669] VGAM1551 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1551 was detected is described hereinabove with reference to Figs. 2-8.

[21670] VGAM1551 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Macaca mulatta rhadinovirus. VGAM1551 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[21671] VGAM1551 gene, herein designated VGAM GENE, encodes

a VGAM1551 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1551 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1551 precursor RNA is designated SEQ ID:1537, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1537 is located at position 113655 relative to the genome of Macaca mulatta rhadinovirus.

[21672] VGAM1551 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1551 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21673] An enzyme complex designated DICER COMPLEX, dices the VGAM1551 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, into VGAM1551 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM1551 RNA is designated SEQ ID:4262, and is provided hereinbelow with reference to the sequence listing part.

[21674] VGAM1551 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1551 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1551 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21675] VGAM1551 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1551 host target RNA, herein designated VGAM HOST TARGET RNA. This

complementary binding is due to the fact that the nucleotide sequence of VGAM1551 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1551 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1551 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21676] The complementary binding of VGAM1551 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1551 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1551

host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1551 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[21677] It is appreciated that VGAM1551 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1551 host target genes. The mRNA of each one of this plurality of VGAM1551 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1551 RNA, herein designated VGAM RNA, and which when bound by VGAM1551 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1551 host target proteins.

[21678] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1551 gene, herein designated VGAM GENE, on one or more VGAM1551 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21679] It is yet further appreciated that a function of VGAM1551 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1551 include diagnosis, prevention and treatment of viral infection by Macaca mulatta rhadinovirus. Specific functions, and accordingly utilities, of VGAM1551 correlate with, and may be deduced from, the identity of the host target genes which VGAM1551 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[21680] Nucleotide sequences of the VGAM1551 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1551 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1551 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM1551 are further described hereinbelow with reference to Table 1.

[21681] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1551 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[21682] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1552 (VGAM1552) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[21683] VGAM1552 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1552 was detected is described hereinabove with reference to Figs. 2-8.

[21684] VGAM1552 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Macaca mulatta rhadinovirus. VGAM1552 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in

the human genome.

[21685] VGAM1552 gene, herein designated VGAM GENE, encodes a VGAM1552 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1552 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1552 precursor RNA is designated SEQ ID:1538, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1538 is located at position 116594 relative to the genome of Macaca mulatta rhadinovirus.

[21686] VGAM1552 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1552 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21687] An enzyme complex designated DICER COMPLEX, dices the VGAM1552 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1552 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM1552 RNA is designated SEQ ID:4263, and is provided hereinbelow with reference to the sequence listing part.

[21688] VGAM1552 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1552 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1552 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21689] VGAM1552 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites

located in untranslated regions of VGAM1552 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1552 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1552 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1552 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21690] The complementary binding of VGAM1552 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1552 host target RNA, herein designated VGAM

HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1552 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1552 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[21691] It is appreciated that VGAM1552 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1552 host target genes. The mRNA of each one of this plurality of VGAM1552 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1552 RNA, herein designated VGAM RNA, and which when bound by VGAM1552 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1552 host target proteins.

[21692] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1552 gene, herein designated VGAM GENE, on one or more VGAM1552 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove

with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21693] It is yet further appreciated that a function of VGAM1552 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1552 include diagnosis, prevention and treatment of viral infection by Macaca mulatta rhadinovirus. Specific functions, and accordingly utilities, of VGAM1552 correlate with, and may be deduced from, the identity of the host target genes which VGAM1552 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[21694] Nucleotide sequences of the VGAM1552 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1552 RNA, herein designated VGAM RNA, and

a schematic representation of the secondary folding of VGAM1552 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1552 are further described hereinbelow with reference to Table 1.

[21695] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1552 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[21696] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1553 (VGAM1553) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[21697] VGAM1553 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1553 was detected is described hereinabove with reference to Figs. 2-8.

[21698] VGAM1553 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Macaca mulatta rhadi-

novirus. VGAM1553 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[21699] VGAM1553 gene, herein designated VGAM GENE, encodes a VGAM1553 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1553 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1553 precursor RNA is designated SEQ ID:1539, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1539 is located at position 113170 relative to the genome of Macaca mulatta rhadinovirus.

[21700] VGAM1553 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1553 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21701] An enzyme complex designated DICER COMPLEX, dices the VGAM1553 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1553 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 51%) nucleotide sequence of VGAM1553 RNA is designated SEQ ID:4264, and is provided hereinbelow with reference to the sequence listing part.

[21702] VGAM1553 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1553 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1553 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21703] VGAM1553 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1553 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1553 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1553 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1553 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21704] The complementary binding of VGAM1553 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM1553 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1553 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1553 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[21705] It is appreciated that VGAM1553 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1553 host target genes. The mRNA of each one of this plurality of VGAM1553 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1553 RNA, herein designated VGAM RNA, and which when bound by VGAM1553 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1553 host target proteins.

[21706] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1553 gene, herein designated VGAM GENE, on one or more VGAM1553 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21707] It is yet further appreciated that a function of VGAM1553 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1553 include diagnosis, prevention and treatment of viral infection by Macaca mulatta rhadinovirus. Specific functions, and accordingly utilities, of VGAM1553 correlate with, and may be deduced from, the identity of the host target genes which VGAM1553 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[21708] Nucleotide sequences of the VGAM1553 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the diced VGAM1553 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1553 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1553 are further described hereinbelow with reference to Table 1.

[21709] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1553 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[21710] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1554 (VGAM1554) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[21711] VGAM1554 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1554 was detected is described hereinabove with reference to Figs. 2-8.

[21712] VGAM1554 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Macaca mulatta rhadinovirus. VGAM1554 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[21713] VGAM1554 gene, herein designated VGAM GENE, encodes a VGAM1554 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1554 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1554 precursor RNA is designated SEQ ID:1540, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1540 is located at position 118520 relative to the genome of Macaca mulatta rhadinovirus.

[21714] VGAM1554 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1554 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21715] An enzyme complex designated DICER COMPLEX, dices the VGAM1554 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1554 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM1554 RNA is designated SEQ ID:4265, and is provided hereinbelow with reference to the sequence listing part.

[21716] VGAM1554 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1554 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1554 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and

a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21717] VGAM1554 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1554 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1554 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1554 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1554 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both

3UTR and 5UTR regions.

[21718] The complementary binding of VGAM1554 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1554 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1554 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1554 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[21719] It is appreciated that VGAM1554 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1554 host target genes. The mRNA of each one of this plurality of VGAM1554 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1554 RNA, herein designated VGAM RNA, and which when bound by VGAM1554 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1554 host target proteins.

[21720] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM1554 gene, herein designated VGAM GENE, on one or more VGAM1554 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21721] It is yet further appreciated that a function of VGAM1554 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1554 include diagnosis, prevention and treatment of viral infection by Macaca mulatta rhadinovirus. Specific functions, and accordingly utilities, of VGAM1554 correlate with, and may be deduced from, the identity of the host target genes which VGAM1554 binds and inhibits, and the function of these host target genes,

as elaborated hereinbelow.

[21722] Nucleotide sequences of the VGAM1554 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1554 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1554 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1554 are further described hereinbelow with reference to Table 1.

[21723] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1554 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[21724] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1555 (VGAM1555) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[21725] VGAM1555 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene.

The method by which VGAM1555 was detected is described hereinabove with reference to Figs. 2-8.

[21726] VGAM1555 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Macaca mulatta rhadinovirus. VGAM1555 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[21727] VGAM1555 gene, herein designated VGAM GENE, encodes a VGAM1555 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1555 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1555 precursor RNA is designated SEQ ID:1541, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1541 is located at position 118330 relative to the genome of Macaca mulatta rhadinovirus.

[21728] VGAM1555 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1555 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21729] An enzyme complex designated DICER COMPLEX, dices the VGAM1555 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1555 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 78%) nucleotide sequence of VGAM1555 RNA is designated SEQ ID:4266, and is provided hereinbelow with reference to the sequence listing part.

[21730] VGAM1555 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1555 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1555 host target RNA, herein designated VGAM HOST TARGET RNA, comprises

three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21731] VGAM1555 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1555 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1555 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1555 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1555 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an

example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21732] The complementary binding of VGAM1555 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1555 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1555 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1555 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[21733] It is appreciated that VGAM1555 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1555 host target genes. The mRNA of each one of this plurality of VGAM1555 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1555 RNA, herein designated VGAM RNA, and which when bound by VGAM1555 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1555 host target proteins.

[21734] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1555 gene, herein designated VGAM GENE, on one or more VGAM1555 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21735] It is yet further appreciated that a function of VGAM1555 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1555 include diagnosis, prevention and treatment of viral infection by Macaca mulatta rhadinovirus. Specific functions, and accordingly utilities, of VGAM1555 correlate with, and may be deduced from, the

identity of the host target genes which VGAM1555 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[21736] Nucleotide sequences of the VGAM1555 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1555 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1555 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1555 are further described hereinbelow with reference to Table 1.

[21737] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1555 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[21738] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1556 (VGAM1556) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[21739] VGAM1556 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1556 was detected is described hereinabove with reference to Figs. 2-8.

[21740] VGAM1556 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Macaca mulatta rhadinovirus. VGAM1556 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[21741] VGAM1556 gene, herein designated VGAM GENE, encodes a VGAM1556 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1556 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1556 precursor RNA is designated SEQ ID:1542, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1542 is located at position 114675 relative to the genome of Macaca mulatta rhadinovirus.

[21742] VGAM1556 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1556 folded

precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21743] An enzyme complex designated DICER COMPLEX, dices the VGAM1556 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1556 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 51%) nucleotide sequence of VGAM1556 RNA is designated SEQ ID:4267, and is provided hereinbelow with reference to the sequence listing part.

[21744] VGAM1556 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1556 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM1556 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21745] VGAM1556 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1556 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1556 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1556 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1556 host target RNA, herein designated VGAM HOST TARGET RNA.

It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21746] The complementary binding of VGAM1556 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1556 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1556 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1556 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[21747] It is appreciated that VGAM1556 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1556 host target genes. The mRNA of each one of this plurality of VGAM1556 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1556 RNA, herein designated VGAM RNA, and which when bound by VGAM1556 RNA, herein designated VGAM RNA, causes inhibition of translation of

respective one or more VGAM1556 host target proteins.

[21748] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1556 gene, herein designated VGAM GENE, on one or more VGAM1556 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21749] It is yet further appreciated that a function of VGAM1556 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1556 include diagnosis, prevention and treatment of viral infection by Macaca mulatta rhadi-

novirus. Specific functions, and accordingly utilities, of VGAM1556 correlate with, and may be deduced from, the identity of the host target genes which VGAM1556 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[21750] Nucleotide sequences of the VGAM1556 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1556 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1556 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1556 are further described hereinbelow with reference to Table 1.

[21751] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1556 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[21752] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1557 (VGAM1557) viral gene, which modulates expression of respective host target genes thereof, the func-

tion and utility of which host target genes is known in the art.

[21753] VGAM1557 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1557 was detected is described hereinabove with reference to Figs. 2-8.

[21754] VGAM1557 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Macaca mulatta rhadinovirus. VGAM1557 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[21755] VGAM1557 gene, herein designated VGAM GENE, encodes a VGAM1557 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1557 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1557 precursor RNA is designated SEQ ID:1543, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1543 is located at position 114790 relative to the genome of Macaca mulatta rhadinovirus.

[21756] VGAM1557 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1557 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21757] An enzyme complex designated DICER COMPLEX, dices the VGAM1557 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1557 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM1557 RNA is designated SEQ ID:4268, and is provided hereinbelow with reference to the sequence listing part.

[21758] VGAM1557 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1557 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1557 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21759] VGAM1557 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1557 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1557 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1557 RNA, herein designated VGAM RNA, may have a different number of host target

binding sites in untranslated regions of a VGAM1557 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21760] The complementary binding of VGAM1557 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1557 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1557 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1557 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[21761] It is appreciated that VGAM1557 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1557 host target genes. The mRNA of each one of this plurality of VGAM1557 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1557 RNA, herein designated VGAM

RNA, and which when bound by VGAM1557 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1557 host target proteins.

[21762] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1557 gene, herein designated VGAM GENE, on one or more VGAM1557 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21763] It is yet further appreciated that a function of VGAM1557 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM1557 include diagnosis, prevention and treatment of viral infection by Macaca mulatta rhadinovirus. Specific functions, and accordingly utilities, of VGAM1557 correlate with, and may be deduced from, the identity of the host target genes which VGAM1557 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[21764] Nucleotide sequences of the VGAM1557 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1557 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1557 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1557 are further described hereinbelow with reference to Table 1.

[21765] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1557 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[21766] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Mes-

senger 1558 (VGAM1558) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[21767] VGAM1558 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1558 was detected is described hereinabove with reference to Figs. 2-8.

[21768] VGAM1558 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Bean common mosaic virus. VGAM1558 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[21769] VGAM1558 gene, herein designated VGAM GENE, encodes a VGAM1558 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1558 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1558 precursor RNA is designated SEQ ID:1544, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1544 is located at position 8996

relative to the genome of Bean common mosaic virus.

[21770] VGAM1558 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1558 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21771] An enzyme complex designated DICER COMPLEX, dices the VGAM1558 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1558 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM1558 RNA is designated SEQ ID:4269, and is provided hereinbelow with reference to the sequence listing part.

[21772] VGAM1558 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1558 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1558 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21773] VGAM1558 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1558 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1558 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1558 RNA, herein designated

VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1558 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21774] The complementary binding of VGAM1558 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1558 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1558 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1558 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[21775] It is appreciated that VGAM1558 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1558 host target genes. The mRNA of each one of this plurality of VGAM1558 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM1558 RNA, herein designated VGAM RNA, and which when bound by VGAM1558 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1558 host target proteins.

[21776] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1558 gene, herein designated VGAM GENE, on one or more VGAM1558 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21777] It is yet further appreciated that a function of VGAM1558 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1558 include diagnosis, prevention and treatment of viral infection by Bean common mosaic virus. Specific functions, and accordingly utilities, of VGAM1558 correlate with, and may be deduced from, the identity of the host target genes which VGAM1558 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[21778] Nucleotide sequences of the VGAM1558 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1558 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1558 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1558 are further described hereinbelow with reference to Table 1.

[21779] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1558 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[21780] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present

invention, referred to here as Viral Genomic Address Messenger 1559 (VGAM1559) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[21781] VGAM1559 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1559 was detected is described hereinabove with reference to Figs. 2-8.

[21782] VGAM1559 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Bean common mosaic virus. VGAM1559 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[21783] VGAM1559 gene, herein designated VGAM GENE, encodes a VGAM1559 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1559 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1559 precursor RNA is designated SEQ ID:1545, and is provided hereinbelow with reference to the sequence listing part. Nu-

cleotide sequence SEQ ID:1545 is located at position 3572 relative to the genome of Bean common mosaic virus.

[21784] VGAM1559 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1559 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21785] An enzyme complex designated DICER COMPLEX, dices the VGAM1559 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1559 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM1559 RNA is designated SEQ ID:4270, and is provided hereinbelow with reference to the sequence

listing part.

[21786] VGAM1559 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1559 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1559 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21787] VGAM1559 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1559 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1559 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not

meant to be limiting VGAM1559 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1559 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21788] The complementary binding of VGAM1559 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1559 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1559 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1559 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[21789] It is appreciated that VGAM1559 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1559 host target genes. The mRNA of each one of this plurality of VGAM1559 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM1559 RNA, herein designated VGAM RNA, and which when bound by VGAM1559 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1559 host target proteins.

[21790] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1559 gene, herein designated VGAM GENE, on one or more VGAM1559 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21791] It is yet further appreciated that a function of VGAM1559

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1559 include diagnosis, prevention and treatment of viral infection by Bean common mosaic virus. Specific functions, and accordingly utilities, of VGAM1559 correlate with, and may be deduced from, the identity of the host target genes which VGAM1559 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[21792] Nucleotide sequences of the VGAM1559 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1559 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1559 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1559 are further described hereinbelow with reference to Table 1.

[21793] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1559 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[21794] Fig. 1 further provides a conceptual description of another

novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1560 (VGAM1560) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[21795] VGAM1560 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1560 was detected is described hereinabove with reference to Figs. 2-8.

[21796] VGAM1560 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Bean common mosaic virus. VGAM1560 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[21797] VGAM1560 gene, herein designated VGAM GENE, encodes a VGAM1560 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1560 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1560 precursor RNA is designated SEQ ID:1546, and is provided here-

inbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1546 is located at position 6352 relative to the genome of Bean common mosaic virus.

[21798] VGAM1560 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1560 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21799] An enzyme complex designated DICER COMPLEX, dices the VGAM1560 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1560 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM1560 RNA is designated SEQ ID:4271, and

is provided hereinbelow with reference to the sequence listing part.

[21800] VGAM1560 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1560 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1560 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21801] VGAM1560 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1560 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1560 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites

shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1560 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1560 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21802] The complementary binding of VGAM1560 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1560 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1560 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1560 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[21803] It is appreciated that VGAM1560 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1560 host target genes. The mRNA of each one of this plurality of VGAM1560 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1560 RNA, herein designated VGAM RNA, and which when bound by VGAM1560 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1560 host target proteins.

[21804] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1560 gene, herein designated VGAM GENE, on one or more VGAM1560 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21805] It is yet further appreciated that a function of VGAM1560 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1560 include diagnosis, prevention and treatment of viral infection by Bean common mosaic virus. Specific functions, and accordingly utilities, of VGAM1560 correlate with, and may be deduced from, the identity of the host target genes which VGAM1560 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[21806] Nucleotide sequences of the VGAM1560 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1560 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1560 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1560 are further described hereinbelow with reference to Table 1.

[21807] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1560 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[21808] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1561 (VGAM1561) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[21809] VGAM1561 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1561 was detected is described hereinabove with reference to Figs. 2-8.

[21810] VGAM1561 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Bean common mosaic virus. VGAM1561 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[21811] VGAM1561 gene, herein designated VGAM GENE, encodes a VGAM1561 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1561 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1561 precur-

sor RNA is designated SEQ ID:1547, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1547 is located at position 7254 relative to the genome of Bean common mosaic virus.

[21812] VGAM1561 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1561 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21813] An enzyme complex designated DICER COMPLEX, dices the VGAM1561 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1561 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 73%) nucleotide se-

quence of VGAM1561 RNA is designated SEQ ID:4272, and is provided hereinbelow with reference to the sequence listing part.

[21814] VGAM1561 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1561 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1561 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21815] VGAM1561 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1561 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1561 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is ap-

preciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1561 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1561 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21816] The complementary binding of VGAM1561 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1561 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1561 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1561 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[21817] It is appreciated that VGAM1561 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1561 host target genes. The mRNA of

each one of this plurality of VGAM1561 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1561 RNA, herein designated VGAM RNA, and which when bound by VGAM1561 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1561 host target proteins.

[21818] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1561 gene, herein designated VGAM GENE, on one or more VGAM1561 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science

294,779 (2001)).

[21819] It is yet further appreciated that a function of VGAM1561 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1561 include diagnosis, prevention and treatment of viral infection by Bean common mosaic virus. Specific functions, and accordingly utilities, of VGAM1561 correlate with, and may be deduced from, the identity of the host target genes which VGAM1561 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[21820] Nucleotide sequences of the VGAM1561 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1561 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1561 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1561 are further described hereinbelow with reference to Table 1.

[21821] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1561 RNA, herein designated VGAM RNA, are de-

scribed hereinbelow with reference to Table 2.

[21822] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1562 (VGAM1562) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[21823] VGAM1562 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1562 was detected is described hereinabove with reference to Figs. 2-8.

[21824] VGAM1562 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Bean common mosaic virus. VGAM1562 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[21825] VGAM1562 gene, herein designated VGAM GENE, encodes a VGAM1562 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1562 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly

similar to the nucleotide sequence of VGAM1562 precursor RNA is designated SEQ ID:1548, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1548 is located at position 2292 relative to the genome of Bean common mosaic virus.

[21826] VGAM1562 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1562 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21827] An enzyme complex designated DICER COMPLEX, dices the VGAM1562 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1562 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 42%) nucleotide sequence of VGAM1562 RNA is designated SEQ ID:4273, and is provided hereinbelow with reference to the sequence listing part.

[21828] VGAM1562 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1562 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1562 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21829] VGAM1562 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1562 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1562 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I,

BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1562 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1562 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21830] The complementary binding of VGAM1562 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1562 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1562 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1562 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[21831] It is appreciated that VGAM1562 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM1562 host target genes. The mRNA of each one of this plurality of VGAM1562 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1562 RNA, herein designated VGAM RNA, and which when bound by VGAM1562 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1562 host target proteins.

[21832] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1562 gene, herein designated VGAM GENE, on one or more VGAM1562 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21833] It is yet further appreciated that a function of VGAM1562 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1562 include diagnosis, prevention and treatment of viral infection by Bean common mosaic virus. Specific functions, and accordingly utilities, of VGAM1562 correlate with, and may be deduced from, the identity of the host target genes which VGAM1562 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[21834] Nucleotide sequences of the VGAM1562 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1562 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1562 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1562 are further described hereinbelow with reference to Table 1.

[21835] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites

to VGAM1562 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[21836] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1563 (VGAM1563) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[21837] VGAM1563 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1563 was detected is described hereinabove with reference to Figs. 2-8.

[21838] VGAM1563 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Bean common mosaic virus. VGAM1563 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[21839] VGAM1563 gene, herein designated VGAM GENE, encodes a VGAM1563 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1563 precursor RNA, herein designated VGAM PRECURSOR RNA, does not en-

code a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1563 precursor RNA is designated SEQ ID:1549, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1549 is located at position 9514 relative to the genome of Bean common mosaic virus.

[21840] VGAM1563 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1563 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21841] An enzyme complex designated DICER COMPLEX, dices the VGAM1563 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1563 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 51%) nucleotide sequence of VGAM1563 RNA is designated SEQ ID:4274, and is provided hereinbelow with reference to the sequence listing part.

[21842] VGAM1563 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1563 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1563 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21843] VGAM1563 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1563 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1563 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3

such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1563 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1563 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21844] The complementary binding of VGAM1563 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1563 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1563 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1563 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[21845] It is appreciated that VGAM1563 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1563 host target genes. The mRNA of each one of this plurality of VGAM1563 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1563 RNA, herein designated VGAM RNA, and which when bound by VGAM1563 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1563 host target proteins.

[21846] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1563 gene, herein designated VGAM GENE, on one or more VGAM1563 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21847] It is yet further appreciated that a function of VGAM1563 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1563 include diagnosis, prevention and treatment of viral infection by Bean common mosaic virus. Specific functions, and accordingly utilities, of VGAM1563 correlate with, and may be deduced from, the identity of the host target genes which VGAM1563 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[21848] Nucleotide sequences of the VGAM1563 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1563 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1563 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1563 are further described hereinbelow with reference to Table 1.

[21849] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the

complementarity of each of these host target binding sites to VGAM1563 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[21850] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1564 (VGAM1564) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[21851] VGAM1564 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1564 was detected is described hereinabove with reference to Figs. 2-8.

[21852] VGAM1564 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human herpesvirus 5. VGAM1564 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[21853] VGAM1564 gene, herein designated VGAM GENE, encodes a VGAM1564 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1564 precursor RNA,

herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1564 precursor RNA is designated SEQ ID:1550, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1550 is located at position 167115 relative to the genome of Human herpesvirus 5.

[21854] VGAM1564 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1564 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21855] An enzyme complex designated DICER COMPLEX, dices the VGAM1564 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1564 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 90%) nucleotide sequence of VGAM1564 RNA is designated SEQ ID:4275, and is provided hereinbelow with reference to the sequence listing part.

[21856] VGAM1564 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1564 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1564 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21857] VGAM1564 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1564 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1564 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host

target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1564 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1564 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21858] The complementary binding of VGAM1564 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1564 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1564 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1564 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[21859] It is appreciated that VGAM1564 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1564 host target genes. The mRNA of each one of this plurality of VGAM1564 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1564 RNA, herein designated VGAM RNA, and which when bound by VGAM1564 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1564 host target proteins.

[21860] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1564 gene, herein designated VGAM GENE, on one or more VGAM1564 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21861] It is yet further appreciated that a function of VGAM1564 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1564 include diagnosis, prevention and treatment of viral infection by Human herpesvirus 5. Specific functions, and accordingly utilities, of VGAM1564 correlate with, and may be deduced from, the identity of the host target genes which VGAM1564 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[21862] Nucleotide sequences of the VGAM1564 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1564 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1564 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1564 are further described hereinbelow with reference to Table 1.

[21863] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1564 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[21864] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1565 (VGAM1565) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[21865] VGAM1565 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1565 was detected is described hereinabove with reference to Figs. 2-8.

[21866] VGAM1565 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human herpesvirus 5. VGAM1565 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[21867] VGAM1565 gene, herein designated VGAM GENE, encodes a VGAM1565 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and un-

like most ordinary genes, VGAM1565 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1565 precursor RNA is designated SEQ ID:1551, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1551 is located at position 170917 relative to the genome of Human herpesvirus 5.

[21868] VGAM1565 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1565 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21869] An enzyme complex designated DICER COMPLEX, dices the VGAM1565 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1565 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM1565 RNA is designated SEQ ID:4276, and is provided hereinbelow with reference to the sequence listing part.

[21870] VGAM1565 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1565 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1565 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21871] VGAM1565 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1565 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1565 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed

sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1565 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1565 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21872] The complementary binding of VGAM1565 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1565 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1565 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1565 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target

protein is therefore outlined by a broken line.

[21873] It is appreciated that VGAM1565 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1565 host target genes. The mRNA of each one of this plurality of VGAM1565 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1565 RNA, herein designated VGAM RNA, and which when bound by VGAM1565 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1565 host target proteins.

[21874] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1565 gene, herein designated VGAM GENE, on one or more VGAM1565 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21875] It is yet further appreciated that a function of VGAM1565 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1565 include diagnosis, prevention and treatment of viral infection by Human herpesvirus 5. Specific functions, and accordingly utilities, of VGAM1565 correlate with, and may be deduced from, the identity of the host target genes which VGAM1565 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[21876] Nucleotide sequences of the VGAM1565 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1565 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1565 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1565 are further described hereinbelow with reference to Table 1.

[21877] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1565 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[21878] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1566 (VGAM1566) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[21879] VGAM1566 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1566 was detected is described hereinabove with reference to Figs. 2-8.

[21880] VGAM1566 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human herpesvirus 5. VGAM1566 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[21881] VGAM1566 gene, herein designated VGAM GENE, encodes a VGAM1566 precursor RNA, herein designated VGAM

PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1566 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1566 precursor RNA is designated SEQ ID:1552, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1552 is located at position 165653 relative to the genome of Human herpesvirus 5.

[21882] VGAM1566 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1566 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21883] An enzyme complex designated DICER COMPLEX, dices the VGAM1566 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1566 RNA, herein designated VGAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 70%) nucleotide sequence of VGAM1566 RNA is designated SEQ ID:4277, and is provided hereinbelow with reference to the sequence listing part.

[21884] VGAM1566 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1566 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1566 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21885] VGAM1566 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1566 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1566 RNA, herein designated

VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1566 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1566 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21886] The complementary binding of VGAM1566 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1566 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1566 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1566 host target protein, herein desig-

nated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[21887] It is appreciated that VGAM1566 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1566 host target genes. The mRNA of each one of this plurality of VGAM1566 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1566 RNA, herein designated VGAM RNA, and which when bound by VGAM1566 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1566 host target proteins.

[21888] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1566 gene, herein designated VGAM GENE, on one or more VGAM1566 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21889] It is yet further appreciated that a function of VGAM1566 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1566 include diagnosis, prevention and treatment of viral infection by Human herpesvirus 5. Specific functions, and accordingly utilities, of VGAM1566 correlate with, and may be deduced from, the identity of the host target genes which VGAM1566 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[21890] Nucleotide sequences of the VGAM1566 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1566 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1566 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1566 are further described hereinbelow with reference to Table 1.

[21891] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1566 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[21892] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1567 (VGAM1567) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[21893] VGAM1567 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1567 was detected is described hereinabove with reference to Figs. 2-8.

[21894] VGAM1567 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human herpesvirus 5. VGAM1567 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[21895] VGAM1567 gene, herein designated VGAM GENE, encodes

a VGAM1567 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1567 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1567 precursor RNA is designated SEQ ID:1553, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1553 is located at position 69308 relative to the genome of Human herpesvirus 5.

[21896] VGAM1567 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1567 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21897] An enzyme complex designated DICER COMPLEX, dices the VGAM1567 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1567 RNA,

herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 48%) nucleotide sequence of VGAM1567 RNA is designated SEQ ID:4278, and is provided hereinbelow with reference to the sequence listing part.

[21898] VGAM1567 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1567 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1567 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21899] VGAM1567 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1567 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM1567 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1567 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1567 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21900] The complementary binding of VGAM1567 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1567 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1567 host target RNA, herein designated VGAM HOST TARGET

RNA, into VGAM1567 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[21901] It is appreciated that VGAM1567 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1567 host target genes. The mRNA of each one of this plurality of VGAM1567 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1567 RNA, herein designated VGAM RNA, and which when bound by VGAM1567 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1567 host target proteins.

[21902] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1567 gene, herein designated VGAM GENE, on one or more VGAM1567 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21903] It is yet further appreciated that a function of VGAM1567 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1567 include diagnosis, prevention and treatment of viral infection by Human herpesvirus 5. Specific functions, and accordingly utilities, of VGAM1567 correlate with, and may be deduced from, the identity of the host target genes which VGAM1567 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[21904] Nucleotide sequences of the VGAM1567 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1567 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1567 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1567 are further

described hereinbelow with reference to Table 1.

[21905] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1567 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[21906] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1568 (VGAM1568) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[21907] VGAM1568 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1568 was detected is described hereinabove with reference to Figs. 2-8.

[21908] VGAM1568 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human herpesvirus 5. VGAM1568 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[21909] VGAM1568 gene, herein designated VGAM GENE, encodes a VGAM1568 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1568 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1568 precursor RNA is designated SEQ ID:1554, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1554 is located at position 61146 relative to the genome of Human herpesvirus 5.

[21910] VGAM1568 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1568 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21911] An enzyme complex designated DICER COMPLEX, dices the VGAM1568 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, into VGAM1568 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM1568 RNA is designated SEQ ID:4279, and is provided hereinbelow with reference to the sequence listing part.

[21912] VGAM1568 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1568 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1568 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21913] VGAM1568 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1568 host target RNA, herein designated VGAM HOST TARGET RNA. This

complementary binding is due to the fact that the nucleotide sequence of VGAM1568 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1568 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1568 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21914] The complementary binding of VGAM1568 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1568 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1568

host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1568 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[21915] It is appreciated that VGAM1568 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1568 host target genes. The mRNA of each one of this plurality of VGAM1568 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1568 RNA, herein designated VGAM RNA, and which when bound by VGAM1568 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1568 host target proteins.

[21916] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1568 gene, herein designated VGAM GENE, on one or more VGAM1568 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21917] It is yet further appreciated that a function of VGAM1568 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1568 include diagnosis, prevention and treatment of viral infection by Human herpesvirus 5. Specific functions, and accordingly utilities, of VGAM1568 correlate with, and may be deduced from, the identity of the host target genes which VGAM1568 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[21918] Nucleotide sequences of the VGAM1568 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1568 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1568 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM1568 are further described hereinbelow with reference to Table 1.

[21919] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1568 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[21920] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1569 (VGAM1569) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[21921] VGAM1569 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1569 was detected is described hereinabove with reference to Figs. 2-8.

[21922] VGAM1569 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human herpesvirus 5. VGAM1569 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the

human genome.

[21923] VGAM1569 gene, herein designated VGAM GENE, encodes a VGAM1569 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1569 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1569 precursor RNA is designated SEQ ID:1555, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1555 is located at position 66671 relative to the genome of Human herpesvirus 5.

[21924] VGAM1569 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1569 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21925] An enzyme complex designated DICER COMPLEX, dices

the VGAM1569 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1569 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 82%) nucleotide sequence of VGAM1569 RNA is designated SEQ ID:4280, and is provided hereinbelow with reference to the sequence listing part.

[21926] VGAM1569 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1569 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1569 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21927] VGAM1569 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1569 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1569 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1569 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1569 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21928] The complementary binding of VGAM1569 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1569 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM1569 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1569 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[21929] It is appreciated that VGAM1569 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1569 host target genes. The mRNA of each one of this plurality of VGAM1569 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1569 RNA, herein designated VGAM RNA, and which when bound by VGAM1569 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1569 host target proteins.

[21930] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1569 gene, herein designated VGAM GENE, on one or more VGAM1569 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21931] It is yet further appreciated that a function of VGAM1569 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1569 include diagnosis, prevention and treatment of viral infection by Human herpesvirus 5. Specific functions, and accordingly utilities, of VGAM1569 correlate with, and may be deduced from, the identity of the host target genes which VGAM1569 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[21932] Nucleotide sequences of the VGAM1569 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1569 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of

VGAM1569 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1569 are further described hereinbelow with reference to Table 1.

[21933] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1569 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[21934] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1570 (VGAM1570) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[21935] VGAM1570 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1570 was detected is described hereinabove with reference to Figs. 2-8.

[21936] VGAM1570 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human herpesvirus 5. VGAM1570 host target gene, herein designated VGAM

HOST TARGET GENE, is a human gene contained in the human genome.

[21937] VGAM1570 gene, herein designated VGAM GENE, encodes a VGAM1570 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1570 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1570 precursor RNA is designated SEQ ID:1556, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1556 is located at position 65530 relative to the genome of Human herpesvirus 5.

[21938] VGAM1570 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1570 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21939] An enzyme complex designated DICER COMPLEX, dices the VGAM1570 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1570 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 50%) nucleotide sequence of VGAM1570 RNA is designated SEQ ID:4281, and is provided hereinbelow with reference to the sequence listing part.

[21940] VGAM1570 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1570 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1570 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21941] VGAM1570 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites

located in untranslated regions of VGAM1570 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1570 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1570 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1570 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21942] The complementary binding of VGAM1570 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1570 host target RNA, herein designated VGAM

HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1570 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1570 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[21943] It is appreciated that VGAM1570 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1570 host target genes. The mRNA of each one of this plurality of VGAM1570 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1570 RNA, herein designated VGAM RNA, and which when bound by VGAM1570 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1570 host target proteins.

[21944] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1570 gene, herein designated VGAM GENE, on one or more VGAM1570 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove

with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21945] It is yet further appreciated that a function of VGAM1570 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1570 include diagnosis, prevention and treatment of viral infection by Human herpesvirus 5. Specific functions, and accordingly utilities, of VGAM1570 correlate with, and may be deduced from, the identity of the host target genes which VGAM1570 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[21946] Nucleotide sequences of the VGAM1570 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1570 RNA, herein designated VGAM RNA, and

a schematic representation of the secondary folding of VGAM1570 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1570 are further described hereinbelow with reference to Table 1.

[21947] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1570 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[21948] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1571 (VGAM1571) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[21949] VGAM1571 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1571 was detected is described hereinabove with reference to Figs. 2-8.

[21950] VGAM1571 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rhopalosiphum padi

virus. VGAM1571 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[21951] VGAM1571 gene, herein designated VGAM GENE, encodes a VGAM1571 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1571 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1571 precursor RNA is designated SEQ ID:1557, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1557 is located at position 4 relative to the genome of Rhopalosiphum padi virus.

[21952] VGAM1571 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1571 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[21953] An enzyme complex designated DICER COMPLEX, dices the VGAM1571 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1571 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM1571 RNA is designated SEQ ID:4282, and is provided hereinbelow with reference to the sequence listing part.

[21954] VGAM1571 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1571 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1571 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21955] VGAM1571 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM1571 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1571 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1571 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1571 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21956] The complementary binding of VGAM1571 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM1571 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1571 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1571 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[21957] It is appreciated that VGAM1571 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1571 host target genes. The mRNA of each one of this plurality of VGAM1571 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1571 RNA, herein designated VGAM RNA, and which when bound by VGAM1571 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1571 host target proteins.

[21958] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1571 gene, herein designated VGAM GENE, on one or more VGAM1571 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21959] It is yet further appreciated that a function of VGAM1571 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1571 include diagnosis, prevention and treatment of viral infection by Rhopalosiphum padi virus. Specific functions, and accordingly utilities, of VGAM1571 correlate with, and may be deduced from, the identity of the host target genes which VGAM1571 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[21960] Nucleotide sequences of the VGAM1571 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

diced VGAM1571 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1571 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1571 are further described hereinbelow with reference to Table 1.

[21961] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1571 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[21962] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1572 (VGAM1572) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[21963] VGAM1572 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1572 was detected is described hereinabove with reference to Figs. 2-8.

[21964] VGAM1572 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of Rhopalosiphum padi virus. VGAM1572 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[21965] VGAM1572 gene, herein designated VGAM GENE, encodes a VGAM1572 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1572 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1572 precursor RNA is designated SEQ ID:1558, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1558 is located at position 3435 relative to the genome of Rhopalosiphum padi virus.

[21966] VGAM1572 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1572 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21967] An enzyme complex designated DICER COMPLEX, dices the VGAM1572 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1572 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM1572 RNA is designated SEQ ID:4283, and is provided hereinbelow with reference to the sequence listing part.

[21968] VGAM1572 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1572 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1572 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21969] VGAM1572 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1572 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1572 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1572 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1572 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21970] The complementary binding of VGAM1572 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM1572 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1572 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1572 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[21971] It is appreciated that VGAM1572 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1572 host target genes. The mRNA of each one of this plurality of VGAM1572 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1572 RNA, herein designated VGAM RNA, and which when bound by VGAM1572 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1572 host target proteins.

[21972] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1572 gene, herein designated VGAM GENE, on one or more VGAM1572 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21973] It is yet further appreciated that a function of VGAM1572 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1572 include diagnosis, prevention and treatment of viral infection by Rhopalosiphum padi virus. Specific functions, and accordingly utilities, of VGAM1572 correlate with, and may be deduced from, the identity of the host target genes which VGAM1572 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[21974] Nucleotide sequences of the VGAM1572 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the diced VGAM1572 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1572 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1572 are further described hereinbelow with reference to Table 1.

[21975] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1572 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[21976] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1573 (VGAM1573) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[21977] VGAM1573 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1573 was detected is described hereinabove with reference to Figs. 2-8.

[21978] VGAM1573 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rhopalosiphum padi virus. VGAM1573 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[21979] VGAM1573 gene, herein designated VGAM GENE, encodes a VGAM1573 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1573 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1573 precursor RNA is designated SEQ ID:1559, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1559 is located at position 3711 relative to the genome of Rhopalosiphum padi virus.

[21980] VGAM1573 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1573 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21981] An enzyme complex designated DICER COMPLEX, dices the VGAM1573 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1573 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM1573 RNA is designated SEQ ID:4284, and is provided hereinbelow with reference to the sequence listing part.

[21982] VGAM1573 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1573 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1573 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN COD-

ING and 3UTR respectively.

[21983] VGAM1573 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1573 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1573 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1573 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1573 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21984] The complementary binding of VGAM1573 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1573 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1573 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1573 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[21985] It is appreciated that VGAM1573 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1573 host target genes. The mRNA of each one of this plurality of VGAM1573 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1573 RNA, herein designated VGAM RNA, and which when bound by VGAM1573 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1573 host target proteins.

[21986] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1573 gene, herein designated VGAM GENE, on one

or more VGAM1573 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21987] It is yet further appreciated that a function of VGAM1573 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1573 include diagnosis, prevention and treatment of viral infection by Rhopalosiphum padi virus. Specific functions, and accordingly utilities, of VGAM1573 correlate with, and may be deduced from, the identity of the host target genes which VGAM1573 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[21988] Nucleotide sequences of the VGAM1573 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1573 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1573 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1573 are further described hereinbelow with reference to Table 1.

[21989] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1573 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[21990] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1574 (VGAM1574) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[21991] VGAM1574 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1574 was detected is de-

scribed hereinabove with reference to Figs. 2-8.

[21992] VGAM1574 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rhopalosiphum padi virus. VGAM1574 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[21993] VGAM1574 gene, herein designated VGAM GENE, encodes a VGAM1574 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1574 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1574 precursor RNA is designated SEQ ID:1560, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1560 is located at position 7836 relative to the genome of Rhopalosiphum padi virus.

[21994] VGAM1574 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1574 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21995] An enzyme complex designated DICER COMPLEX, dices the VGAM1574 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1574 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM1574 RNA is designated SEQ ID:4285, and is provided hereinbelow with reference to the sequence listing part.

[21996] VGAM1574 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1574 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1574 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and

a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21997] VGAM1574 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1574 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1574 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1574 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1574 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both

3UTR and 5UTR regions.

[21998] The complementary binding of VGAM1574 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1574 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1574 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1574 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[21999] It is appreciated that VGAM1574 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1574 host target genes. The mRNA of each one of this plurality of VGAM1574 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1574 RNA, herein designated VGAM RNA, and which when bound by VGAM1574 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1574 host target proteins.

[22000] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM1574 gene, herein designated VGAM GENE, on one or more VGAM1574 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22001] It is yet further appreciated that a function of VGAM1574 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1574 include diagnosis, prevention and treatment of viral infection by Rhopalosiphum padi virus. Specific functions, and accordingly utilities, of VGAM1574 correlate with, and may be deduced from, the identity of the host target genes which VGAM1574 binds and inhibits, and the function of these host target genes, as

elaborated hereinbelow.

[22002] Nucleotide sequences of the VGAM1574 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1574 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1574 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1574 are further described hereinbelow with reference to Table 1.

[22003] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1574 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[22004] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1575 (VGAM1575) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[22005] VGAM1575 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene.

The method by which VGAM1575 was detected is described hereinabove with reference to Figs. 2-8.

[22006] VGAM1575 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rhopalosiphum padi virus. VGAM1575 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[22007] VGAM1575 gene, herein designated VGAM GENE, encodes a VGAM1575 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1575 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1575 precursor RNA is designated SEQ ID:1561, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1561 is located at position 923 relative to the genome of Rhopalosiphum padi virus.

[22008] VGAM1575 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1575 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22009] An enzyme complex designated DICER COMPLEX, dices the VGAM1575 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1575 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 71%) nucleotide sequence of VGAM1575 RNA is designated SEQ ID:4286, and is provided hereinbelow with reference to the sequence listing part.

[22010] VGAM1575 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1575 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1575 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding

gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22011] VGAM1575 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1575 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1575 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1575 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1575 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be lo-

cated in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22012] The complementary binding of VGAM1575 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1575 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1575 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1575 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[22013] It is appreciated that VGAM1575 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1575 host target genes. The mRNA of each one of this plurality of VGAM1575 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1575 RNA, herein designated VGAM RNA, and which when bound by VGAM1575 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1575 host target proteins.

[22014] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM1575 gene, herein designated VGAM GENE, on one or more VGAM1575 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22015] It is yet further appreciated that a function of VGAM1575 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1575 include diagnosis, prevention and treatment of viral infection by Rhopalosiphum padi virus. Specific functions, and accordingly utilities, of VGAM1575 correlate with, and may be deduced from, the identity of the host target genes which VGAM1575 binds and in-

hibits, and the function of these host target genes, as elaborated hereinbelow.

[22016] Nucleotide sequences of the VGAM1575 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1575 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1575 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1575 are further described hereinbelow with reference to Table 1.

[22017] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1575 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[22018] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1576 (VGAM1576) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[22019] VGAM1576 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1576 was detected is described hereinabove with reference to Figs. 2-8.

[22020] VGAM1576 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rhopalosiphum padi virus. VGAM1576 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[22021] VGAM1576 gene, herein designated VGAM GENE, encodes a VGAM1576 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1576 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1576 precursor RNA is designated SEQ ID:1562, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1562 is located at position 3322 relative to the genome of Rhopalosiphum padi virus.

[22022] VGAM1576 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1576 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22023] An enzyme complex designated DICER COMPLEX, dices the VGAM1576 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1576 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM1576 RNA is designated SEQ ID:4287, and is provided hereinbelow with reference to the sequence listing part.

[22024] VGAM1576 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1576 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1576 host target RNA, herein designated VGAM HOST TARGET RNA, comprises

three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22025] VGAM1576 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1576 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1576 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1576 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1576 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an

example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22026] The complementary binding of VGAM1576 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1576 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1576 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1576 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[22027] It is appreciated that VGAM1576 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1576 host target genes. The mRNA of each one of this plurality of VGAM1576 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1576 RNA, herein designated VGAM RNA, and which when bound by VGAM1576 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1576 host target proteins.

[22028] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1576 gene, herein designated VGAM GENE, on one or more VGAM1576 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22029] It is yet further appreciated that a function of VGAM1576 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1576 include diagnosis, prevention and treatment of viral infection by Rhopalosiphum padi virus. Specific functions, and accordingly utilities, of VGAM1576 correlate with, and may be deduced from, the identity of

the host target genes which VGAM1576 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[22030] Nucleotide sequences of the VGAM1576 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1576 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1576 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1576 are further described hereinbelow with reference to Table 1.

[22031] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1576 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[22032] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1577 (VGAM1577) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[22033] VGAM1577 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1577 was detected is described hereinabove with reference to Figs. 2-8.

[22034] VGAM1577 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rhopalosiphum padi virus. VGAM1577 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[22035] VGAM1577 gene, herein designated VGAM GENE, encodes a VGAM1577 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1577 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1577 precursor RNA is designated SEQ ID:1563, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1563 is located at position 2545 relative to the genome of Rhopalosiphum padi virus.

[22036] VGAM1577 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1577 folded precursor RNA, herein designated VGAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22037] An enzyme complex designated DICER COMPLEX, dices the VGAM1577 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1577 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 90%) nucleotide sequence of VGAM1577 RNA is designated SEQ ID:4288, and is provided hereinbelow with reference to the sequence listing part.

[22038] VGAM1577 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1577 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1577 host target RNA,

herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22039] VGAM1577 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1577 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1577 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1577 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1577 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host tar-

get binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22040] The complementary binding of VGAM1577 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1577 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1577 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1577 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[22041] It is appreciated that VGAM1577 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1577 host target genes. The mRNA of each one of this plurality of VGAM1577 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1577 RNA, herein designated VGAM RNA, and which when bound by VGAM1577 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1577 host target proteins.

[22042] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1577 gene, herein designated VGAM GENE, on one or more VGAM1577 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22043] It is yet further appreciated that a function of VGAM1577 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1577 include diagnosis, prevention and treatment of viral infection by Rhopalosiphum padi virus. Specific functions, and accordingly utilities, of VGAM1577

correlate with, and may be deduced from, the identity of the host target genes which VGAM1577 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[22044] Nucleotide sequences of the VGAM1577 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1577 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1577 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1577 are further described hereinbelow with reference to Table 1.

[22045] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1577 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[22046] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1578 (VGAM1578) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the

art.

[22047] VGAM1578 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1578 was detected is described hereinabove with reference to Figs. 2-8.

[22048] VGAM1578 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rhopalosiphum padi virus. VGAM1578 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[22049] VGAM1578 gene, herein designated VGAM GENE, encodes a VGAM1578 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1578 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1578 precursor RNA is designated SEQ ID:1564, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1564 is located at position 3984 relative to the genome of Rhopalosiphum padi virus.

[22050] VGAM1578 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1578 folded

precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22051] An enzyme complex designated DICER COMPLEX, dices the VGAM1578 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1578 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM1578 RNA is designated SEQ ID:4289, and is provided hereinbelow with reference to the sequence listing part.

[22052] VGAM1578 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1578 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM1578 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22053] VGAM1578 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1578 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1578 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1578 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1578 host target RNA, herein designated VGAM HOST TARGET RNA.

It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22054] The complementary binding of VGAM1578 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1578 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1578 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1578 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[22055] It is appreciated that VGAM1578 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1578 host target genes. The mRNA of each one of this plurality of VGAM1578 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1578 RNA, herein designated VGAM RNA, and which when bound by VGAM1578 RNA, herein designated VGAM RNA, causes inhibition of translation of

respective one or more VGAM1578 host target proteins.

[22056] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1578 gene, herein designated VGAM GENE, on one or more VGAM1578 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22057] It is yet further appreciated that a function of VGAM1578 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1578 include diagnosis, prevention and treatment of viral infection by Rhopalosiphum padi virus.

Specific functions, and accordingly utilities, of VGAM1578 correlate with, and may be deduced from, the identity of the host target genes which VGAM1578 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[22058] Nucleotide sequences of the VGAM1578 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1578 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1578 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1578 are further described hereinbelow with reference to Table 1.

[22059] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1578 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[22060] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1579 (VGAM1579) viral gene, which modulates expression of respective host target genes thereof, the func-

tion and utility of which host target genes is known in the art.

[22061] VGAM1579 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1579 was detected is described hereinabove with reference to Figs. 2-8.

[22062] VGAM1579 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rhopalosiphum padi virus. VGAM1579 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[22063] VGAM1579 gene, herein designated VGAM GENE, encodes a VGAM1579 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1579 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1579 precursor RNA is designated SEQ ID:1565, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1565 is located at position 8880 relative to the genome of Rhopalosiphum padi virus.

[22064] VGAM1579 precursor RNA, herein designated VGAM PRE-

CURSOR RNA, folds onto itself, forming VGAM1579 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22065] An enzyme complex designated DICER COMPLEX, dices the VGAM1579 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1579 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM1579 RNA is designated SEQ ID:4290, and is provided hereinbelow with reference to the sequence listing part.

[22066] VGAM1579 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM1579 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1579 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22067] VGAM1579 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1579 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1579 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1579 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1579 host

target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22068] The complementary binding of VGAM1579 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1579 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1579 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1579 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[22069] It is appreciated that VGAM1579 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1579 host target genes. The mRNA of each one of this plurality of VGAM1579 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1579 RNA, herein designated VGAM RNA, and which when bound by VGAM1579 RNA, herein

designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1579 host target proteins.

[22070] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1579 gene, herein designated VGAM GENE, on one or more VGAM1579 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22071] It is yet further appreciated that a function of VGAM1579 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1579 include diagnosis, prevention and

treatment of viral infection by Rhopalosiphum padi virus. Specific functions, and accordingly utilities, of VGAM1579 correlate with, and may be deduced from, the identity of the host target genes which VGAM1579 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[22072] Nucleotide sequences of the VGAM1579 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1579 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1579 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1579 are further described hereinbelow with reference to Table 1.

[22073] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1579 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[22074] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1580 (VGAM1580) viral gene, which modulates ex-

pression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[22075] VGAM1580 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1580 was detected is described hereinabove with reference to Figs. 2-8.

[22076] VGAM1580 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rhopalosiphum padi virus. VGAM1580 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[22077] VGAM1580 gene, herein designated VGAM GENE, encodes a VGAM1580 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1580 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1580 precursor RNA is designated SEQ ID:1566, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1566 is located at position 8018 relative to the genome of Rhopalosiphum padi virus.

[22078] VGAM1580 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1580 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22079] An enzyme complex designated DICER COMPLEX, dices the VGAM1580 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1580 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of VGAM1580 RNA is designated SEQ ID:4291, and is provided hereinbelow with reference to the sequence listing part.

[22080] VGAM1580 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1580 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1580 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22081] VGAM1580 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1580 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1580 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1580 RNA, herein designated VGAM RNA, may have a different number of host target

binding sites in untranslated regions of a VGAM1580 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22082] The complementary binding of VGAM1580 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1580 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1580 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1580 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[22083] It is appreciated that VGAM1580 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1580 host target genes. The mRNA of each one of this plurality of VGAM1580 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1580 RNA, herein designated VGAM

RNA, and which when bound by VGAM1580 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1580 host target proteins.

[22084] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1580 gene, herein designated VGAM GENE, on one or more VGAM1580 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22085] It is yet further appreciated that a function of VGAM1580 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM1580 include diagnosis, prevention and treatment of viral infection by Rhopalosiphum padi virus. Specific functions, and accordingly utilities, of VGAM1580 correlate with, and may be deduced from, the identity of the host target genes which VGAM1580 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[22086] Nucleotide sequences of the VGAM1580 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1580 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1580 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1580 are further described hereinbelow with reference to Table 1.

[22087] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1580 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[22088] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Mes-

senger 1581 (VGAM1581) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[22089] VGAM1581 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1581 was detected is described hereinabove with reference to Figs. 2-8.

[22090] VGAM1581 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Saimiriine herpesvirus 2. VGAM1581 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[22091] VGAM1581 gene, herein designated VGAM GENE, encodes a VGAM1581 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1581 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1581 precursor RNA is designated SEQ ID:1567, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1567 is located at position

94704 relative to the genome of Saimiriine herpesvirus 2.

[22092] VGAM1581 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1581 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22093] An enzyme complex designated DICER COMPLEX, dices the VGAM1581 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1581 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 57%) nucleotide sequence of VGAM1581 RNA is designated SEQ ID:4292, and is provided hereinbelow with reference to the sequence listing part.

[22094] VGAM1581 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1581 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1581 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22095] VGAM1581 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1581 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1581 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1581 RNA, herein designated

VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1581 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22096] The complementary binding of VGAM1581 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1581 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1581 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1581 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[22097] It is appreciated that VGAM1581 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1581 host target genes. The mRNA of each one of this plurality of VGAM1581 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM1581 RNA, herein designated VGAM RNA, and which when bound by VGAM1581 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1581 host target proteins.

[22098] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1581 gene, herein designated VGAM GENE, on one or more VGAM1581 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22099] It is yet further appreciated that a function of VGAM1581 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1581 include diagnosis, prevention and treatment of viral infection by Saimiriine herpesvirus 2. Specific functions, and accordingly utilities, of VGAM1581 correlate with, and may be deduced from, the identity of the host target genes which VGAM1581 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[22100] Nucleotide sequences of the VGAM1581 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1581 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1581 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1581 are further described hereinbelow with reference to Table 1.

[22101] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1581 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[22102] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present

invention, referred to here as Viral Genomic Address Messenger 1582 (VGAM1582) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[22103] VGAM1582 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1582 was detected is described hereinabove with reference to Figs. 2-8.

[22104] VGAM1582 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Saimiriine herpesvirus 2. VGAM1582 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[22105] VGAM1582 gene, herein designated VGAM GENE, encodes a VGAM1582 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1582 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1582 precursor RNA is designated SEQ ID:1568, and is provided hereinbelow with reference to the sequence listing part. Nu-

cleotide sequence SEQ ID:1568 is located at position 90201 relative to the genome of Saimiriine herpesvirus 2.

[22106] VGAM1582 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1582 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22107] An enzyme complex designated DICER COMPLEX, dices the VGAM1582 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1582 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM1582 RNA is designated SEQ ID:4293, and is provided hereinbelow with reference to the sequence

listing part.

[22108] VGAM1582 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1582 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1582 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22109] VGAM1582 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1582 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1582 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not

meant to be limiting VGAM1582 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1582 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22110] The complementary binding of VGAM1582 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1582 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1582 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1582 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[22111] It is appreciated that VGAM1582 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1582 host target genes. The mRNA of each one of this plurality of VGAM1582 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM1582 RNA, herein designated VGAM RNA, and which when bound by VGAM1582 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1582 host target proteins.

[22112] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1582 gene, herein designated VGAM GENE, on one or more VGAM1582 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22113] It is yet further appreciated that a function of VGAM1582

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1582 include diagnosis, prevention and treatment of viral infection by Saimiriine herpesvirus 2. Specific functions, and accordingly utilities, of VGAM1582 correlate with, and may be deduced from, the identity of the host target genes which VGAM1582 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[22114] Nucleotide sequences of the VGAM1582 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1582 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1582 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1582 are further described hereinbelow with reference to Table 1.

[22115] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1582 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[22116] Fig. 1 further provides a conceptual description of another

novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1583 (VGAM1583) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[22117] VGAM1583 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1583 was detected is described hereinabove with reference to Figs. 2-8.

[22118] VGAM1583 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Saimiriine herpesvirus 2. VGAM1583 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[22119] VGAM1583 gene, herein designated VGAM GENE, encodes a VGAM1583 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1583 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1583 precursor RNA is designated SEQ ID:1569, and is provided here-

inbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1569 is located at position 93157 relative to the genome of Saimiriine herpesvirus 2.

[22120] VGAM1583 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1583 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22121] An enzyme complex designated DICER COMPLEX, dices the VGAM1583 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1583 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 63%) nucleotide sequence of VGAM1583 RNA is designated SEQ ID:4294, and

is provided hereinbelow with reference to the sequence listing part.

[22122] VGAM1583 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1583 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1583 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22123] VGAM1583 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1583 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1583 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites

shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1583 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1583 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22124] The complementary binding of VGAM1583 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1583 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1583 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1583 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[22125] It is appreciated that VGAM1583 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1583 host target genes. The mRNA of each one of this plurality of VGAM1583 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1583 RNA, herein designated VGAM RNA, and which when bound by VGAM1583 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1583 host target proteins.

[22126] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1583 gene, herein designated VGAM GENE, on one or more VGAM1583 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22127] It is yet further appreciated that a function of VGAM1583 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1583 include diagnosis, prevention and treatment of viral infection by Saimiriine herpesvirus 2. Specific functions, and accordingly utilities, of VGAM1583 correlate with, and may be deduced from, the identity of the host target genes which VGAM1583 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[22128] Nucleotide sequences of the VGAM1583 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1583 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1583 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1583 are further described hereinbelow with reference to Table 1.

[22129] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1583 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[22130] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1584 (VGAM1584) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[22131] VGAM1584 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1584 was detected is described hereinabove with reference to Figs. 2-8.

[22132] VGAM1584 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Saimiriine herpesvirus 2. VGAM1584 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[22133] VGAM1584 gene, herein designated VGAM GENE, encodes a VGAM1584 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1584 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1584 precur-

sor RNA is designated SEQ ID:1570, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1570 is located at position 91273 relative to the genome of Saimiriine herpesvirus 2.

[22134] VGAM1584 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1584 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22135] An enzyme complex designated DICER COMPLEX, dices the VGAM1584 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1584 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 56%) nucleotide se-

quence of VGAM1584 RNA is designated SEQ ID:4295, and is provided hereinbelow with reference to the sequence listing part.

[22136] VGAM1584 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1584 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1584 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22137] VGAM1584 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1584 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1584 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is ap-

preciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1584 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1584 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22138] The complementary binding of VGAM1584 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1584 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1584 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1584 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[22139] It is appreciated that VGAM1584 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1584 host target genes. The mRNA of

each one of this plurality of VGAM1584 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1584 RNA, herein designated VGAM RNA, and which when bound by VGAM1584 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1584 host target proteins.

[22140] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1584 gene, herein designated VGAM GENE, on one or more VGAM1584 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science

294,779 (2001)).

[22141] It is yet further appreciated that a function of VGAM1584 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1584 include diagnosis, prevention and treatment of viral infection by Saimiriine herpesvirus 2. Specific functions, and accordingly utilities, of VGAM1584 correlate with, and may be deduced from, the identity of the host target genes which VGAM1584 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[22142] Nucleotide sequences of the VGAM1584 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1584 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1584 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1584 are further described hereinbelow with reference to Table 1.

[22143] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1584 RNA, herein designated VGAM RNA, are de-

scribed hereinbelow with reference to Table 2.

[22144] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1585 (VGAM1585) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[22145] VGAM1585 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1585 was detected is described hereinabove with reference to Figs. 2-8.

[22146] VGAM1585 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Saimiriine herpesvirus 2. VGAM1585 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[22147] VGAM1585 gene, herein designated VGAM GENE, encodes a VGAM1585 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1585 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly

similar to the nucleotide sequence of VGAM1585 precursor RNA is designated SEQ ID:1571, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1571 is located at position 87716 relative to the genome of Saimiriine herpesvirus 2.

[22148] VGAM1585 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1585 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22149] An enzyme complex designated DICER COMPLEX, dices the VGAM1585 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1585 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 48%) nucleotide sequence of VGAM1585 RNA is designated SEQ ID:4296, and is provided hereinbelow with reference to the sequence listing part.

[22150] VGAM1585 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1585 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1585 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22151] VGAM1585 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1585 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1585 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I,

BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1585 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1585 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22152] The complementary binding of VGAM1585 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1585 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1585 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1585 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[22153] It is appreciated that VGAM1585 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM1585 host target genes. The mRNA of each one of this plurality of VGAM1585 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1585 RNA, herein designated VGAM RNA, and which when bound by VGAM1585 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1585 host target proteins.

[22154] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1585 gene, herein designated VGAM GENE, on one or more VGAM1585 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22155] It is yet further appreciated that a function of VGAM1585 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1585 include diagnosis, prevention and treatment of viral infection by Saimiriine herpesvirus 2. Specific functions, and accordingly utilities, of VGAM1585 correlate with, and may be deduced from, the identity of the host target genes which VGAM1585 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[22156] Nucleotide sequences of the VGAM1585 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1585 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1585 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1585 are further described hereinbelow with reference to Table 1.

[22157] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites

to VGAM1585 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[22158] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1586 (VGAM1586) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[22159] VGAM1586 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1586 was detected is described hereinabove with reference to Figs. 2-8.

[22160] VGAM1586 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Saimiriine herpesvirus 2. VGAM1586 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[22161] VGAM1586 gene, herein designated VGAM GENE, encodes a VGAM1586 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1586 precursor RNA, herein designated VGAM PRECURSOR RNA, does not en-

code a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1586 precursor RNA is designated SEQ ID:1572, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1572 is located at position 86610 relative to the genome of Saimiriine herpesvirus 2.

[22162] VGAM1586 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1586 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22163] An enzyme complex designated DICER COMPLEX, dices the VGAM1586 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1586 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 74%) nucleotide sequence of VGAM1586 RNA is designated SEQ ID:4297, and is provided hereinbelow with reference to the sequence listing part.

[22164] VGAM1586 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1586 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1586 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22165] VGAM1586 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1586 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1586 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3

such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1586 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1586 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22166] The complementary binding of VGAM1586 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1586 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1586 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1586 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[22167] It is appreciated that VGAM1586 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1586 host target genes. The mRNA of each one of this plurality of VGAM1586 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1586 RNA, herein designated VGAM RNA, and which when bound by VGAM1586 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1586 host target proteins.

[22168] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1586 gene, herein designated VGAM GENE, on one or more VGAM1586 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22169] It is yet further appreciated that a function of VGAM1586 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1586 include diagnosis, prevention and treatment of viral infection by Saimiriine herpesvirus 2. Specific functions, and accordingly utilities, of VGAM1586 correlate with, and may be deduced from, the identity of the host target genes which VGAM1586 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[22170] Nucleotide sequences of the VGAM1586 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1586 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1586 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1586 are further described hereinbelow with reference to Table 1.

[22171] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the

complementarity of each of these host target binding sites to VGAM1586 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[22172] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1587 (VGAM1587) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[22173] VGAM1587 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1587 was detected is described hereinabove with reference to Figs. 2-8.

[22174] VGAM1587 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Saimiriine herpesvirus 2. VGAM1587 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[22175] VGAM1587 gene, herein designated VGAM GENE, encodes a VGAM1587 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1587 precursor RNA,

herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1587 precursor RNA is designated SEQ ID:1573, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1573 is located at position 93438 relative to the genome of Saimiriine herpesvirus 2.

[22176] VGAM1587 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1587 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22177] An enzyme complex designated DICER COMPLEX, dices the VGAM1587 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1587 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM1587 RNA is designated SEQ ID:4298, and is provided hereinbelow with reference to the sequence listing part.

[22178] VGAM1587 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1587 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1587 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22179] VGAM1587 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1587 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1587 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host

target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1587 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1587 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22180] The complementary binding of VGAM1587 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1587 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1587 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1587 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[22181] It is appreciated that VGAM1587 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1587 host target genes. The mRNA of each one of this plurality of VGAM1587 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1587 RNA, herein designated VGAM RNA, and which when bound by VGAM1587 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1587 host target proteins.

[22182] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1587 gene, herein designated VGAM GENE, on one or more VGAM1587 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22183] It is yet further appreciated that a function of VGAM1587 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1587 include diagnosis, prevention and treatment of viral infection by Saimiriine herpesvirus 2. Specific functions, and accordingly utilities, of VGAM1587 correlate with, and may be deduced from, the identity of the host target genes which VGAM1587 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[22184] Nucleotide sequences of the VGAM1587 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1587 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1587 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1587 are further described hereinbelow with reference to Table 1.

[22185] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1587 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[22186] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1588 (VGAM1588) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[22187] VGAM1588 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1588 was detected is described hereinabove with reference to Figs. 2-8.

[22188] VGAM1588 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Saimiriine herpesvirus 2. VGAM1588 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[22189] VGAM1588 gene, herein designated VGAM GENE, encodes a VGAM1588 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and un-

like most ordinary genes, VGAM1588 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1588 precursor RNA is designated SEQ ID:1574, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1574 is located at position 90393 relative to the genome of Saimiriine herpesvirus 2.

[22190] VGAM1588 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1588 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22191] An enzyme complex designated DICER COMPLEX, dices the VGAM1588 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1588 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM1588 RNA is designated SEQ ID:4299, and is provided hereinbelow with reference to the sequence listing part.

[22192] VGAM1588 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1588 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1588 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22193] VGAM1588 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1588 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1588 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed

sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1588 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1588 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22194] The complementary binding of VGAM1588 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1588 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1588 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1588 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target

protein is therefore outlined by a broken line.

[22195] It is appreciated that VGAM1588 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1588 host target genes. The mRNA of each one of this plurality of VGAM1588 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1588 RNA, herein designated VGAM RNA, and which when bound by VGAM1588 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1588 host target proteins.

[22196] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1588 gene, herein designated VGAM GENE, on one or more VGAM1588 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22197] It is yet further appreciated that a function of VGAM1588 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1588 include diagnosis, prevention and treatment of viral infection by Saimiriine herpesvirus 2. Specific functions, and accordingly utilities, of VGAM1588 correlate with, and may be deduced from, the identity of the host target genes which VGAM1588 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[22198] Nucleotide sequences of the VGAM1588 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1588 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1588 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1588 are further described hereinbelow with reference to Table 1.

[22199] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1588 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[22200] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1589 (VGAM1589) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[22201] VGAM1589 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1589 was detected is described hereinabove with reference to Figs. 2-8.

[22202] VGAM1589 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ateline herpesvirus 3. VGAM1589 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[22203] VGAM1589 gene, herein designated VGAM GENE, encodes a VGAM1589 precursor RNA, herein designated VGAM

PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1589 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1589 precursor RNA is designated SEQ ID:1575, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1575 is located at position 88982 relative to the genome of Ateline herpesvirus 3.

[22204] VGAM1589 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1589 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22205] An enzyme complex designated DICER COMPLEX, dices the VGAM1589 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1589 RNA, herein designated VGAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 52%) nucleotide sequence of VGAM1589 RNA is designated SEQ ID:4300, and is provided hereinbelow with reference to the sequence listing part.

[22206] VGAM1589 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1589 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1589 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22207] VGAM1589 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1589 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1589 RNA, herein designated

VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1589 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1589 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22208] The complementary binding of VGAM1589 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1589 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1589 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1589 host target protein, herein desig-

nated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[22209] It is appreciated that VGAM1589 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1589 host target genes. The mRNA of each one of this plurality of VGAM1589 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1589 RNA, herein designated VGAM RNA, and which when bound by VGAM1589 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1589 host target proteins.

[22210] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1589 gene, herein designated VGAM GENE, on one or more VGAM1589 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22211] It is yet further appreciated that a function of VGAM1589 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1589 include diagnosis, prevention and treatment of viral infection by Ateline herpesvirus 3. Specific functions, and accordingly utilities, of VGAM1589 correlate with, and may be deduced from, the identity of the host target genes which VGAM1589 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[22212] Nucleotide sequences of the VGAM1589 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1589 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1589 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1589 are further described hereinbelow with reference to Table 1.

[22213] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1589 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[22214] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1590 (VGAM1590) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[22215] VGAM1590 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1590 was detected is described hereinabove with reference to Figs. 2-8.

[22216] VGAM1590 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ateline herpesvirus 3. VGAM1590 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[22217] VGAM1590 gene, herein designated VGAM GENE, encodes

a VGAM1590 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1590 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1590 precursor RNA is designated SEQ ID:1576, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1576 is located at position 91163 relative to the genome of Ateline herpesvirus 3.

[22218] VGAM1590 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1590 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22219] An enzyme complex designated DICER COMPLEX, dices the VGAM1590 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1590 RNA,

herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM1590 RNA is designated SEQ ID:4301, and is provided hereinbelow with reference to the sequence listing part.

[22220] VGAM1590 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1590 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1590 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22221] VGAM1590 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1590 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM1590 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1590 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1590 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22222] The complementary binding of VGAM1590 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1590 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1590 host target RNA, herein designated VGAM HOST TARGET

RNA, into VGAM1590 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[22223] It is appreciated that VGAM1590 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1590 host target genes. The mRNA of each one of this plurality of VGAM1590 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1590 RNA, herein designated VGAM RNA, and which when bound by VGAM1590 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1590 host target proteins.

[22224] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1590 gene, herein designated VGAM GENE, on one or more VGAM1590 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22225] It is yet further appreciated that a function of VGAM1590 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1590 include diagnosis, prevention and treatment of viral infection by Ateline herpesvirus 3. Specific functions, and accordingly utilities, of VGAM1590 correlate with, and may be deduced from, the identity of the host target genes which VGAM1590 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[22226] Nucleotide sequences of the VGAM1590 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1590 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1590 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1590 are further

described hereinbelow with reference to Table 1.

[22227] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1590 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[22228] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1591 (VGAM1591) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[22229] VGAM1591 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1591 was detected is described hereinabove with reference to Figs. 2-8.

[22230] VGAM1591 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ateline herpesvirus 3. VGAM1591 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[22231] VGAM1591 gene, herein designated VGAM GENE, encodes a VGAM1591 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1591 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1591 precursor RNA is designated SEQ ID:1577, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1577 is located at position 90226 relative to the genome of Ateline herpesvirus 3.

[22232] VGAM1591 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1591 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22233] An enzyme complex designated DICER COMPLEX, dices the VGAM1591 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, into VGAM1591 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 66%) nucleotide sequence of VGAM1591 RNA is designated SEQ ID:4302, and is provided hereinbelow with reference to the sequence listing part.

[22234] VGAM1591 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1591 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1591 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22235] VGAM1591 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1591 host target RNA, herein designated VGAM HOST TARGET RNA. This

complementary binding is due to the fact that the nucleotide sequence of VGAM1591 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1591 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1591 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22236] The complementary binding of VGAM1591 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1591 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1591

host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1591 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[22237] It is appreciated that VGAM1591 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1591 host target genes. The mRNA of each one of this plurality of VGAM1591 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1591 RNA, herein designated VGAM RNA, and which when bound by VGAM1591 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1591 host target proteins.

[22238] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1591 gene, herein designated VGAM GENE, on one or more VGAM1591 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22239] It is yet further appreciated that a function of VGAM1591 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1591 include diagnosis, prevention and treatment of viral infection by Ateline herpesvirus 3. Specific functions, and accordingly utilities, of VGAM1591 correlate with, and may be deduced from, the identity of the host target genes which VGAM1591 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[22240] Nucleotide sequences of the VGAM1591 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1591 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1591 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM1591 are further described hereinbelow with reference to Table 1.

[22241] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1591 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[22242] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1592 (VGAM1592) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[22243] VGAM1592 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1592 was detected is described hereinabove with reference to Figs. 2-8.

[22244] VGAM1592 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ateline herpesvirus 3. VGAM1592 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the

human genome.

[22245] VGAM1592 gene, herein designated VGAM GENE, encodes a VGAM1592 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1592 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1592 precursor RNA is designated SEQ ID:1578, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1578 is located at position 89710 relative to the genome of Ateline herpesvirus 3.

[22246] VGAM1592 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1592 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22247] An enzyme complex designated DICER COMPLEX, dices

the VGAM1592 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1592 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM1592 RNA is designated SEQ ID:4303, and is provided hereinbelow with reference to the sequence listing part.

[22248] VGAM1592 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1592 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1592 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22249] VGAM1592 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1592 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1592 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1592 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1592 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22250] The complementary binding of VGAM1592 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1592 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM1592 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1592 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[22251] It is appreciated that VGAM1592 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1592 host target genes. The mRNA of each one of this plurality of VGAM1592 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1592 RNA, herein designated VGAM RNA, and which when bound by VGAM1592 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1592 host target proteins.

[22252] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1592 gene, herein designated VGAM GENE, on one or more VGAM1592 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22253] It is yet further appreciated that a function of VGAM1592 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1592 include diagnosis, prevention and treatment of viral infection by Ateline herpesvirus 3. Specific functions, and accordingly utilities, of VGAM1592 correlate with, and may be deduced from, the identity of the host target genes which VGAM1592 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[22254] Nucleotide sequences of the VGAM1592 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1592 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of

VGAM1592 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1592 are further described hereinbelow with reference to Table 1.

[22255] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1592 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[22256] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1593 (VGAM1593) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[22257] VGAM1593 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1593 was detected is described hereinabove with reference to Figs. 2-8.

[22258] VGAM1593 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ateline herpesvirus 3. VGAM1593 host target gene, herein designated VGAM

HOST TARGET GENE, is a human gene contained in the human genome.

[22259] VGAM1593 gene, herein designated VGAM GENE, encodes a VGAM1593 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1593 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1593 precursor RNA is designated SEQ ID:1579, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1579 is located at position 86183 relative to the genome of Ateline herpesvirus 3.

[22260] VGAM1593 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1593 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22261] An enzyme complex designated DICER COMPLEX, dices the VGAM1593 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1593 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of VGAM1593 RNA is designated SEQ ID:4304, and is provided hereinbelow with reference to the sequence listing part.

[22262] VGAM1593 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1593 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1593 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22263] VGAM1593 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites

located in untranslated regions of VGAM1593 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1593 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1593 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1593 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22264] The complementary binding of VGAM1593 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1593 host target RNA, herein designated VGAM

HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1593 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1593 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[22265] It is appreciated that VGAM1593 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1593 host target genes. The mRNA of each one of this plurality of VGAM1593 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1593 RNA, herein designated VGAM RNA, and which when bound by VGAM1593 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1593 host target proteins.

[22266] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1593 gene, herein designated VGAM GENE, on one or more VGAM1593 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove

with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22267] It is yet further appreciated that a function of VGAM1593 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1593 include diagnosis, prevention and treatment of viral infection by Ateline herpesvirus 3. Specific functions, and accordingly utilities, of VGAM1593 correlate with, and may be deduced from, the identity of the host target genes which VGAM1593 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[22268] Nucleotide sequences of the VGAM1593 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1593 RNA, herein designated VGAM RNA, and

a schematic representation of the secondary folding of VGAM1593 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1593 are further described hereinbelow with reference to Table 1.

[22269] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1593 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[22270] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1594 (VGAM1594) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[22271] VGAM1594 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1594 was detected is described hereinabove with reference to Figs. 2-8.

[22272] VGAM1594 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Leek yellow stripe po-

tyvirus. VGAM1594 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[22273] VGAM1594 gene, herein designated VGAM GENE, encodes a VGAM1594 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1594 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1594 precursor RNA is designated SEQ ID:1580, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1580 is located at position 10003 relative to the genome of Leek yellow stripe potyvirus.

[22274] VGAM1594 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1594 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22275] An enzyme complex designated DICER COMPLEX, dices the VGAM1594 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1594 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 76%) nucleotide sequence of VGAM1594 RNA is designated SEQ ID:4305, and is provided hereinbelow with reference to the sequence listing part.

[22276] VGAM1594 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1594 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1594 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22277] VGAM1594 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1594 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1594 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1594 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1594 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22278] The complementary binding of VGAM1594 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM1594 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1594 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1594 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[22279] It is appreciated that VGAM1594 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1594 host target genes. The mRNA of each one of this plurality of VGAM1594 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1594 RNA, herein designated VGAM RNA, and which when bound by VGAM1594 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1594 host target proteins.

[22280] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1594 gene, herein designated VGAM GENE, on one or more VGAM1594 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22281] It is yet further appreciated that a function of VGAM1594 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1594 include diagnosis, prevention and treatment of viral infection by Leek yellow stripe potyvirus. Specific functions, and accordingly utilities, of VGAM1594 correlate with, and may be deduced from, the identity of the host target genes which VGAM1594 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[22282] Nucleotide sequences of the VGAM1594 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the diced VGAM1594 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1594 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1594 are further described hereinbelow with reference to Table 1.

[22283] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1594 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[22284] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1595 (VGAM1595) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[22285] VGAM1595 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1595 was detected is described hereinabove with reference to Figs. 2-8.

[22286] VGAM1595 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Leek yellow stripe potyvirus. VGAM1595 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[22287] VGAM1595 gene, herein designated VGAM GENE, encodes a VGAM1595 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1595 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1595 precursor RNA is designated SEQ ID:1581, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1581 is located at position 6252 relative to the genome of Leek yellow stripe potyvirus.

[22288] VGAM1595 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1595 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22289] An enzyme complex designated DICER COMPLEX, dices the VGAM1595 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1595 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM1595 RNA is designated SEQ ID:4306, and is provided hereinbelow with reference to the sequence listing part.

[22290] VGAM1595 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1595 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1595 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN COD-

ING and 3UTR respectively.

[22291] VGAM1595 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1595 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1595 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1595 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1595 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22292] The complementary binding of VGAM1595 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1595 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1595 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1595 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[22293] It is appreciated that VGAM1595 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1595 host target genes. The mRNA of each one of this plurality of VGAM1595 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1595 RNA, herein designated VGAM RNA, and which when bound by VGAM1595 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1595 host target proteins.

[22294] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1595 gene, herein designated VGAM GENE, on one

or more VGAM1595 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22295] It is yet further appreciated that a function of VGAM1595 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1595 include diagnosis, prevention and treatment of viral infection by Leek yellow stripe potyvirus. Specific functions, and accordingly utilities, of VGAM1595 correlate with, and may be deduced from, the identity of the host target genes which VGAM1595 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[22296] Nucleotide sequences of the VGAM1595 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1595 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1595 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1595 are further described hereinbelow with reference to Table 1.

[22297] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1595 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[22298] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1596 (VGAM1596) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[22299] VGAM1596 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1596 was detected is de-

scribed hereinabove with reference to Figs. 2-8.

[22300] VGAM1596 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Leek yellow stripe potyvirus. VGAM1596 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[22301] VGAM1596 gene, herein designated VGAM GENE, encodes a VGAM1596 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1596 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1596 precursor RNA is designated SEQ ID:1582, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1582 is located at position 3823 relative to the genome of Leek yellow stripe potyvirus.

[22302] VGAM1596 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1596 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22303] An enzyme complex designated DICER COMPLEX, dices the VGAM1596 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1596 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM1596 RNA is designated SEQ ID:4307, and is provided hereinbelow with reference to the sequence listing part.

[22304] VGAM1596 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1596 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1596 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and

a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22305] VGAM1596 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1596 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1596 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1596 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1596 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both

3UTR and 5UTR regions.

[22306] The complementary binding of VGAM1596 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1596 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1596 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1596 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[22307] It is appreciated that VGAM1596 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1596 host target genes. The mRNA of each one of this plurality of VGAM1596 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1596 RNA, herein designated VGAM RNA, and which when bound by VGAM1596 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1596 host target proteins.

[22308] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM1596 gene, herein designated VGAM GENE, on one or more VGAM1596 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22309] It is yet further appreciated that a function of VGAM1596 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1596 include diagnosis, prevention and treatment of viral infection by Leek yellow stripe potyvirus. Specific functions, and accordingly utilities, of VGAM1596 correlate with, and may be deduced from, the identity of the host target genes which VGAM1596 binds and inhibits, and the function of these host target genes,

as elaborated hereinbelow.

[22310] Nucleotide sequences of the VGAM1596 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1596 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1596 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1596 are further described hereinbelow with reference to Table 1.

[22311] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1596 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[22312] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1597 (VGAM1597) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[22313] VGAM1597 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene.

The method by which VGAM1597 was detected is described hereinabove with reference to Figs. 2-8.

[22314] VGAM1597 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Leek yellow stripe potyvirus. VGAM1597 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[22315] VGAM1597 gene, herein designated VGAM GENE, encodes a VGAM1597 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1597 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1597 precursor RNA is designated SEQ ID:1583, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1583 is located at position 5446 relative to the genome of Leek yellow stripe potyvirus.

[22316] VGAM1597 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1597 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22317] An enzyme complex designated DICER COMPLEX, dices the VGAM1597 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1597 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 73%) nucleotide sequence of VGAM1597 RNA is designated SEQ ID:4308, and is provided hereinbelow with reference to the sequence listing part.

[22318] VGAM1597 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1597 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1597 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding

gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22319] VGAM1597 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1597 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1597 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1597 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1597 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be lo-

cated in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22320] The complementary binding of VGAM1597 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1597 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1597 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1597 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[22321] It is appreciated that VGAM1597 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1597 host target genes. The mRNA of each one of this plurality of VGAM1597 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1597 RNA, herein designated VGAM RNA, and which when bound by VGAM1597 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1597 host target proteins.

[22322] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM1597 gene, herein designated VGAM GENE, on one or more VGAM1597 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22323] It is yet further appreciated that a function of VGAM1597 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1597 include diagnosis, prevention and treatment of viral infection by Leek yellow stripe potyvirus. Specific functions, and accordingly utilities, of VGAM1597 correlate with, and may be deduced from, the identity of the host target genes which VGAM1597 binds

and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[22324] Nucleotide sequences of the VGAM1597 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1597 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1597 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1597 are further described hereinbelow with reference to Table 1.

[22325] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1597 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[22326] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1598 (VGAM1598) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[22327] VGAM1598 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1598 was detected is described hereinabove with reference to Figs. 2-8.

[22328] VGAM1598 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human adenovirus E. VGAM1598 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[22329] VGAM1598 gene, herein designated VGAM GENE, encodes a VGAM1598 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1598 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1598 precursor RNA is designated SEQ ID:1584, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1584 is located at position 32869 relative to the genome of Human adenovirus E.

[22330] VGAM1598 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1598 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22331] An enzyme complex designated DICER COMPLEX, dices the VGAM1598 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1598 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM1598 RNA is designated SEQ ID:4309, and is provided hereinbelow with reference to the sequence listing part.

[22332] VGAM1598 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1598 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1598 host target RNA, herein designated VGAM HOST TARGET RNA, comprises

three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22333] VGAM1598 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1598 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1598 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1598 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1598 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an

example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22334] The complementary binding of VGAM1598 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1598 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1598 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1598 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[22335] It is appreciated that VGAM1598 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1598 host target genes. The mRNA of each one of this plurality of VGAM1598 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1598 RNA, herein designated VGAM RNA, and which when bound by VGAM1598 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1598 host target proteins.

[22336] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1598 gene, herein designated VGAM GENE, on one or more VGAM1598 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22337] It is yet further appreciated that a function of VGAM1598 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1598 include diagnosis, prevention and treatment of viral infection by Human adenovirus E. Specific functions, and accordingly utilities, of VGAM1598 correlate with, and may be deduced from, the identity of

the host target genes which VGAM1598 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[22338] Nucleotide sequences of the VGAM1598 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1598 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1598 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1598 are further described hereinbelow with reference to Table 1.

[22339] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1598 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[22340] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1599 (VGAM1599) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[22341] VGAM1599 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1599 was detected is described hereinabove with reference to Figs. 2-8.

[22342] VGAM1599 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human adenovirus E. VGAM1599 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[22343] VGAM1599 gene, herein designated VGAM GENE, encodes a VGAM1599 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1599 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1599 precursor RNA is designated SEQ ID:1585, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1585 is located at position 24788 relative to the genome of Human adenovirus E.

[22344] VGAM1599 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1599 folded precursor RNA, herein designated VGAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22345] An enzyme complex designated DICER COMPLEX, dices the VGAM1599 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1599 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM1599 RNA is designated SEQ ID:4310, and is provided hereinbelow with reference to the sequence listing part.

[22346] VGAM1599 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1599 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1599 host target RNA,

herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22347] VGAM1599 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1599 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1599 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1599 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1599 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host tar-

get binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22348] The complementary binding of VGAM1599 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1599 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1599 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1599 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[22349] It is appreciated that VGAM1599 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1599 host target genes. The mRNA of each one of this plurality of VGAM1599 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1599 RNA, herein designated VGAM RNA, and which when bound by VGAM1599 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1599 host target proteins.

[22350] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1599 gene, herein designated VGAM GENE, on one or more VGAM1599 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22351] It is yet further appreciated that a function of VGAM1599 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1599 include diagnosis, prevention and treatment of viral infection by Human adenovirus E. Specific functions, and accordingly utilities, of VGAM1599

correlate with, and may be deduced from, the identity of the host target genes which VGAM1599 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[22352] Nucleotide sequences of the VGAM1599 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1599 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1599 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1599 are further described hereinbelow with reference to Table 1.

[22353] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1599 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[22354] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1600 (VGAM1600) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the

art.

[22355] VGAM1600 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1600 was detected is described hereinabove with reference to Figs. 2-8.

[22356] VGAM1600 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human adenovirus E. VGAM1600 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[22357] VGAM1600 gene, herein designated VGAM GENE, encodes a VGAM1600 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1600 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1600 precursor RNA is designated SEQ ID:1586, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1586 is located at position 23495 relative to the genome of Human adenovirus E.

[22358] VGAM1600 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1600 folded

precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22359] An enzyme complex designated DICER COMPLEX, dices the VGAM1600 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1600 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM1600 RNA is designated SEQ ID:4311, and is provided hereinbelow with reference to the sequence listing part.

[22360] VGAM1600 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1600 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM1600 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22361] VGAM1600 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1600 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1600 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1600 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1600 host target RNA, herein designated VGAM HOST TARGET RNA.

It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22362] The complementary binding of VGAM1600 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1600 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1600 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1600 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[22363] It is appreciated that VGAM1600 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1600 host target genes. The mRNA of each one of this plurality of VGAM1600 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1600 RNA, herein designated VGAM RNA, and which when bound by VGAM1600 RNA, herein designated VGAM RNA, causes inhibition of translation of

respective one or more VGAM1600 host target proteins.

[22364] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1600 gene, herein designated VGAM GENE, on one or more VGAM1600 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22365] It is yet further appreciated that a function of VGAM1600 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1600 include diagnosis, prevention and treatment of viral infection by Human adenovirus E. Spe-

cific functions, and accordingly utilities, of VGAM1600 correlate with, and may be deduced from, the identity of the host target genes which VGAM1600 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[22366] Nucleotide sequences of the VGAM1600 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1600 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1600 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1600 are further described hereinbelow with reference to Table 1.

[22367] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1600 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[22368] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1601 (VGAM1601) viral gene, which modulates expression of respective host target genes thereof, the func-

tion and utility of which host target genes is known in the art.

[22369] VGAM1601 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1601 was detected is described hereinabove with reference to Figs. 2-8.

[22370] VGAM1601 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human adenovirus E. VGAM1601 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[22371] VGAM1601 gene, herein designated VGAM GENE, encodes a VGAM1601 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1601 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1601 precursor RNA is designated SEQ ID:1587, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1587 is located at position 32517 relative to the genome of Human adenovirus E.

[22372] VGAM1601 precursor RNA, herein designated VGAM PRE-

CURSOR RNA, folds onto itself, forming VGAM1601 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22373] An enzyme complex designated DICER COMPLEX, dices the VGAM1601 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1601 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 65%) nucleotide sequence of VGAM1601 RNA is designated SEQ ID:4312, and is provided hereinbelow with reference to the sequence listing part.

[22374] VGAM1601 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM1601 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1601 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22375] VGAM1601 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1601 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1601 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1601 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1601 host

target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22376] The complementary binding of VGAM1601 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1601 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1601 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1601 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[22377] It is appreciated that VGAM1601 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1601 host target genes. The mRNA of each one of this plurality of VGAM1601 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1601 RNA, herein designated VGAM RNA, and which when bound by VGAM1601 RNA, herein

designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1601 host target proteins.

[22378] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1601 gene, herein designated VGAM GENE, on one or more VGAM1601 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22379] It is yet further appreciated that a function of VGAM1601 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1601 include diagnosis, prevention and

treatment of viral infection by Human adenovirus E. Specific functions, and accordingly utilities, of VGAM1601 correlate with, and may be deduced from, the identity of the host target genes which VGAM1601 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[22380] Nucleotide sequences of the VGAM1601 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1601 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1601 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1601 are further described hereinbelow with reference to Table 1.

[22381] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1601 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[22382] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1602 (VGAM1602) viral gene, which modulates ex-

pression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[22383] VGAM1602 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1602 was detected is described hereinabove with reference to Figs. 2-8.

[22384] VGAM1602 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human adenovirus E. VGAM1602 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[22385] VGAM1602 gene, herein designated VGAM GENE, encodes a VGAM1602 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1602 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1602 precursor RNA is designated SEQ ID:1588, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1588 is located at position 27497 relative to the genome of Human adenovirus E.

[22386] VGAM1602 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1602 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22387] An enzyme complex designated DICER COMPLEX, dices the VGAM1602 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1602 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 90%) nucleotide sequence of VGAM1602 RNA is designated SEQ ID:4313, and is provided hereinbelow with reference to the sequence listing part.

[22388] VGAM1602 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1602 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1602 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22389] VGAM1602 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1602 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1602 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1602 RNA, herein designated VGAM RNA, may have a different number of host target

binding sites in untranslated regions of a VGAM1602 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22390] The complementary binding of VGAM1602 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1602 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1602 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1602 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[22391] It is appreciated that VGAM1602 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1602 host target genes. The mRNA of each one of this plurality of VGAM1602 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1602 RNA, herein designated VGAM

RNA, and which when bound by VGAM1602 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1602 host target proteins.

[22392] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1602 gene, herein designated VGAM GENE, on one or more VGAM1602 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22393] It is yet further appreciated that a function of VGAM1602 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM1602 include diagnosis, prevention and treatment of viral infection by Human adenovirus E. Specific functions, and accordingly utilities, of VGAM1602 correlate with, and may be deduced from, the identity of the host target genes which VGAM1602 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[22394] Nucleotide sequences of the VGAM1602 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1602 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1602 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1602 are further described hereinbelow with reference to Table 1.

[22395] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1602 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[22396] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Mes-

senger 1603 (VGAM1603) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[22397] VGAM1603 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1603 was detected is described hereinabove with reference to Figs. 2-8.

[22398] VGAM1603 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Taura syndrome virus. VGAM1603 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[22399] VGAM1603 gene, herein designated VGAM GENE, encodes a VGAM1603 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1603 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1603 precursor RNA is designated SEQ ID:1589, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1589 is located at position 4189

relative to the genome of Taura syndrome virus.

[22400] VGAM1603 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1603 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22401] An enzyme complex designated DICER COMPLEX, dices the VGAM1603 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1603 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM1603 RNA is designated SEQ ID:4314, and is provided hereinbelow with reference to the sequence listing part.

[22402] VGAM1603 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1603 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1603 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22403] VGAM1603 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1603 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1603 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1603 RNA, herein designated

VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1603 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22404] The complementary binding of VGAM1603 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1603 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1603 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1603 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[22405] It is appreciated that VGAM1603 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1603 host target genes. The mRNA of each one of this plurality of VGAM1603 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM1603 RNA, herein designated VGAM RNA, and which when bound by VGAM1603 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1603 host target proteins.

[22406] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1603 gene, herein designated VGAM GENE, on one or more VGAM1603 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22407] It is yet further appreciated that a function of VGAM1603 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1603 include diagnosis, prevention and treatment of viral infection by Taura syndrome virus. Specific functions, and accordingly utilities, of VGAM1603 correlate with, and may be deduced from, the identity of the host target genes which VGAM1603 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[22408] Nucleotide sequences of the VGAM1603 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1603 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1603 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1603 are further described hereinbelow with reference to Table 1.

[22409] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1603 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[22410] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present

invention, referred to here as Viral Genomic Address Messenger 1604 (VGAM1604) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[22411] VGAM1604 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1604 was detected is described hereinabove with reference to Figs. 2-8.

[22412] VGAM1604 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Taura syndrome virus. VGAM1604 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[22413] VGAM1604 gene, herein designated VGAM GENE, encodes a VGAM1604 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1604 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1604 precursor RNA is designated SEQ ID:1590, and is provided hereinbelow with reference to the sequence listing part. Nu-

cleotide sequence SEQ ID:1590 is located at position 2524 relative to the genome of Taura syndrome virus.

[22414] VGAM1604 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1604 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22415] An enzyme complex designated DICER COMPLEX, dices the VGAM1604 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1604 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM1604 RNA is designated SEQ ID:4315, and is provided hereinbelow with reference to the sequence

listing part.

[22416] VGAM1604 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1604 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1604 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22417] VGAM1604 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1604 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1604 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not

meant to be limiting VGAM1604 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1604 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22418] The complementary binding of VGAM1604 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1604 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1604 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1604 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[22419] It is appreciated that VGAM1604 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1604 host target genes. The mRNA of each one of this plurality of VGAM1604 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM1604 RNA, herein designated VGAM RNA, and which when bound by VGAM1604 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1604 host target proteins.

[22420] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1604 gene, herein designated VGAM GENE, on one or more VGAM1604 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22421] It is yet further appreciated that a function of VGAM1604

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1604 include diagnosis, prevention and treatment of viral infection by Taura syndrome virus. Specific functions, and accordingly utilities, of VGAM1604 correlate with, and may be deduced from, the identity of the host target genes which VGAM1604 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[22422] Nucleotide sequences of the VGAM1604 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1604 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1604 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1604 are further described hereinbelow with reference to Table 1.

[22423] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1604 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[22424] Fig. 1 further provides a conceptual description of another

novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1605 (VGAM1605) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[22425] VGAM1605 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1605 was detected is described hereinabove with reference to Figs. 2-8.

[22426] VGAM1605 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Taura syndrome virus. VGAM1605 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[22427] VGAM1605 gene, herein designated VGAM GENE, encodes a VGAM1605 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1605 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1605 precursor RNA is designated SEQ ID:1591, and is provided here-

inbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1591 is located at position 8483 relative to the genome of Taura syndrome virus.

[22428] VGAM1605 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1605 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22429] An enzyme complex designated DICER COMPLEX, dices the VGAM1605 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1605 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM1605 RNA is designated SEQ ID:4316, and

is provided hereinbelow with reference to the sequence listing part.

[22430] VGAM1605 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1605 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1605 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22431] VGAM1605 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1605 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1605 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites

shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1605 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1605 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22432] The complementary binding of VGAM1605 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1605 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1605 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1605 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[22433] It is appreciated that VGAM1605 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1605 host target genes. The mRNA of each one of this plurality of VGAM1605 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1605 RNA, herein designated VGAM RNA, and which when bound by VGAM1605 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1605 host target proteins.

[22434] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1605 gene, herein designated VGAM GENE, on one or more VGAM1605 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22435] It is yet further appreciated that a function of VGAM1605 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1605 include diagnosis, prevention and treatment of viral infection by Taura syndrome virus. Specific functions, and accordingly utilities, of VGAM1605 correlate with, and may be deduced from, the identity of the host target genes which VGAM1605 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[22436] Nucleotide sequences of the VGAM1605 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1605 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1605 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1605 are further described hereinbelow with reference to Table 1.

[22437] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1605 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[22438] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1606 (VGAM1606) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[22439] VGAM1606 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1606 was detected is described hereinabove with reference to Figs. 2-8.

[22440] VGAM1606 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Taura syndrome virus. VGAM1606 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[22441] VGAM1606 gene, herein designated VGAM GENE, encodes

a VGAM1606 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1606 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1606 precursor RNA is designated SEQ ID:1592, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1592 is located at position 7811 relative to the genome of Taura syndrome virus.

[22442] VGAM1606 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1606 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22443] An enzyme complex designated DICER COMPLEX, dices the VGAM1606 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1606 RNA,

herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM1606 RNA is designated SEQ ID:4317, and is provided hereinbelow with reference to the sequence listing part.

[22444] VGAM1606 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1606 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1606 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22445] VGAM1606 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1606 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM1606 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1606 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1606 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22446] The complementary binding of VGAM1606 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1606 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1606 host target RNA, herein designated VGAM HOST TARGET

RNA, into VGAM1606 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[22447] It is appreciated that VGAM1606 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1606 host target genes. The mRNA of each one of this plurality of VGAM1606 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1606 RNA, herein designated VGAM RNA, and which when bound by VGAM1606 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1606 host target proteins.

[22448] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1606 gene, herein designated VGAM GENE, on one or more VGAM1606 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22449] It is yet further appreciated that a function of VGAM1606 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1606 include diagnosis, prevention and treatment of viral infection by Taura syndrome virus. Specific functions, and accordingly utilities, of VGAM1606 correlate with, and may be deduced from, the identity of the host target genes which VGAM1606 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[22450] Nucleotide sequences of the VGAM1606 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1606 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1606 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1606 are further

described hereinbelow with reference to Table 1.

[22451] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1606 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[22452] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1607 (VGAM1607) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[22453] VGAM1607 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1607 was detected is described hereinabove with reference to Figs. 2-8.

[22454] VGAM1607 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Taura syndrome virus. VGAM1607 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[22455] VGAM1607 gene, herein designated VGAM GENE, encodes a VGAM1607 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1607 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1607 precursor RNA is designated SEQ ID:1593, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1593 is located at position 567 relative to the genome of Taura syndrome virus.

[22456] VGAM1607 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1607 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22457] An enzyme complex designated DICER COMPLEX, dices the VGAM1607 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, into VGAM1607 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of VGAM1607 RNA is designated SEQ ID:4318, and is provided hereinbelow with reference to the sequence listing part.

[22458] VGAM1607 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1607 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1607 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22459] VGAM1607 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1607 host target RNA, herein designated VGAM HOST TARGET RNA. This

complementary binding is due to the fact that the nucleotide sequence of VGAM1607 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1607 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1607 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22460] The complementary binding of VGAM1607 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1607 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1607

host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1607 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[22461] It is appreciated that VGAM1607 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1607 host target genes. The mRNA of each one of this plurality of VGAM1607 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1607 RNA, herein designated VGAM RNA, and which when bound by VGAM1607 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1607 host target proteins.

[22462] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1607 gene, herein designated VGAM GENE, on one or more VGAM1607 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22463] It is yet further appreciated that a function of VGAM1607 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1607 include diagnosis, prevention and treatment of viral infection by Taura syndrome virus. Specific functions, and accordingly utilities, of VGAM1607 correlate with, and may be deduced from, the identity of the host target genes which VGAM1607 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[22464] Nucleotide sequences of the VGAM1607 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1607 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1607 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM1607 are further described hereinbelow with reference to Table 1.

[22465] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1607 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[22466] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1608 (VGAM1608) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[22467] VGAM1608 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1608 was detected is described hereinabove with reference to Figs. 2-8.

[22468] VGAM1608 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Taura syndrome virus. VGAM1608 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the

human genome.

[22469] VGAM1608 gene, herein designated VGAM GENE, encodes a VGAM1608 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1608 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1608 precursor RNA is designated SEQ ID:1594, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1594 is located at position 3052 relative to the genome of Taura syndrome virus.

[22470] VGAM1608 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1608 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22471] An enzyme complex designated DICER COMPLEX, dices

the VGAM1608 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1608 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 48%) nucleotide sequence of VGAM1608 RNA is designated SEQ ID:4319, and is provided hereinbelow with reference to the sequence listing part.

[22472] VGAM1608 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1608 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1608 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22473] VGAM1608 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1608 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1608 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1608 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1608 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22474] The complementary binding of VGAM1608 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1608 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM1608 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1608 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[22475] It is appreciated that VGAM1608 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1608 host target genes. The mRNA of each one of this plurality of VGAM1608 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1608 RNA, herein designated VGAM RNA, and which when bound by VGAM1608 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1608 host target proteins.

[22476] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1608 gene, herein designated VGAM GENE, on one or more VGAM1608 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22477] It is yet further appreciated that a function of VGAM1608 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1608 include diagnosis, prevention and treatment of viral infection by Taura syndrome virus. Specific functions, and accordingly utilities, of VGAM1608 correlate with, and may be deduced from, the identity of the host target genes which VGAM1608 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[22478] Nucleotide sequences of the VGAM1608 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1608 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of

VGAM1608 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1608 are further described hereinbelow with reference to Table 1.

[22479] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1608 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[22480] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1609 (VGAM1609) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[22481] VGAM1609 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1609 was detected is described hereinabove with reference to Figs. 2-8.

[22482] VGAM1609 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Chimpanzee cytomegalovirus. VGAM1609 host target gene, herein desig-

nated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[22483] VGAM1609 gene, herein designated VGAM GENE, encodes a VGAM1609 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1609 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1609 precursor RNA is designated SEQ ID:1595, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1595 is located at position 8708 relative to the genome of Chimpanzee cytomegalovirus.

[22484] VGAM1609 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1609 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22485] An enzyme complex designated DICER COMPLEX, dices the VGAM1609 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1609 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM1609 RNA is designated SEQ ID:4320, and is provided hereinbelow with reference to the sequence listing part.

[22486] VGAM1609 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1609 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1609 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22487] VGAM1609 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites

located in untranslated regions of VGAM1609 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1609 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1609 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1609 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22488] The complementary binding of VGAM1609 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1609 host target RNA, herein designated VGAM

HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1609 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1609 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[22489] It is appreciated that VGAM1609 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1609 host target genes. The mRNA of each one of this plurality of VGAM1609 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1609 RNA, herein designated VGAM RNA, and which when bound by VGAM1609 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1609 host target proteins.

[22490] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1609 gene, herein designated VGAM GENE, on one or more VGAM1609 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove

with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22491] It is yet further appreciated that a function of VGAM1609 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1609 include diagnosis, prevention and treatment of viral infection by Chimpanzee cytomegalovirus. Specific functions, and accordingly utilities, of VGAM1609 correlate with, and may be deduced from, the identity of the host target genes which VGAM1609 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[22492] Nucleotide sequences of the VGAM1609 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1609 RNA, herein designated VGAM RNA, and

a schematic representation of the secondary folding of VGAM1609 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1609 are further described hereinbelow with reference to Table 1.

[22493] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1609 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[22494] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1610 (VGAM1610) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[22495] VGAM1610 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1610 was detected is described hereinabove with reference to Figs. 2-8.

[22496] VGAM1610 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Chimpanzee cy-

tomegalovirus. VGAM1610 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[22497] VGAM1610 gene, herein designated VGAM GENE, encodes a VGAM1610 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1610 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1610 precursor RNA is designated SEQ ID:1596, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1596 is located at position 5615 relative to the genome of Chimpanzee cytomegalovirus.

[22498] VGAM1610 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1610 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[22499] An enzyme complex designated DICER COMPLEX, dices the VGAM1610 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1610 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM1610 RNA is designated SEQ ID:4321, and is provided hereinbelow with reference to the sequence listing part.

[22500] VGAM1610 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1610 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1610 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22501] VGAM1610 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM1610 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1610 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1610 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1610 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22502] The complementary binding of VGAM1610 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM1610 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1610 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1610 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[22503] It is appreciated that VGAM1610 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1610 host target genes. The mRNA of each one of this plurality of VGAM1610 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1610 RNA, herein designated VGAM RNA, and which when bound by VGAM1610 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1610 host target proteins.

[22504] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1610 gene, herein designated VGAM GENE, on one or more VGAM1610 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22505] It is yet further appreciated that a function of VGAM1610 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1610 include diagnosis, prevention and treatment of viral infection by Chimpanzee cytomegalovirus. Specific functions, and accordingly utilities, of VGAM1610 correlate with, and may be deduced from, the identity of the host target genes which VGAM1610 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[22506] Nucleotide sequences of the VGAM1610 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

diced VGAM1610 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1610 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1610 are further described hereinbelow with reference to Table 1.

[22507] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1610 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[22508] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1611 (VGAM1611) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[22509] VGAM1611 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1611 was detected is described hereinabove with reference to Figs. 2-8.

[22510] VGAM1611 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of Chimpanzee cytomegalovirus. VGAM1611 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[22511] VGAM1611 gene, herein designated VGAM GENE, encodes a VGAM1611 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1611 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1611 precursor RNA is designated SEQ ID:1597, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1597 is located at position 10114 relative to the genome of Chimpanzee cytomegalovirus.

[22512] VGAM1611 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1611 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22513] An enzyme complex designated DICER COMPLEX, dices the VGAM1611 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1611 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM1611 RNA is designated SEQ ID:4322, and is provided hereinbelow with reference to the sequence listing part.

[22514] VGAM1611 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1611 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1611 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN COD-

ING and 3UTR respectively.

[22515] VGAM1611 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1611 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1611 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1611 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1611 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22516] The complementary binding of VGAM1611 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1611 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1611 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1611 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[22517] It is appreciated that VGAM1611 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1611 host target genes. The mRNA of each one of this plurality of VGAM1611 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1611 RNA, herein designated VGAM RNA, and which when bound by VGAM1611 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1611 host target proteins.

[22518] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1611 gene, herein designated VGAM GENE, on one

or more VGAM1611 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22519] It is yet further appreciated that a function of VGAM1611 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1611 include diagnosis, prevention and treatment of viral infection by Chimpanzee cytomegalovirus. Specific functions, and accordingly utilities, of VGAM1611 correlate with, and may be deduced from, the identity of the host target genes which VGAM1611 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[22520] Nucleotide sequences of the VGAM1611 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1611 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1611 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1611 are further described hereinbelow with reference to Table 1.

[22521] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1611 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[22522] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1612 (VGAM1612) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[22523] VGAM1612 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1612 was detected is de-

scribed hereinabove with reference to Figs. 2-8.

[22524] VGAM1612 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Chimpanzee cytomegalovirus. VGAM1612 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[22525] VGAM1612 gene, herein designated VGAM GENE, encodes a VGAM1612 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1612 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1612 precursor RNA is designated SEQ ID:1598, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1598 is located at position 1800 relative to the genome of Chimpanzee cytomegalovirus.

[22526] VGAM1612 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1612 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22527] An enzyme complex designated DICER COMPLEX, dices the VGAM1612 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1612 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM1612 RNA is designated SEQ ID:4323, and is provided hereinbelow with reference to the sequence listing part.

[22528] VGAM1612 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1612 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1612 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and

a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22529] VGAM1612 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1612 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1612 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1612 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1612 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both

3UTR and 5UTR regions.

[22530] The complementary binding of VGAM1612 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1612 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1612 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1612 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[22531] It is appreciated that VGAM1612 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1612 host target genes. The mRNA of each one of this plurality of VGAM1612 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1612 RNA, herein designated VGAM RNA, and which when bound by VGAM1612 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1612 host target proteins.

[22532] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM1612 gene, herein designated VGAM GENE, on one or more VGAM1612 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22533] It is yet further appreciated that a function of VGAM1612 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1612 include diagnosis, prevention and treatment of viral infection by Chimpanzee cytomegalovirus. Specific functions, and accordingly utilities, of VGAM1612 correlate with, and may be deduced from, the identity of the host target genes which VGAM1612 binds and inhibits, and the function of these

host target genes, as elaborated hereinbelow.

[22534] Nucleotide sequences of the VGAM1612 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1612 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1612 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1612 are further described hereinbelow with reference to Table 1.

[22535] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1612 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[22536] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1613 (VGAM1613) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[22537] VGAM1613 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene.

The method by which VGAM1613 was detected is described hereinabove with reference to Figs. 2-8.

[22538] VGAM1613 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Chimpanzee cytomegalovirus. VGAM1613 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[22539] VGAM1613 gene, herein designated VGAM GENE, encodes a VGAM1613 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1613 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1613 precursor RNA is designated SEQ ID:1599, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1599 is located at position 4267 relative to the genome of Chimpanzee cytomegalovirus.

[22540] VGAM1613 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1613 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22541] An enzyme complex designated DICER COMPLEX, dices the VGAM1613 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1613 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 67%) nucleotide sequence of VGAM1613 RNA is designated SEQ ID:4324, and is provided hereinbelow with reference to the sequence listing part.

[22542] VGAM1613 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1613 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1613 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding

gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22543] VGAM1613 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1613 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1613 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1613 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1613 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be lo-

cated in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22544] The complementary binding of VGAM1613 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1613 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1613 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1613 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[22545] It is appreciated that VGAM1613 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1613 host target genes. The mRNA of each one of this plurality of VGAM1613 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1613 RNA, herein designated VGAM RNA, and which when bound by VGAM1613 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1613 host target proteins.

[22546] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM1613 gene, herein designated VGAM GENE, on one or more VGAM1613 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22547] It is yet further appreciated that a function of VGAM1613 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1613 include diagnosis, prevention and treatment of viral infection by Chimpanzee cytomegalovirus. Specific functions, and accordingly utilities, of VGAM1613 correlate with, and may be deduced from, the identity of the host target genes which

VGAM1613 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[22548] Nucleotide sequences of the VGAM1613 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1613 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1613 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1613 are further described hereinbelow with reference to Table 1.

[22549] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1613 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[22550] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1614 (VGAM1614) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[22551] VGAM1614 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1614 was detected is described hereinabove with reference to Figs. 2-8.

[22552] VGAM1614 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Chimpanzee cytomegalovirus. VGAM1614 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[22553] VGAM1614 gene, herein designated VGAM GENE, encodes a VGAM1614 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1614 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1614 precursor RNA is designated SEQ ID:1600, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1600 is located at position 6443 relative to the genome of Chimpanzee cytomegalovirus.

[22554] VGAM1614 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1614 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22555] An enzyme complex designated DICER COMPLEX, dices the VGAM1614 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1614 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 72%) nucleotide sequence of VGAM1614 RNA is designated SEQ ID:4325, and is provided hereinbelow with reference to the sequence listing part.

[22556] VGAM1614 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1614 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1614 host target RNA, herein designated VGAM HOST TARGET RNA, comprises

three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22557] VGAM1614 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1614 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1614 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1614 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1614 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an

example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22558] The complementary binding of VGAM1614 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1614 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1614 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1614 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[22559] It is appreciated that VGAM1614 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1614 host target genes. The mRNA of each one of this plurality of VGAM1614 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1614 RNA, herein designated VGAM RNA, and which when bound by VGAM1614 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1614 host target proteins.

[22560] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1614 gene, herein designated VGAM GENE, on one or more VGAM1614 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22561] It is yet further appreciated that a function of VGAM1614 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1614 include diagnosis, prevention and treatment of viral infection by Chimpanzee cytomegalovirus. Specific functions, and accordingly utilities, of VGAM1614 correlate with, and may be deduced

from, the identity of the host target genes which VGAM1614 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[22562] Nucleotide sequences of the VGAM1614 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1614 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1614 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1614 are further described hereinbelow with reference to Table 1.

[22563] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1614 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[22564] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1615 (VGAM1615) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[22565] VGAM1615 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1615 was detected is described hereinabove with reference to Figs. 2-8.

[22566] VGAM1615 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Chimpanzee cytomegalovirus. VGAM1615 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[22567] VGAM1615 gene, herein designated VGAM GENE, encodes a VGAM1615 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1615 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1615 precursor RNA is designated SEQ ID:1601, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1601 is located at position 1492 relative to the genome of Chimpanzee cytomegalovirus.

[22568] VGAM1615 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1615 folded precursor RNA, herein designated VGAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22569] An enzyme complex designated DICER COMPLEX, dices the VGAM1615 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1615 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM1615 RNA is designated SEQ ID:4326, and is provided hereinbelow with reference to the sequence listing part.

[22570] VGAM1615 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1615 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1615 host target RNA,

herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22571] VGAM1615 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1615 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1615 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1615 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1615 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host tar-

get binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22572] The complementary binding of VGAM1615 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1615 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1615 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1615 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[22573] It is appreciated that VGAM1615 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1615 host target genes. The mRNA of each one of this plurality of VGAM1615 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1615 RNA, herein designated VGAM RNA, and which when bound by VGAM1615 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1615 host target proteins.

[22574] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1615 gene, herein designated VGAM GENE, on one or more VGAM1615 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22575] It is yet further appreciated that a function of VGAM1615 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1615 include diagnosis, prevention and treatment of viral infection by Chimpanzee cytomegalovirus. Specific functions, and accordingly utili-

ties, of VGAM1615 correlate with, and may be deduced from, the identity of the host target genes which VGAM1615 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[22576] Nucleotide sequences of the VGAM1615 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1615 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1615 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1615 are further described hereinbelow with reference to Table 1.

[22577] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1615 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[22578] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1616 (VGAM1616) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the

art.

[22579] VGAM1616 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1616 was detected is described hereinabove with reference to Figs. 2-8.

[22580] VGAM1616 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Chimpanzee cytomegalovirus. VGAM1616 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[22581] VGAM1616 gene, herein designated VGAM GENE, encodes a VGAM1616 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1616 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1616 precursor RNA is designated SEQ ID:1602, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1602 is located at position 2891 relative to the genome of Chimpanzee cytomegalovirus.

[22582] VGAM1616 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1616 folded

precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22583] An enzyme complex designated DICER COMPLEX, dices the VGAM1616 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1616 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM1616 RNA is designated SEQ ID:4327, and is provided hereinbelow with reference to the sequence listing part.

[22584] VGAM1616 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1616 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM1616 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22585] VGAM1616 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1616 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1616 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1616 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1616 host target RNA, herein designated VGAM HOST TARGET RNA.

It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22586] The complementary binding of VGAM1616 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1616 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1616 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1616 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[22587] It is appreciated that VGAM1616 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1616 host target genes. The mRNA of each one of this plurality of VGAM1616 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1616 RNA, herein designated VGAM RNA, and which when bound by VGAM1616 RNA, herein designated VGAM RNA, causes inhibition of translation of

respective one or more VGAM1616 host target proteins.

[22588] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1616 gene, herein designated VGAM GENE, on one or more VGAM1616 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22589] It is yet further appreciated that a function of VGAM1616 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1616 include diagnosis, prevention and treatment of viral infection by Chimpanzee cy-

tomegalovirus. Specific functions, and accordingly utilities, of VGAM1616 correlate with, and may be deduced from, the identity of the host target genes which VGAM1616 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[22590] Nucleotide sequences of the VGAM1616 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1616 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1616 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1616 are further described hereinbelow with reference to Table 1.

[22591] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1616 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[22592] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1617 (VGAM1617) viral gene, which modulates expression of respective host target genes thereof, the func-

tion and utility of which host target genes is known in the art.

[22593] VGAM1617 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1617 was detected is described hereinabove with reference to Figs. 2-8.

[22594] VGAM1617 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Fowl adenovirus D. VGAM1617 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[22595] VGAM1617 gene, herein designated VGAM GENE, encodes a VGAM1617 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1617 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1617 precursor RNA is designated SEQ ID:1603, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1603 is located at position 10492 relative to the genome of Fowl adenovirus D.

[22596] VGAM1617 precursor RNA, herein designated VGAM PRE-

CURSOR RNA, folds onto itself, forming VGAM1617 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22597] An enzyme complex designated DICER COMPLEX, dices the VGAM1617 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1617 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM1617 RNA is designated SEQ ID:4328, and is provided hereinbelow with reference to the sequence listing part.

[22598] VGAM1617 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM1617 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1617 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22599] VGAM1617 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1617 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1617 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1617 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1617 host

target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22600] The complementary binding of VGAM1617 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1617 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1617 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1617 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[22601] It is appreciated that VGAM1617 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1617 host target genes. The mRNA of each one of this plurality of VGAM1617 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1617 RNA, herein designated VGAM RNA, and which when bound by VGAM1617 RNA, herein

designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1617 host target proteins.

[22602] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1617 gene, herein designated VGAM GENE, on one or more VGAM1617 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22603] It is yet further appreciated that a function of VGAM1617 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1617 include diagnosis, prevention and

treatment of viral infection by Fowl adenovirus D. Specific functions, and accordingly utilities, of VGAM1617 correlate with, and may be deduced from, the identity of the host target genes which VGAM1617 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[22604] Nucleotide sequences of the VGAM1617 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1617 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1617 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1617 are further described hereinbelow with reference to Table 1.

[22605] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1617 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[22606] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1618 (VGAM1618) viral gene, which modulates ex-

pression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[22607] VGAM1618 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1618 was detected is described hereinabove with reference to Figs. 2-8.

[22608] VGAM1618 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Fowl adenovirus D. VGAM1618 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[22609] VGAM1618 gene, herein designated VGAM GENE, encodes a VGAM1618 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1618 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1618 precursor RNA is designated SEQ ID:1604, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1604 is located at position 5025 relative to the genome of Fowl adenovirus D.

[22610] VGAM1618 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1618 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22611] An enzyme complex designated DICER COMPLEX, dices the VGAM1618 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1618 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM1618 RNA is designated SEQ ID:4329, and is provided hereinbelow with reference to the sequence listing part.

[22612] VGAM1618 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1618 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1618 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22613] VGAM1618 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1618 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1618 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1618 RNA, herein designated VGAM RNA, may have a different number of host target

binding sites in untranslated regions of a VGAM1618 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22614] The complementary binding of VGAM1618 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1618 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1618 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1618 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[22615] It is appreciated that VGAM1618 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1618 host target genes. The mRNA of each one of this plurality of VGAM1618 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1618 RNA, herein designated VGAM

RNA, and which when bound by VGAM1618 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1618 host target proteins.

[22616] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1618 gene, herein designated VGAM GENE, on one or more VGAM1618 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22617] It is yet further appreciated that a function of VGAM1618 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM1618 include diagnosis, prevention and treatment of viral infection by Fowl adenovirus D. Specific functions, and accordingly utilities, of VGAM1618 correlate with, and may be deduced from, the identity of the host target genes which VGAM1618 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[22618] Nucleotide sequences of the VGAM1618 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1618 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1618 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1618 are further described hereinbelow with reference to Table 1.

[22619] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1618 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[22620] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Mes-

senger 1619 (VGAM1619) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[22621] VGAM1619 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1619 was detected is described hereinabove with reference to Figs. 2-8.

[22622] VGAM1619 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Fowl adenovirus D. VGAM1619 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[22623] VGAM1619 gene, herein designated VGAM GENE, encodes a VGAM1619 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1619 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1619 precursor RNA is designated SEQ ID:1605, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1605 is located at position 4810

relative to the genome of Fowl adenovirus D.

[22624] VGAM1619 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1619 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22625] An enzyme complex designated DICER COMPLEX, dices the VGAM1619 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1619 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM1619 RNA is designated SEQ ID:4330, and is provided hereinbelow with reference to the sequence listing part.

[22626] VGAM1619 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1619 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1619 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22627] VGAM1619 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1619 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1619 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1619 RNA, herein designated

VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1619 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22628] The complementary binding of VGAM1619 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1619 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1619 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1619 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[22629] It is appreciated that VGAM1619 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1619 host target genes. The mRNA of each one of this plurality of VGAM1619 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM1619 RNA, herein designated VGAM RNA, and which when bound by VGAM1619 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1619 host target proteins.

[22630] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1619 gene, herein designated VGAM GENE, on one or more VGAM1619 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22631] It is yet further appreciated that a function of VGAM1619 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1619 include diagnosis, prevention and treatment of viral infection by Fowl adenovirus D. Specific functions, and accordingly utilities, of VGAM1619 correlate with, and may be deduced from, the identity of the host target genes which VGAM1619 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[22632] Nucleotide sequences of the VGAM1619 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1619 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1619 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1619 are further described hereinbelow with reference to Table 1.

[22633] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1619 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[22634] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present

invention, referred to here as Viral Genomic Address Messenger 1620 (VGAM1620) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[22635] VGAM1620 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1620 was detected is described hereinabove with reference to Figs. 2-8.

[22636] VGAM1620 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Fowl adenovirus D. VGAM1620 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[22637] VGAM1620 gene, herein designated VGAM GENE, encodes a VGAM1620 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1620 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1620 precursor RNA is designated SEQ ID:1606, and is provided hereinbelow with reference to the sequence listing part. Nu-

cleotide sequence SEQ ID:1606 is located at position 9503 relative to the genome of Fowl adenovirus D.

[22638] VGAM1620 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1620 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22639] An enzyme complex designated DICER COMPLEX, dices the VGAM1620 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1620 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM1620 RNA is designated SEQ ID:4331, and is provided hereinbelow with reference to the sequence

listing part.

[22640] VGAM1620 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1620 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1620 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22641] VGAM1620 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1620 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1620 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not

meant to be limiting VGAM1620 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1620 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22642] The complementary binding of VGAM1620 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1620 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1620 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1620 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[22643] It is appreciated that VGAM1620 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1620 host target genes. The mRNA of each one of this plurality of VGAM1620 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM1620 RNA, herein designated VGAM RNA, and which when bound by VGAM1620 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1620 host target proteins.

[22644] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1620 gene, herein designated VGAM GENE, on one or more VGAM1620 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22645] It is yet further appreciated that a function of VGAM1620

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1620 include diagnosis, prevention and treatment of viral infection by Fowl adenovirus D. Specific functions, and accordingly utilities, of VGAM1620 correlate with, and may be deduced from, the identity of the host target genes which VGAM1620 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[22646] Nucleotide sequences of the VGAM1620 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1620 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1620 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1620 are further described hereinbelow with reference to Table 1.

[22647] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1620 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[22648] Fig. 1 further provides a conceptual description of another

novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1621 (VGAM1621) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[22649] VGAM1621 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1621 was detected is described hereinabove with reference to Figs. 2-8.

[22650] VGAM1621 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Fowl adenovirus D. VGAM1621 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[22651] VGAM1621 gene, herein designated VGAM GENE, encodes a VGAM1621 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1621 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1621 precursor RNA is designated SEQ ID:1607, and is provided here-

inbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1607 is located at position 4619 relative to the genome of Fowl adenovirus D.

[22652] VGAM1621 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1621 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22653] An enzyme complex designated DICER COMPLEX, dices the VGAM1621 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1621 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of VGAM1621 RNA is designated SEQ ID:4332, and

is provided hereinbelow with reference to the sequence listing part.

[22654] VGAM1621 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1621 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1621 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22655] VGAM1621 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1621 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1621 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites

shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1621 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1621 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22656] The complementary binding of VGAM1621 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1621 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1621 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1621 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[22657] It is appreciated that VGAM1621 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1621 host target genes. The mRNA of each one of this plurality of VGAM1621 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1621 RNA, herein designated VGAM RNA, and which when bound by VGAM1621 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1621 host target proteins.

[22658] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1621 gene, herein designated VGAM GENE, on one or more VGAM1621 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22659] It is yet further appreciated that a function of VGAM1621 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1621 include diagnosis, prevention and treatment of viral infection by Fowl adenovirus D. Specific functions, and accordingly utilities, of VGAM1621 correlate with, and may be deduced from, the identity of the host target genes which VGAM1621 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[22660] Nucleotide sequences of the VGAM1621 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1621 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1621 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1621 are further described hereinbelow with reference to Table 1.

[22661] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1621 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[22662] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1622 (VGAM1622) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[22663] VGAM1622 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1622 was detected is described hereinabove with reference to Figs. 2-8.

[22664] VGAM1622 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Bovine herpesvirus 4. VGAM1622 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[22665] VGAM1622 gene, herein designated VGAM GENE, encodes a VGAM1622 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1622 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1622 precur-

sor RNA is designated SEQ ID:1608, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1608 is located at position 87319 relative to the genome of Bovine herpesvirus 4.

[22666] VGAM1622 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1622 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22667] An enzyme complex designated DICER COMPLEX, dices the VGAM1622 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1622 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide se-

quence of VGAM1622 RNA is designated SEQ ID:4333, and is provided hereinbelow with reference to the sequence listing part.

[22668] VGAM1622 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1622 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1622 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22669] VGAM1622 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1622 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1622 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is ap-

preciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1622 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1622 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22670] The complementary binding of VGAM1622 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1622 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1622 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1622 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[22671] It is appreciated that VGAM1622 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1622 host target genes. The mRNA of

each one of this plurality of VGAM1622 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1622 RNA, herein designated VGAM RNA, and which when bound by VGAM1622 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1622 host target proteins.

[22672] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1622 gene, herein designated VGAM GENE, on one or more VGAM1622 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science

294,779 (2001)).

[22673] It is yet further appreciated that a function of VGAM1622 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1622 include diagnosis, prevention and treatment of viral infection by Bovine herpesvirus 4. Specific functions, and accordingly utilities, of VGAM1622 correlate with, and may be deduced from, the identity of the host target genes which VGAM1622 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[22674] Nucleotide sequences of the VGAM1622 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1622 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1622 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1622 are further described hereinbelow with reference to Table 1.

[22675] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1622 RNA, herein designated VGAM RNA, are de-

scribed hereinbelow with reference to Table 2.

[22676] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1623 (VGAM1623) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[22677] VGAM1623 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1623 was detected is described hereinabove with reference to Figs. 2-8.

[22678] VGAM1623 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Bovine herpesvirus 4. VGAM1623 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[22679] VGAM1623 gene, herein designated VGAM GENE, encodes a VGAM1623 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1623 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly

similar to the nucleotide sequence of VGAM1623 precursor RNA is designated SEQ ID:1609, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1609 is located at position 83968 relative to the genome of Bovine herpesvirus 4.

[22680] VGAM1623 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1623 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22681] An enzyme complex designated DICER COMPLEX, dices the VGAM1623 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1623 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 42%) nucleotide sequence of VGAM1623 RNA is designated SEQ ID:4334, and is provided hereinbelow with reference to the sequence listing part.

[22682] VGAM1623 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1623 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1623 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22683] VGAM1623 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1623 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1623 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I,

BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1623 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1623 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22684] The complementary binding of VGAM1623 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1623 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1623 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1623 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[22685] It is appreciated that VGAM1623 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM1623 host target genes. The mRNA of each one of this plurality of VGAM1623 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1623 RNA, herein designated VGAM RNA, and which when bound by VGAM1623 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1623 host target proteins.

[22686] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1623 gene, herein designated VGAM GENE, on one or more VGAM1623 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22687] It is yet further appreciated that a function of VGAM1623 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1623 include diagnosis, prevention and treatment of viral infection by Bovine herpesvirus 4. Specific functions, and accordingly utilities, of VGAM1623 correlate with, and may be deduced from, the identity of the host target genes which VGAM1623 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[22688] Nucleotide sequences of the VGAM1623 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1623 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1623 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1623 are further described hereinbelow with reference to Table 1.

[22689] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites

to VGAM1623 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[22690] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1624 (VGAM1624) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[22691] VGAM1624 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1624 was detected is described hereinabove with reference to Figs. 2-8.

[22692] VGAM1624 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Bovine herpesvirus 4. VGAM1624 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[22693] VGAM1624 gene, herein designated VGAM GENE, encodes a VGAM1624 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1624 precursor RNA, herein designated VGAM PRECURSOR RNA, does not en-

code a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1624 precursor RNA is designated SEQ ID:1610, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1610 is located at position 86638 relative to the genome of Bovine herpesvirus 4.

[22694] VGAM1624 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1624 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22695] An enzyme complex designated DICER COMPLEX, dices the VGAM1624 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1624 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 52%) nucleotide sequence of VGAM1624 RNA is designated SEQ ID:4335, and is provided hereinbelow with reference to the sequence listing part.

[22696] VGAM1624 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1624 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1624 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22697] VGAM1624 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1624 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1624 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3

such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1624 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1624 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22698] The complementary binding of VGAM1624 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1624 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1624 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1624 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[22699] It is appreciated that VGAM1624 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1624 host target genes. The mRNA of each one of this plurality of VGAM1624 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1624 RNA, herein designated VGAM RNA, and which when bound by VGAM1624 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1624 host target proteins.

[22700] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1624 gene, herein designated VGAM GENE, on one or more VGAM1624 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22701] It is yet further appreciated that a function of VGAM1624 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1624 include diagnosis, prevention and treatment of viral infection by Bovine herpesvirus 4. Specific functions, and accordingly utilities, of VGAM1624 correlate with, and may be deduced from, the identity of the host target genes which VGAM1624 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[22702] Nucleotide sequences of the VGAM1624 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1624 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1624 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1624 are further described hereinbelow with reference to Table 1.

[22703] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the

complementarity of each of these host target binding sites to VGAM1624 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[22704] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1625 (VGAM1625) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[22705] VGAM1625 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1625 was detected is described hereinabove with reference to Figs. 2-8.

[22706] VGAM1625 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Bovine herpesvirus 4. VGAM1625 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[22707] VGAM1625 gene, herein designated VGAM GENE, encodes a VGAM1625 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1625 precursor RNA,

herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1625 precursor RNA is designated SEQ ID:1611, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1611 is located at position 86511 relative to the genome of Bovine herpesvirus 4.

[22708] VGAM1625 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1625 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22709] An enzyme complex designated DICER COMPLEX, dices the VGAM1625 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1625 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM1625 RNA is designated SEQ ID:4336, and is provided hereinbelow with reference to the sequence listing part.

[22710] VGAM1625 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1625 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1625 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22711] VGAM1625 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1625 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1625 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host

target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1625 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1625 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22712] The complementary binding of VGAM1625 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1625 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1625 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1625 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[22713] It is appreciated that VGAM1625 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1625 host target genes. The mRNA of each one of this plurality of VGAM1625 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1625 RNA, herein designated VGAM RNA, and which when bound by VGAM1625 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1625 host target proteins.

[22714] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1625 gene, herein designated VGAM GENE, on one or more VGAM1625 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22715] It is yet further appreciated that a function of VGAM1625 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1625 include diagnosis, prevention and treatment of viral infection by Bovine herpesvirus 4. Specific functions, and accordingly utilities, of VGAM1625 correlate with, and may be deduced from, the identity of the host target genes which VGAM1625 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[22716] Nucleotide sequences of the VGAM1625 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1625 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1625 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1625 are further described hereinbelow with reference to Table 1.

[22717] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1625 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[22718] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1626 (VGAM1626) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[22719] VGAM1626 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1626 was detected is described hereinabove with reference to Figs. 2-8.

[22720] VGAM1626 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Bovine herpesvirus 4. VGAM1626 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[22721] VGAM1626 gene, herein designated VGAM GENE, encodes a VGAM1626 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and un-

like most ordinary genes, VGAM1626 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1626 precursor RNA is designated SEQ ID:1612, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1612 is located at position 80653 relative to the genome of Bovine herpesvirus 4.

[22722] VGAM1626 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1626 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22723] An enzyme complex designated DICER COMPLEX, dices the VGAM1626 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1626 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide sequence of VGAM1626 RNA is designated SEQ ID:4337, and is provided hereinbelow with reference to the sequence listing part.

[22724] VGAM1626 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1626 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1626 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22725] VGAM1626 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1626 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1626 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed

sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1626 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1626 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22726] The complementary binding of VGAM1626 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1626 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1626 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1626 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target

protein is therefore outlined by a broken line.

[22727] It is appreciated that VGAM1626 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1626 host target genes. The mRNA of each one of this plurality of VGAM1626 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1626 RNA, herein designated VGAM RNA, and which when bound by VGAM1626 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1626 host target proteins.

[22728] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1626 gene, herein designated VGAM GENE, on one or more VGAM1626 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22729] It is yet further appreciated that a function of VGAM1626 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1626 include diagnosis, prevention and treatment of viral infection by Bovine herpesvirus 4. Specific functions, and accordingly utilities, of VGAM1626 correlate with, and may be deduced from, the identity of the host target genes which VGAM1626 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[22730] Nucleotide sequences of the VGAM1626 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1626 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1626 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1626 are further described hereinbelow with reference to Table 1.

[22731] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1626 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[22732] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1627 (VGAM1627) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[22733] VGAM1627 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1627 was detected is described hereinabove with reference to Figs. 2-8.

[22734] VGAM1627 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Bovine herpesvirus 4. VGAM1627 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[22735] VGAM1627 gene, herein designated VGAM GENE, encodes a VGAM1627 precursor RNA, herein designated VGAM

PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1627 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1627 precursor RNA is designated SEQ ID:1613, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1613 is located at position 80799 relative to the genome of Bovine herpesvirus 4.

[22736] VGAM1627 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1627 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22737] An enzyme complex designated DICER COMPLEX, dices the VGAM1627 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1627 RNA, herein designated VGAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM1627 RNA is designated SEQ ID:4338, and is provided hereinbelow with reference to the sequence listing part.

[22738] VGAM1627 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1627 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1627 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22739] VGAM1627 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1627 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1627 RNA, herein designated

VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1627 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1627 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22740] The complementary binding of VGAM1627 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1627 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1627 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1627 host target protein, herein desig-

nated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[22741] It is appreciated that VGAM1627 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1627 host target genes. The mRNA of each one of this plurality of VGAM1627 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1627 RNA, herein designated VGAM RNA, and which when bound by VGAM1627 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1627 host target proteins.

[22742] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1627 gene, herein designated VGAM GENE, on one or more VGAM1627 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22743] It is yet further appreciated that a function of VGAM1627 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1627 include diagnosis, prevention and treatment of viral infection by Bovine herpesvirus 4. Specific functions, and accordingly utilities, of VGAM1627 correlate with, and may be deduced from, the identity of the host target genes which VGAM1627 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[22744] Nucleotide sequences of the VGAM1627 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1627 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1627 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1627 are further described hereinbelow with reference to Table 1.

[22745] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1627 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[22746] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1628 (VGAM1628) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[22747] VGAM1628 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1628 was detected is described hereinabove with reference to Figs. 2-8.

[22748] VGAM1628 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Bovine herpesvirus 4. VGAM1628 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[22749] VGAM1628 gene, herein designated VGAM GENE, encodes

a VGAM1628 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1628 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1628 precursor RNA is designated SEQ ID:1614, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1614 is located at position 83406 relative to the genome of Bovine herpesvirus 4.

[22750] VGAM1628 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1628 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22751] An enzyme complex designated DICER COMPLEX, dices the VGAM1628 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1628 RNA,

herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 49%) nucleotide sequence of VGAM1628 RNA is designated SEQ ID:4339, and is provided hereinbelow with reference to the sequence listing part.

[22752] VGAM1628 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1628 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1628 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22753] VGAM1628 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1628 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM1628 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1628 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1628 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22754] The complementary binding of VGAM1628 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1628 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1628 host target RNA, herein designated VGAM HOST TARGET

RNA, into VGAM1628 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[22755] It is appreciated that VGAM1628 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1628 host target genes. The mRNA of each one of this plurality of VGAM1628 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1628 RNA, herein designated VGAM RNA, and which when bound by VGAM1628 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1628 host target proteins.

[22756] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1628 gene, herein designated VGAM GENE, on one or more VGAM1628 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22757] It is yet further appreciated that a function of VGAM1628 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1628 include diagnosis, prevention and treatment of viral infection by Bovine herpesvirus 4. Specific functions, and accordingly utilities, of VGAM1628 correlate with, and may be deduced from, the identity of the host target genes which VGAM1628 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[22758] Nucleotide sequences of the VGAM1628 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1628 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1628 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1628 are further

described hereinbelow with reference to Table 1.

[22759] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1628 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[22760] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1629 (VGAM1629) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[22761] VGAM1629 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1629 was detected is described hereinabove with reference to Figs. 2-8.

[22762] VGAM1629 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Bovine herpesvirus 4. VGAM1629 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[22763] VGAM1629 gene, herein designated VGAM GENE, encodes a VGAM1629 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1629 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1629 precursor RNA is designated SEQ ID:1615, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1615 is located at position 88808 relative to the genome of Bovine herpesvirus 4.

[22764] VGAM1629 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1629 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22765] An enzyme complex designated DICER COMPLEX, dices the VGAM1629 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, into VGAM1629 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM1629 RNA is designated SEQ ID:4340, and is provided hereinbelow with reference to the sequence listing part.

[22766] VGAM1629 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1629 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1629 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22767] VGAM1629 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1629 host target RNA, herein designated VGAM HOST TARGET RNA. This

complementary binding is due to the fact that the nucleotide sequence of VGAM1629 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1629 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1629 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22768] The complementary binding of VGAM1629 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1629 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1629

host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1629 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[22769] It is appreciated that VGAM1629 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1629 host target genes. The mRNA of each one of this plurality of VGAM1629 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1629 RNA, herein designated VGAM RNA, and which when bound by VGAM1629 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1629 host target proteins.

[22770] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1629 gene, herein designated VGAM GENE, on one or more VGAM1629 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22771] It is yet further appreciated that a function of VGAM1629 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1629 include diagnosis, prevention and treatment of viral infection by Bovine herpesvirus 4. Specific functions, and accordingly utilities, of VGAM1629 correlate with, and may be deduced from, the identity of the host target genes which VGAM1629 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[22772] Nucleotide sequences of the VGAM1629 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1629 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1629 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM1629 are further described hereinbelow with reference to Table 1.

[22773] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1629 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[22774] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1630 (VGAM1630) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[22775] VGAM1630 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1630 was detected is described hereinabove with reference to Figs. 2-8.

[22776] VGAM1630 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Bovine herpesvirus 4. VGAM1630 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the

human genome.

[22777] VGAM1630 gene, herein designated VGAM GENE, encodes a VGAM1630 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1630 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1630 precursor RNA is designated SEQ ID:1616, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1616 is located at position 84159 relative to the genome of Bovine herpesvirus 4.

[22778] VGAM1630 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1630 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22779] An enzyme complex designated DICER COMPLEX, dices

the VGAM1630 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1630 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 63%) nucleotide sequence of VGAM1630 RNA is designated SEQ ID:4341, and is provided hereinbelow with reference to the sequence listing part.

[22780] VGAM1630 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1630 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1630 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22781] VGAM1630 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1630 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1630 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1630 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1630 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22782] The complementary binding of VGAM1630 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1630 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM1630 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1630 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[22783] It is appreciated that VGAM1630 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1630 host target genes. The mRNA of each one of this plurality of VGAM1630 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1630 RNA, herein designated VGAM RNA, and which when bound by VGAM1630 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1630 host target proteins.

[22784] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1630 gene, herein designated VGAM GENE, on one or more VGAM1630 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22785] It is yet further appreciated that a function of VGAM1630 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1630 include diagnosis, prevention and treatment of viral infection by Bovine herpesvirus 4. Specific functions, and accordingly utilities, of VGAM1630 correlate with, and may be deduced from, the identity of the host target genes which VGAM1630 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[22786] Nucleotide sequences of the VGAM1630 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1630 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of

VGAM1630 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1630 are further described hereinbelow with reference to Table 1.

[22787] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1630 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[22788] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1631 (VGAM1631) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[22789] VGAM1631 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1631 was detected is described hereinabove with reference to Figs. 2-8.

[22790] VGAM1631 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Bovine herpesvirus 4. VGAM1631 host target gene, herein designated VGAM

HOST TARGET GENE, is a human gene contained in the human genome.

[22791] VGAM1631 gene, herein designated VGAM GENE, encodes a VGAM1631 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1631 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1631 precursor RNA is designated SEQ ID:1617, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1617 is located at position 90442 relative to the genome of Bovine herpesvirus 4.

[22792] VGAM1631 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1631 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22793] An enzyme complex designated DICER COMPLEX, dices the VGAM1631 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1631 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM1631 RNA is designated SEQ ID:4342, and is provided hereinbelow with reference to the sequence listing part.

[22794] VGAM1631 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1631 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1631 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22795] VGAM1631 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites

located in untranslated regions of VGAM1631 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1631 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1631 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1631 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22796] The complementary binding of VGAM1631 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1631 host target RNA, herein designated VGAM

HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1631 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1631 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[22797] It is appreciated that VGAM1631 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1631 host target genes. The mRNA of each one of this plurality of VGAM1631 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1631 RNA, herein designated VGAM RNA, and which when bound by VGAM1631 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1631 host target proteins.

[22798] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1631 gene, herein designated VGAM GENE, on one or more VGAM1631 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove

with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22799] It is yet further appreciated that a function of VGAM1631 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1631 include diagnosis, prevention and treatment of viral infection by Bovine herpesvirus 4. Specific functions, and accordingly utilities, of VGAM1631 correlate with, and may be deduced from, the identity of the host target genes which VGAM1631 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[22800] Nucleotide sequences of the VGAM1631 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1631 RNA, herein designated VGAM RNA, and

a schematic representation of the secondary folding of VGAM1631 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1631 are further described hereinbelow with reference to Table 1.

[22801] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1631 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[22802] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1632 (VGAM1632) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[22803] VGAM1632 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1632 was detected is described hereinabove with reference to Figs. 2-8.

[22804] VGAM1632 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Bovine herpesvirus 4.

VGAM1632 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[22805] VGAM1632 gene, herein designated VGAM GENE, encodes a VGAM1632 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1632 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1632 precursor RNA is designated SEQ ID:1618, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1618 is located at position 85979 relative to the genome of Bovine herpesvirus 4.

[22806] VGAM1632 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1632 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[22807] An enzyme complex designated DICER COMPLEX, dices the VGAM1632 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1632 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM1632 RNA is designated SEQ ID:4343, and is provided hereinbelow with reference to the sequence listing part.

[22808] VGAM1632 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1632 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1632 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22809] VGAM1632 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM1632 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1632 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1632 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1632 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22810] The complementary binding of VGAM1632 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM1632 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1632 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1632 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[22811] It is appreciated that VGAM1632 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1632 host target genes. The mRNA of each one of this plurality of VGAM1632 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1632 RNA, herein designated VGAM RNA, and which when bound by VGAM1632 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1632 host target proteins.

[22812] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1632 gene, herein designated VGAM GENE, on one or more VGAM1632 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22813] It is yet further appreciated that a function of VGAM1632 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1632 include diagnosis, prevention and treatment of viral infection by Bovine herpesvirus 4. Specific functions, and accordingly utilities, of VGAM1632 correlate with, and may be deduced from, the identity of the host target genes which VGAM1632 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[22814] Nucleotide sequences of the VGAM1632 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

diced VGAM1632 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1632 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1632 are further described hereinbelow with reference to Table 1.

[22815] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1632 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[22816] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1633 (VGAM1633) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[22817] VGAM1633 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1633 was detected is described hereinabove with reference to Figs. 2-8.

[22818] VGAM1633 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of Bovine herpesvirus 4. VGAM1633 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[22819] VGAM1633 gene, herein designated VGAM GENE, encodes a VGAM1633 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1633 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1633 precursor RNA is designated SEQ ID:1619, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1619 is located at position 85246 relative to the genome of Bovine herpesvirus 4.

[22820] VGAM1633 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1633 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22821] An enzyme complex designated DICER COMPLEX, dices the VGAM1633 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1633 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM1633 RNA is designated SEQ ID:4344, and is provided hereinbelow with reference to the sequence listing part.

[22822] VGAM1633 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1633 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1633 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22823] VGAM1633 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1633 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1633 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1633 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1633 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22824] The complementary binding of VGAM1633 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM1633 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1633 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1633 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[22825] It is appreciated that VGAM1633 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1633 host target genes. The mRNA of each one of this plurality of VGAM1633 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1633 RNA, herein designated VGAM RNA, and which when bound by VGAM1633 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1633 host target proteins.

[22826] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1633 gene, herein designated VGAM GENE, on one or more VGAM1633 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22827] It is yet further appreciated that a function of VGAM1633 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1633 include diagnosis, prevention and treatment of viral infection by Bovine herpesvirus 4. Specific functions, and accordingly utilities, of VGAM1633 correlate with, and may be deduced from, the identity of the host target genes which VGAM1633 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[22828] Nucleotide sequences of the VGAM1633 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the diced VGAM1633 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1633 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1633 are further described hereinbelow with reference to Table 1.

[22829] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1633 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[22830] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1634 (VGAM1634) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[22831] VGAM1634 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1634 was detected is described hereinabove with reference to Figs. 2-8.

[22832] VGAM1634 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Bovine herpesvirus 4. VGAM1634 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[22833] VGAM1634 gene, herein designated VGAM GENE, encodes a VGAM1634 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1634 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1634 precursor RNA is designated SEQ ID:1620, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1620 is located at position 81295 relative to the genome of Bovine herpesvirus 4.

[22834] VGAM1634 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1634 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22835] An enzyme complex designated DICER COMPLEX, dices the VGAM1634 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1634 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM1634 RNA is designated SEQ ID:4345, and is provided hereinbelow with reference to the sequence listing part.

[22836] VGAM1634 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1634 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1634 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN COD-

ING and 3UTR respectively.

[22837] VGAM1634 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1634 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1634 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1634 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1634 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22838] The complementary binding of VGAM1634 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1634 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1634 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1634 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[22839] It is appreciated that VGAM1634 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1634 host target genes. The mRNA of each one of this plurality of VGAM1634 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1634 RNA, herein designated VGAM RNA, and which when bound by VGAM1634 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1634 host target proteins.

[22840] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1634 gene, herein designated VGAM GENE, on one

or more VGAM1634 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22841] It is yet further appreciated that a function of VGAM1634 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1634 include diagnosis, prevention and treatment of viral infection by Bovine herpesvirus 4. Specific functions, and accordingly utilities, of VGAM1634 correlate with, and may be deduced from, the identity of the host target genes which VGAM1634 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[22842] Nucleotide sequences of the VGAM1634 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1634 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1634 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1634 are further described hereinbelow with reference to Table 1.

[22843] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1634 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[22844] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1635 (VGAM1635) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[22845] VGAM1635 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1635 was detected is de-

scribed hereinabove with reference to Figs. 2-8.

[22846] VGAM1635 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human herpesvirus 8. VGAM1635 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[22847] VGAM1635 gene, herein designated VGAM GENE, encodes a VGAM1635 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1635 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1635 precursor RNA is designated SEQ ID:1621, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1621 is located at position 121659 relative to the genome of Human herpesvirus 8.

[22848] VGAM1635 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1635 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22849] An enzyme complex designated DICER COMPLEX, dices the VGAM1635 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1635 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 81%) nucleotide sequence of VGAM1635 RNA is designated SEQ ID:4346, and is provided hereinbelow with reference to the sequence listing part.

[22850] VGAM1635 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1635 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1635 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and

a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22851] VGAM1635 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1635 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1635 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1635 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1635 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both

3UTR and 5UTR regions.

[22852] The complementary binding of VGAM1635 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1635 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1635 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1635 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[22853] It is appreciated that VGAM1635 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1635 host target genes. The mRNA of each one of this plurality of VGAM1635 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1635 RNA, herein designated VGAM RNA, and which when bound by VGAM1635 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1635 host target proteins.

[22854] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM1635 gene, herein designated VGAM GENE, on one or more VGAM1635 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22855] It is yet further appreciated that a function of VGAM1635 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1635 include diagnosis, prevention and treatment of viral infection by Human herpesvirus 8. Specific functions, and accordingly utilities, of VGAM1635 correlate with, and may be deduced from, the identity of the host target genes which VGAM1635 binds and inhibits, and the function of these host target genes, as

elaborated hereinbelow.

[22856] Nucleotide sequences of the VGAM1635 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1635 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1635 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1635 are further described hereinbelow with reference to Table 1.

[22857] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1635 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[22858] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1636 (VGAM1636) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[22859] VGAM1636 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene.

The method by which VGAM1636 was detected is described hereinabove with reference to Figs. 2-8.

[22860] VGAM1636 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human herpesvirus 8. VGAM1636 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[22861] VGAM1636 gene, herein designated VGAM GENE, encodes a VGAM1636 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1636 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1636 precursor RNA is designated SEQ ID:1622, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1622 is located at position 119152 relative to the genome of Human herpesvirus 8.

[22862] VGAM1636 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1636 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22863] An enzyme complex designated DICER COMPLEX, dices the VGAM1636 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1636 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 47%) nucleotide sequence of VGAM1636 RNA is designated SEQ ID:4347, and is provided hereinbelow with reference to the sequence listing part.

[22864] VGAM1636 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1636 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1636 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding

gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22865] VGAM1636 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1636 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1636 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1636 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1636 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be lo-

cated in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22866] The complementary binding of VGAM1636 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1636 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1636 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1636 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[22867] It is appreciated that VGAM1636 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1636 host target genes. The mRNA of each one of this plurality of VGAM1636 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1636 RNA, herein designated VGAM RNA, and which when bound by VGAM1636 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1636 host target proteins.

[22868] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM1636 gene, herein designated VGAM GENE, on one or more VGAM1636 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22869] It is yet further appreciated that a function of VGAM1636 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1636 include diagnosis, prevention and treatment of viral infection by Human herpesvirus 8. Specific functions, and accordingly utilities, of VGAM1636 correlate with, and may be deduced from, the identity of the host target genes which VGAM1636 binds and in-

hibits, and the function of these host target genes, as elaborated hereinbelow.

[22870] Nucleotide sequences of the VGAM1636 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1636 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1636 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1636 are further described hereinbelow with reference to Table 1.

[22871] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1636 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[22872] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1637 (VGAM1637) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[22873] VGAM1637 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1637 was detected is described hereinabove with reference to Figs. 2-8.

[22874] VGAM1637 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human herpesvirus 8. VGAM1637 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[22875] VGAM1637 gene, herein designated VGAM GENE, encodes a VGAM1637 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1637 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1637 precursor RNA is designated SEQ ID:1623, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1623 is located at position 122480 relative to the genome of Human herpesvirus 8.

[22876] VGAM1637 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1637 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22877] An enzyme complex designated DICER COMPLEX, dices the VGAM1637 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1637 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 63%) nucleotide sequence of VGAM1637 RNA is designated SEQ ID:4348, and is provided hereinbelow with reference to the sequence listing part.

[22878] VGAM1637 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1637 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1637 host target RNA, herein designated VGAM HOST TARGET RNA, comprises

three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22879] VGAM1637 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1637 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1637 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1637 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1637 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an

example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22880] The complementary binding of VGAM1637 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1637 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1637 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1637 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[22881] It is appreciated that VGAM1637 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1637 host target genes. The mRNA of each one of this plurality of VGAM1637 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1637 RNA, herein designated VGAM RNA, and which when bound by VGAM1637 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1637 host target proteins.

[22882] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1637 gene, herein designated VGAM GENE, on one or more VGAM1637 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22883] It is yet further appreciated that a function of VGAM1637 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1637 include diagnosis, prevention and treatment of viral infection by Human herpesvirus 8. Specific functions, and accordingly utilities, of VGAM1637 correlate with, and may be deduced from, the identity of

the host target genes which VGAM1637 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[22884] Nucleotide sequences of the VGAM1637 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1637 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1637 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1637 are further described hereinbelow with reference to Table 1.

[22885] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1637 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[22886] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1638 (VGAM1638) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[22887] VGAM1638 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1638 was detected is described hereinabove with reference to Figs. 2-8.

[22888] VGAM1638 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human herpesvirus 8. VGAM1638 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[22889] VGAM1638 gene, herein designated VGAM GENE, encodes a VGAM1638 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1638 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1638 precursor RNA is designated SEQ ID:1624, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1624 is located at position 124374 relative to the genome of Human herpesvirus 8.

[22890] VGAM1638 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1638 folded precursor RNA, herein designated VGAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22891] An enzyme complex designated DICER COMPLEX, dices the VGAM1638 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1638 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 56%) nucleotide sequence of VGAM1638 RNA is designated SEQ ID:4349, and is provided hereinbelow with reference to the sequence listing part.

[22892] VGAM1638 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1638 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1638 host target RNA,

herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22893] VGAM1638 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1638 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1638 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1638 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1638 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host tar-

get binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22894] The complementary binding of VGAM1638 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1638 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1638 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1638 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[22895] It is appreciated that VGAM1638 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1638 host target genes. The mRNA of each one of this plurality of VGAM1638 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1638 RNA, herein designated VGAM RNA, and which when bound by VGAM1638 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1638 host target proteins.

[22896] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1638 gene, herein designated VGAM GENE, on one or more VGAM1638 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22897] It is yet further appreciated that a function of VGAM1638 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1638 include diagnosis, prevention and treatment of viral infection by Human herpesvirus 8. Specific functions, and accordingly utilities, of VGAM1638

correlate with, and may be deduced from, the identity of the host target genes which VGAM1638 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[22898] Nucleotide sequences of the VGAM1638 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1638 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1638 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1638 are further described hereinbelow with reference to Table 1.

[22899] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1638 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[22900] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1639 (VGAM1639) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the

art.

[22901] VGAM1639 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1639 was detected is described hereinabove with reference to Figs. 2-8.

[22902] VGAM1639 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human herpesvirus 8. VGAM1639 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[22903] VGAM1639 gene, herein designated VGAM GENE, encodes a VGAM1639 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1639 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1639 precursor RNA is designated SEQ ID:1625, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1625 is located at position 121407 relative to the genome of Human herpesvirus 8.

[22904] VGAM1639 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1639 folded

precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22905] An enzyme complex designated DICER COMPLEX, dices the VGAM1639 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1639 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 47%) nucleotide sequence of VGAM1639 RNA is designated SEQ ID:4350, and is provided hereinbelow with reference to the sequence listing part.

[22906] VGAM1639 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1639 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM1639 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22907] VGAM1639 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1639 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1639 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1639 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1639 host target RNA, herein designated VGAM HOST TARGET RNA.

It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22908] The complementary binding of VGAM1639 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1639 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1639 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1639 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[22909] It is appreciated that VGAM1639 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1639 host target genes. The mRNA of each one of this plurality of VGAM1639 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1639 RNA, herein designated VGAM RNA, and which when bound by VGAM1639 RNA, herein designated VGAM RNA, causes inhibition of translation of

respective one or more VGAM1639 host target proteins.

[22910] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1639 gene, herein designated VGAM GENE, on one or more VGAM1639 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22911] It is yet further appreciated that a function of VGAM1639 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1639 include diagnosis, prevention and treatment of viral infection by Human herpesvirus 8. Spe-

cific functions, and accordingly utilities, of VGAM1639 correlate with, and may be deduced from, the identity of the host target genes which VGAM1639 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[22912] Nucleotide sequences of the VGAM1639 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1639 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1639 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1639 are further described hereinbelow with reference to Table 1.

[22913] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1639 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[22914] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1640 (VGAM1640) viral gene, which modulates expression of respective host target genes thereof, the func-

tion and utility of which host target genes is known in the art.

[22915] VGAM1640 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1640 was detected is described hereinabove with reference to Figs. 2-8.

[22916] VGAM1640 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human herpesvirus 8. VGAM1640 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[22917] VGAM1640 gene, herein designated VGAM GENE, encodes a VGAM1640 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1640 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1640 precursor RNA is designated SEQ ID:1626, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1626 is located at position 117446 relative to the genome of Human herpesvirus 8.

[22918] VGAM1640 precursor RNA, herein designated VGAM PRE-

CURSOR RNA, folds onto itself, forming VGAM1640 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22919] An enzyme complex designated DICER COMPLEX, dices the VGAM1640 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1640 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 84%) nucleotide sequence of VGAM1640 RNA is designated SEQ ID:4351, and is provided hereinbelow with reference to the sequence listing part.

[22920] VGAM1640 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM1640 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1640 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22921] VGAM1640 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1640 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1640 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1640 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1640 host

target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22922] The complementary binding of VGAM1640 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1640 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1640 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1640 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[22923] It is appreciated that VGAM1640 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1640 host target genes. The mRNA of each one of this plurality of VGAM1640 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1640 RNA, herein designated VGAM RNA, and which when bound by VGAM1640 RNA, herein

designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1640 host target proteins.

[22924] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1640 gene, herein designated VGAM GENE, on one or more VGAM1640 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22925] It is yet further appreciated that a function of VGAM1640 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1640 include diagnosis, prevention and

treatment of viral infection by Human herpesvirus 8. Specific functions, and accordingly utilities, of VGAM1640 correlate with, and may be deduced from, the identity of the host target genes which VGAM1640 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[22926] Nucleotide sequences of the VGAM1640 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1640 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1640 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1640 are further described hereinbelow with reference to Table 1.

[22927] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1640 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[22928] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1641 (VGAM1641) viral gene, which modulates ex-

pression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[22929] VGAM1641 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1641 was detected is described hereinabove with reference to Figs. 2-8.

[22930] VGAM1641 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cell fusing agent virus. VGAM1641 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[22931] VGAM1641 gene, herein designated VGAM GENE, encodes a VGAM1641 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1641 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1641 precursor RNA is designated SEQ ID:1627, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1627 is located at position 9147 relative to the genome of Cell fusing agent virus.

[22932] VGAM1641 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1641 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22933] An enzyme complex designated DICER COMPLEX, dices the VGAM1641 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1641 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM1641 RNA is designated SEQ ID:4352, and is provided hereinbelow with reference to the sequence listing part.

[22934] VGAM1641 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1641 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1641 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22935] VGAM1641 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1641 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1641 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1641 RNA, herein designated VGAM RNA, may have a different number of host target

binding sites in untranslated regions of a VGAM1641 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22936] The complementary binding of VGAM1641 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1641 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1641 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1641 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[22937] It is appreciated that VGAM1641 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1641 host target genes. The mRNA of each one of this plurality of VGAM1641 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1641 RNA, herein designated VGAM

RNA, and which when bound by VGAM1641 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1641 host target proteins.

[22938] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1641 gene, herein designated VGAM GENE, on one or more VGAM1641 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22939] It is yet further appreciated that a function of VGAM1641 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM1641 include diagnosis, prevention and treatment of viral infection by Cell fusing agent virus. Specific functions, and accordingly utilities, of VGAM1641 correlate with, and may be deduced from, the identity of the host target genes which VGAM1641 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[22940] Nucleotide sequences of the VGAM1641 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1641 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1641 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1641 are further described hereinbelow with reference to Table 1.

[22941] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1641 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[22942] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Mes-

senger 1642 (VGAM1642) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[22943] VGAM1642 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1642 was detected is described hereinabove with reference to Figs. 2-8.

[22944] VGAM1642 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cell fusing agent virus. VGAM1642 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[22945] VGAM1642 gene, herein designated VGAM GENE, encodes a VGAM1642 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1642 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1642 precursor RNA is designated SEQ ID:1628, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1628 is located at position 8550

relative to the genome of Cell fusing agent virus.

[22946] VGAM1642 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1642 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22947] An enzyme complex designated DICER COMPLEX, dices the VGAM1642 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1642 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM1642 RNA is designated SEQ ID:4353, and is provided hereinbelow with reference to the sequence listing part.

[22948] VGAM1642 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1642 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1642 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22949] VGAM1642 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1642 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1642 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1642 RNA, herein designated

VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1642 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22950] The complementary binding of VGAM1642 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1642 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1642 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1642 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[22951] It is appreciated that VGAM1642 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1642 host target genes. The mRNA of each one of this plurality of VGAM1642 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM1642 RNA, herein designated VGAM RNA, and which when bound by VGAM1642 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1642 host target proteins.

[22952] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1642 gene, herein designated VGAM GENE, on one or more VGAM1642 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22953] It is yet further appreciated that a function of VGAM1642 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1642 include diagnosis, prevention and treatment of viral infection by Cell fusing agent virus. Specific functions, and accordingly utilities, of VGAM1642 correlate with, and may be deduced from, the identity of the host target genes which VGAM1642 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[22954] Nucleotide sequences of the VGAM1642 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1642 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1642 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1642 are further described hereinbelow with reference to Table 1.

[22955] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1642 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[22956] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present

invention, referred to here as Viral Genomic Address Messenger 1643 (VGAM1643) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[22957] VGAM1643 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1643 was detected is described hereinabove with reference to Figs. 2-8.

[22958] VGAM1643 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cell fusing agent virus. VGAM1643 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[22959] VGAM1643 gene, herein designated VGAM GENE, encodes a VGAM1643 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1643 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1643 precursor RNA is designated SEQ ID:1629, and is provided hereinbelow with reference to the sequence listing part. Nu-

cleotide sequence SEQ ID:1629 is located at position 1340 relative to the genome of Cell fusing agent virus.

[22960] VGAM1643 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1643 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22961] An enzyme complex designated DICER COMPLEX, dices the VGAM1643 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1643 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM1643 RNA is designated SEQ ID:4354, and is provided hereinbelow with reference to the sequence

listing part.

[22962] VGAM1643 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1643 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1643 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22963] VGAM1643 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1643 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1643 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not

meant to be limiting VGAM1643 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1643 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22964] The complementary binding of VGAM1643 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1643 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1643 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1643 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[22965] It is appreciated that VGAM1643 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1643 host target genes. The mRNA of each one of this plurality of VGAM1643 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM1643 RNA, herein designated VGAM RNA, and which when bound by VGAM1643 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1643 host target proteins.

[22966] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1643 gene, herein designated VGAM GENE, on one or more VGAM1643 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22967] It is yet further appreciated that a function of VGAM1643

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1643 include diagnosis, prevention and treatment of viral infection by Cell fusing agent virus. Specific functions, and accordingly utilities, of VGAM1643 correlate with, and may be deduced from, the identity of the host target genes which VGAM1643 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[22968] Nucleotide sequences of the VGAM1643 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1643 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1643 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1643 are further described hereinbelow with reference to Table 1.

[22969] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1643 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[22970] Fig. 1 further provides a conceptual description of another

novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1644 (VGAM1644) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[22971] VGAM1644 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1644 was detected is described hereinabove with reference to Figs. 2-8.

[22972] VGAM1644 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Dengue virus. VGAM1644 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[22973] VGAM1644 gene, herein designated VGAM GENE, encodes a VGAM1644 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1644 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1644 precursor RNA is designated SEQ ID:1630, and is provided here-

inbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1630 is located at position 10625 relative to the genome of Dengue virus.

[22974] VGAM1644 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1644 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22975] An enzyme complex designated DICER COMPLEX, dices the VGAM1644 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1644 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of VGAM1644 RNA is designated SEQ ID:4355, and

is provided hereinbelow with reference to the sequence listing part.

[22976] VGAM1644 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1644 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1644 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22977] VGAM1644 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1644 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1644 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites

shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1644 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1644 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22978] The complementary binding of VGAM1644 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1644 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1644 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1644 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[22979] It is appreciated that VGAM1644 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1644 host target genes. The mRNA of each one of this plurality of VGAM1644 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1644 RNA, herein designated VGAM RNA, and which when bound by VGAM1644 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1644 host target proteins.

[22980] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1644 gene, herein designated VGAM GENE, on one or more VGAM1644 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22981] It is yet further appreciated that a function of VGAM1644 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1644 include diagnosis, prevention and treatment of viral infection by Dengue virus. Specific functions, and accordingly utilities, of VGAM1644 correlate with, and may be deduced from, the identity of the host target genes which VGAM1644 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[22982] Nucleotide sequences of the VGAM1644 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1644 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1644 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1644 are further described hereinbelow with reference to Table 1.

[22983] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1644 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[22984] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1645 (VGAM1645) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[22985] VGAM1645 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1645 was detected is described hereinabove with reference to Figs. 2-8.

[22986] VGAM1645 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Dengue virus.
VGAM1645 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[22987] VGAM1645 gene, herein designated VGAM GENE, encodes a VGAM1645 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1645 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1645 precur-

sor RNA is designated SEQ ID:1631, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1631 is located at position 5184 relative to the genome of Dengue virus.

[22988] VGAM1645 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1645 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22989] An enzyme complex designated DICER COMPLEX, dices the VGAM1645 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1645 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide se-

quence of VGAM1645 RNA is designated SEQ ID:4356, and is provided hereinbelow with reference to the sequence listing part.

[22990] VGAM1645 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1645 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1645 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22991] VGAM1645 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1645 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1645 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is ap-

preciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1645 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1645 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22992] The complementary binding of VGAM1645 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1645 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1645 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1645 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[22993] It is appreciated that VGAM1645 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1645 host target genes. The mRNA of

each one of this plurality of VGAM1645 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1645 RNA, herein designated VGAM RNA, and which when bound by VGAM1645 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1645 host target proteins.

[22994] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1645 gene, herein designated VGAM GENE, on one or more VGAM1645 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science

294,779 (2001)).

[22995] It is yet further appreciated that a function of VGAM1645 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1645 include diagnosis, prevention and treatment of viral infection by Dengue virus. Specific functions, and accordingly utilities, of VGAM1645 correlate with, and may be deduced from, the identity of the host target genes which VGAM1645 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[22996] Nucleotide sequences of the VGAM1645 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1645 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1645 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1645 are further described hereinbelow with reference to Table 1.

[22997] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1645 RNA, herein designated VGAM RNA, are de-

scribed hereinbelow with reference to Table 2.

[22998] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1646 (VGAM1646) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[22999] VGAM1646 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1646 was detected is described hereinabove with reference to Figs. 2-8.

[23000] VGAM1646 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Dengue virus.
VGAM1646 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[23001] VGAM1646 gene, herein designated VGAM GENE, encodes a VGAM1646 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1646 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly

similar to the nucleotide sequence of VGAM1646 precursor RNA is designated SEQ ID:1632, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1632 is located at position 9914 relative to the genome of Dengue virus.

[23002] VGAM1646 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1646 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23003] An enzyme complex designated DICER COMPLEX, dices the VGAM1646 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1646 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 75%) nucleotide sequence of VGAM1646 RNA is designated SEQ ID:4357, and is provided hereinbelow with reference to the sequence listing part.

[23004] VGAM1646 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1646 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1646 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23005] VGAM1646 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1646 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1646 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I,

BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1646 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1646 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23006] The complementary binding of VGAM1646 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1646 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1646 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1646 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[23007] It is appreciated that VGAM1646 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM1646 host target genes. The mRNA of each one of this plurality of VGAM1646 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1646 RNA, herein designated VGAM RNA, and which when bound by VGAM1646 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1646 host target proteins.

[23008] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1646 gene, herein designated VGAM GENE, on one or more VGAM1646 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23009] It is yet further appreciated that a function of VGAM1646 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1646 include diagnosis, prevention and treatment of viral infection by Dengue virus. Specific functions, and accordingly utilities, of VGAM1646 correlate with, and may be deduced from, the identity of the host target genes which VGAM1646 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[23010] Nucleotide sequences of the VGAM1646 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1646 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1646 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1646 are further described hereinbelow with reference to Table 1.

[23011] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites

to VGAM1646 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[23012] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1647 (VGAM1647) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[23013] VGAM1647 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1647 was detected is described hereinabove with reference to Figs. 2-8.

[23014] VGAM1647 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human herpesvirus 8. VGAM1647 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[23015] VGAM1647 gene, herein designated VGAM GENE, encodes a VGAM1647 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1647 precursor RNA, herein designated VGAM PRECURSOR RNA, does not en-

code a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1647 precursor RNA is designated SEQ ID:1633, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1633 is located at position 104577 relative to the genome of Human herpesvirus 8.

[23016] VGAM1647 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1647 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23017] An enzyme complex designated DICER COMPLEX, dices the VGAM1647 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1647 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM1647 RNA is designated SEQ ID:4358, and is provided hereinbelow with reference to the sequence listing part.

[23018] VGAM1647 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1647 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1647 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23019] VGAM1647 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1647 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1647 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3

such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1647 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1647 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23020] The complementary binding of VGAM1647 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1647 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1647 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1647 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[23021] It is appreciated that VGAM1647 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1647 host target genes. The mRNA of each one of this plurality of VGAM1647 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1647 RNA, herein designated VGAM RNA, and which when bound by VGAM1647 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1647 host target proteins.

[23022] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1647 gene, herein designated VGAM GENE, on one or more VGAM1647 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23023] It is yet further appreciated that a function of VGAM1647 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1647 include diagnosis, prevention and treatment of viral infection by Human herpesvirus 8. Specific functions, and accordingly utilities, of VGAM1647 correlate with, and may be deduced from, the identity of the host target genes which VGAM1647 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[23024] Nucleotide sequences of the VGAM1647 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1647 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1647 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1647 are further described hereinbelow with reference to Table 1.

[23025] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the

complementarity of each of these host target binding sites to VGAM1647 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[23026] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1648 (VGAM1648) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[23027] VGAM1648 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1648 was detected is described hereinabove with reference to Figs. 2-8.

[23028] VGAM1648 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human herpesvirus 8. VGAM1648 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[23029] VGAM1648 gene, herein designated VGAM GENE, encodes a VGAM1648 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1648 precursor RNA,

herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1648 precursor RNA is designated SEQ ID:1634, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1634 is located at position 111049 relative to the genome of Human herpesvirus 8.

[23030] VGAM1648 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1648 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23031] An enzyme complex designated DICER COMPLEX, dices the VGAM1648 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1648 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM1648 RNA is designated SEQ ID:4359, and is provided hereinbelow with reference to the sequence listing part.

[23032] VGAM1648 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1648 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1648 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23033] VGAM1648 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1648 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1648 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host

target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1648 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1648 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23034] The complementary binding of VGAM1648 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1648 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1648 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1648 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[23035] It is appreciated that VGAM1648 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1648 host target genes. The mRNA of each one of this plurality of VGAM1648 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1648 RNA, herein designated VGAM RNA, and which when bound by VGAM1648 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1648 host target proteins.

[23036] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1648 gene, herein designated VGAM GENE, on one or more VGAM1648 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23037] It is yet further appreciated that a function of VGAM1648 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1648 include diagnosis, prevention and treatment of viral infection by Human herpesvirus 8. Specific functions, and accordingly utilities, of VGAM1648 correlate with, and may be deduced from, the identity of the host target genes which VGAM1648 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[23038] Nucleotide sequences of the VGAM1648 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1648 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1648 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1648 are further described hereinbelow with reference to Table 1.

[23039] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1648 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[23040] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1649 (VGAM1649) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[23041] VGAM1649 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1649 was detected is described hereinabove with reference to Figs. 2-8.

[23042] VGAM1649 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human herpesvirus 8. VGAM1649 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[23043] VGAM1649 gene, herein designated VGAM GENE, encodes a VGAM1649 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and un-

like most ordinary genes, VGAM1649 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1649 precursor RNA is designated SEQ ID:1635, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1635 is located at position 105452 relative to the genome of Human herpesvirus 8.

[23044] VGAM1649 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1649 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23045] An enzyme complex designated DICER COMPLEX, dices the VGAM1649 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1649 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 60%) nucleotide sequence of VGAM1649 RNA is designated SEQ ID:4360, and is provided hereinbelow with reference to the sequence listing part.

[23046] VGAM1649 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1649 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1649 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23047] VGAM1649 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1649 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1649 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed

sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1649 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1649 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23048] The complementary binding of VGAM1649 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1649 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1649 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1649 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target

protein is therefore outlined by a broken line.

[23049] It is appreciated that VGAM1649 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1649 host target genes. The mRNA of each one of this plurality of VGAM1649 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1649 RNA, herein designated VGAM RNA, and which when bound by VGAM1649 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1649 host target proteins.

[23050] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1649 gene, herein designated VGAM GENE, on one or more VGAM1649 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23051] It is yet further appreciated that a function of VGAM1649 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1649 include diagnosis, prevention and treatment of viral infection by Human herpesvirus 8. Specific functions, and accordingly utilities, of VGAM1649 correlate with, and may be deduced from, the identity of the host target genes which VGAM1649 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[23052] Nucleotide sequences of the VGAM1649 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1649 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1649 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1649 are further described hereinbelow with reference to Table 1.

[23053] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1649 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[23054] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1650 (VGAM1650) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[23055] VGAM1650 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1650 was detected is described hereinabove with reference to Figs. 2-8.

[23056] VGAM1650 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human herpesvirus 8. VGAM1650 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[23057] VGAM1650 gene, herein designated VGAM GENE, encodes a VGAM1650 precursor RNA, herein designated VGAM

PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1650 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1650 precursor RNA is designated SEQ ID:1636, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1636 is located at position 109181 relative to the genome of Human herpesvirus 8.

[23058] VGAM1650 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1650 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23059] An enzyme complex designated DICER COMPLEX, dices the VGAM1650 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1650 RNA, herein designated VGAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 52%) nucleotide sequence of VGAM1650 RNA is designated SEQ ID:4361, and is provided hereinbelow with reference to the sequence listing part.

[23060] VGAM1650 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1650 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1650 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23061] VGAM1650 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1650 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1650 RNA, herein designated

VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1650 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1650 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23062] The complementary binding of VGAM1650 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1650 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1650 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1650 host target protein, herein desig-

nated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[23063] It is appreciated that VGAM1650 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1650 host target genes. The mRNA of each one of this plurality of VGAM1650 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1650 RNA, herein designated VGAM RNA, and which when bound by VGAM1650 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1650 host target proteins.

[23064] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1650 gene, herein designated VGAM GENE, on one or more VGAM1650 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23065] It is yet further appreciated that a function of VGAM1650 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1650 include diagnosis, prevention and treatment of viral infection by Human herpesvirus 8. Specific functions, and accordingly utilities, of VGAM1650 correlate with, and may be deduced from, the identity of the host target genes which VGAM1650 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[23066] Nucleotide sequences of the VGAM1650 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1650 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1650 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1650 are further described hereinbelow with reference to Table 1.

[23067] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1650 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[23068] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1651 (VGAM1651) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[23069] VGAM1651 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1651 was detected is described hereinabove with reference to Figs. 2-8.

[23070] VGAM1651 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human herpesvirus 8. VGAM1651 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[23071] VGAM1651 gene, herein designated VGAM GENE, encodes

a VGAM1651 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1651 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1651 precursor RNA is designated SEQ ID:1637, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1637 is located at position 106255 relative to the genome of Human herpesvirus 8.

[23072] VGAM1651 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1651 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23073] An enzyme complex designated DICER COMPLEX, dices the VGAM1651 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1651 RNA,

herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 78%) nucleotide sequence of VGAM1651 RNA is designated SEQ ID:4362, and is provided hereinbelow with reference to the sequence listing part.

[23074] VGAM1651 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1651 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1651 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23075] VGAM1651 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1651 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM1651 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1651 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1651 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23076] The complementary binding of VGAM1651 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1651 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1651 host target RNA, herein designated VGAM HOST TARGET

RNA, into VGAM1651 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[23077] It is appreciated that VGAM1651 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1651 host target genes. The mRNA of each one of this plurality of VGAM1651 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1651 RNA, herein designated VGAM RNA, and which when bound by VGAM1651 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1651 host target proteins.

[23078] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1651 gene, herein designated VGAM GENE, on one or more VGAM1651 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23079] It is yet further appreciated that a function of VGAM1651 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1651 include diagnosis, prevention and treatment of viral infection by Human herpesvirus 8. Specific functions, and accordingly utilities, of VGAM1651 correlate with, and may be deduced from, the identity of the host target genes which VGAM1651 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[23080] Nucleotide sequences of the VGAM1651 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1651 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1651 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1651 are further

described hereinbelow with reference to Table 1.

[23081] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1651 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[23082] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1652 (VGAM1652) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[23083] VGAM1652 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1652 was detected is described hereinabove with reference to Figs. 2-8.

[23084] VGAM1652 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Yellow fever virus. VGAM1652 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[23085] VGAM1652 gene, herein designated VGAM GENE, encodes a VGAM1652 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1652 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1652 precursor RNA is designated SEQ ID:1638, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1638 is located at position 10776 relative to the genome of Yellow fever virus.

[23086] VGAM1652 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1652 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23087] An enzyme complex designated DICER COMPLEX, dices the VGAM1652 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, into VGAM1652 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 83%) nucleotide sequence of VGAM1652 RNA is designated SEQ ID:4363, and is provided hereinbelow with reference to the sequence listing part.

[23088] VGAM1652 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1652 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1652 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23089] VGAM1652 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1652 host target RNA, herein designated VGAM HOST TARGET RNA. This

complementary binding is due to the fact that the nucleotide sequence of VGAM1652 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1652 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1652 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23090] The complementary binding of VGAM1652 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1652 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1652

host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1652 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[23091] It is appreciated that VGAM1652 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1652 host target genes. The mRNA of each one of this plurality of VGAM1652 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1652 RNA, herein designated VGAM RNA, and which when bound by VGAM1652 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1652 host target proteins.

[23092] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1652 gene, herein designated VGAM GENE, on one or more VGAM1652 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23093] It is yet further appreciated that a function of VGAM1652 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1652 include diagnosis, prevention and treatment of viral infection by Yellow fever virus. Specific functions, and accordingly utilities, of VGAM1652 correlate with, and may be deduced from, the identity of the host target genes which VGAM1652 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[23094] Nucleotide sequences of the VGAM1652 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1652 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1652 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM1652 are further described hereinbelow with reference to Table 1.

[23095] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1652 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[23096] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1653 (VGAM1653) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[23097] VGAM1653 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1653 was detected is described hereinabove with reference to Figs. 2-8.

[23098] VGAM1653 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Yellow fever virus. VGAM1653 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the

human genome.

[23099] VGAM1653 gene, herein designated VGAM GENE, encodes a VGAM1653 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1653 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1653 precursor RNA is designated SEQ ID:1639, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1639 is located at position 2036 relative to the genome of Yellow fever virus.

[23100] VGAM1653 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1653 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23101] An enzyme complex designated DICER COMPLEX, dices

the VGAM1653 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1653 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM1653 RNA is designated SEQ ID:4364, and is provided hereinbelow with reference to the sequence listing part.

[23102] VGAM1653 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1653 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1653 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23103] VGAM1653 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1653 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1653 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1653 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1653 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23104] The complementary binding of VGAM1653 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1653 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM1653 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1653 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[23105] It is appreciated that VGAM1653 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1653 host target genes. The mRNA of each one of this plurality of VGAM1653 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1653 RNA, herein designated VGAM RNA, and which when bound by VGAM1653 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1653 host target proteins.

[23106] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1653 gene, herein designated VGAM GENE, on one or more VGAM1653 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23107] It is yet further appreciated that a function of VGAM1653 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1653 include diagnosis, prevention and treatment of viral infection by Yellow fever virus. Specific functions, and accordingly utilities, of VGAM1653 correlate with, and may be deduced from, the identity of the host target genes which VGAM1653 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[23108] Nucleotide sequences of the VGAM1653 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1653 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of

VGAM1653 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1653 are further described hereinbelow with reference to Table 1.

[23109] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1653 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[23110] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1654 (VGAM1654) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[23111] VGAM1654 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1654 was detected is described hereinabove with reference to Figs. 2-8.

[23112] VGAM1654 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Yellow fever virus. VGAM1654 host target gene, herein designated VGAM

HOST TARGET GENE, is a human gene contained in the human genome.

[23113] VGAM1654 gene, herein designated VGAM GENE, encodes a VGAM1654 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1654 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1654 precursor RNA is designated SEQ ID:1640, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1640 is located at position 6577 relative to the genome of Yellow fever virus.

[23114] VGAM1654 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1654 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23115] An enzyme complex designated DICER COMPLEX, dices the VGAM1654 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1654 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM1654 RNA is designated SEQ ID:4365, and is provided hereinbelow with reference to the sequence listing part.

[23116] VGAM1654 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1654 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1654 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23117] VGAM1654 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites

located in untranslated regions of VGAM1654 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1654 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1654 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1654 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23118] The complementary binding of VGAM1654 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1654 host target RNA, herein designated VGAM

HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1654 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1654 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[23119] It is appreciated that VGAM1654 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1654 host target genes. The mRNA of each one of this plurality of VGAM1654 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1654 RNA, herein designated VGAM RNA, and which when bound by VGAM1654 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1654 host target proteins.

[23120] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1654 gene, herein designated VGAM GENE, on one or more VGAM1654 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove

with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23121] It is yet further appreciated that a function of VGAM1654 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1654 include diagnosis, prevention and treatment of viral infection by Yellow fever virus. Specific functions, and accordingly utilities, of VGAM1654 correlate with, and may be deduced from, the identity of the host target genes which VGAM1654 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[23122] Nucleotide sequences of the VGAM1654 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1654 RNA, herein designated VGAM RNA, and

a schematic representation of the secondary folding of VGAM1654 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1654 are further described hereinbelow with reference to Table 1.

[23123] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1654 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[23124] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1655 (VGAM1655) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[23125] VGAM1655 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1655 was detected is described hereinabove with reference to Figs. 2-8.

[23126] VGAM1655 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Yellow fever virus.

VGAM1655 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[23127] VGAM1655 gene, herein designated VGAM GENE, encodes a VGAM1655 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1655 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1655 precursor RNA is designated SEQ ID:1641, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1641 is located at position 1472 relative to the genome of Yellow fever virus.

[23128] VGAM1655 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1655 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[23129] An enzyme complex designated DICER COMPLEX, dices the VGAM1655 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1655 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM1655 RNA is designated SEQ ID:4366, and is provided hereinbelow with reference to the sequence listing part.

[23130] VGAM1655 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1655 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1655 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23131] VGAM1655 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM1655 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1655 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1655 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1655 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23132] The complementary binding of VGAM1655 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM1655 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1655 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1655 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[23133] It is appreciated that VGAM1655 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1655 host target genes. The mRNA of each one of this plurality of VGAM1655 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1655 RNA, herein designated VGAM RNA, and which when bound by VGAM1655 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1655 host target proteins.

[23134] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1655 gene, herein designated VGAM GENE, on one or more VGAM1655 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23135] It is yet further appreciated that a function of VGAM1655 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1655 include diagnosis, prevention and treatment of viral infection by Yellow fever virus. Specific functions, and accordingly utilities, of VGAM1655 correlate with, and may be deduced from, the identity of the host target genes which VGAM1655 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[23136] Nucleotide sequences of the VGAM1655 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

diced VGAM1655 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1655 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1655 are further described hereinbelow with reference to Table 1.

[23137] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1655 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[23138] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1656 (VGAM1656) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[23139] VGAM1656 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1656 was detected is described hereinabove with reference to Figs. 2-8.

[23140] VGAM1656 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of Molluscum contagiosum virus. VGAM1656 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[23141] VGAM1656 gene, herein designated VGAM GENE, encodes a VGAM1656 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1656 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1656 precursor RNA is designated SEQ ID:1642, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1642 is located at position 8730 relative to the genome of Molluscum contagiosum virus.

[23142] VGAM1656 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1656 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23143] An enzyme complex designated DICER COMPLEX, dices the VGAM1656 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1656 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM1656 RNA is designated SEQ ID:4367, and is provided hereinbelow with reference to the sequence listing part.

[23144] VGAM1656 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1656 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1656 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23145] VGAM1656 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1656 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1656 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1656 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1656 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23146] The complementary binding of VGAM1656 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM1656 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1656 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1656 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[23147] It is appreciated that VGAM1656 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1656 host target genes. The mRNA of each one of this plurality of VGAM1656 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1656 RNA, herein designated VGAM RNA, and which when bound by VGAM1656 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1656 host target proteins.

[23148] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1656 gene, herein designated VGAM GENE, on one or more VGAM1656 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23149] It is yet further appreciated that a function of VGAM1656 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1656 include diagnosis, prevention and treatment of viral infection by Molluscum contagiosum virus. Specific functions, and accordingly utilities, of VGAM1656 correlate with, and may be deduced from, the identity of the host target genes which VGAM1656 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[23150] Nucleotide sequences of the VGAM1656 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the diced VGAM1656 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1656 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1656 are further described hereinbelow with reference to Table 1.

[23151] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1656 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[23152] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1657 (VGAM1657) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[23153] VGAM1657 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1657 was detected is described hereinabove with reference to Figs. 2-8.

[23154] VGAM1657 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Molluscum contagiosum virus. VGAM1657 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[23155] VGAM1657 gene, herein designated VGAM GENE, encodes a VGAM1657 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1657 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1657 precursor RNA is designated SEQ ID:1643, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1643 is located at position 9944 relative to the genome of Molluscum contagiosum virus.

[23156] VGAM1657 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1657 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23157] An enzyme complex designated DICER COMPLEX, dices the VGAM1657 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1657 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 50%) nucleotide sequence of VGAM1657 RNA is designated SEQ ID:4368, and is provided hereinbelow with reference to the sequence listing part.

[23158] VGAM1657 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1657 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1657 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN COD-

ING and 3UTR respectively.

[23159] VGAM1657 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1657 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1657 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1657 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1657 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23160] The complementary binding of VGAM1657 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1657 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1657 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1657 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[23161] It is appreciated that VGAM1657 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1657 host target genes. The mRNA of each one of this plurality of VGAM1657 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1657 RNA, herein designated VGAM RNA, and which when bound by VGAM1657 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1657 host target proteins.

[23162] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1657 gene, herein designated VGAM GENE, on one

or more VGAM1657 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23163] It is yet further appreciated that a function of VGAM1657 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1657 include diagnosis, prevention and treatment of viral infection by Molluscum contagiosum virus. Specific functions, and accordingly utilities, of VGAM1657 correlate with, and may be deduced from, the identity of the host target genes which VGAM1657 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[23164] Nucleotide sequences of the VGAM1657 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1657 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1657 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1657 are further described hereinbelow with reference to Table 1.

[23165] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1657 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[23166] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1658 (VGAM1658) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[23167] VGAM1658 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1658 was detected is de-

scribed hereinabove with reference to Figs. 2-8.

[23168] VGAM1658 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Molluscum contagiosum virus. VGAM1658 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[23169] VGAM1658 gene, herein designated VGAM GENE, encodes a VGAM1658 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1658 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1658 precursor RNA is designated SEQ ID:1644, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1644 is located at position 9453 relative to the genome of Molluscum contagiosum virus.

[23170] VGAM1658 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1658 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23171] An enzyme complex designated DICER COMPLEX, dices the VGAM1658 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1658 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM1658 RNA is designated SEQ ID:4369, and is provided hereinbelow with reference to the sequence listing part.

[23172] VGAM1658 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1658 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1658 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and

a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23173] VGAM1658 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1658 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1658 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1658 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1658 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both

3UTR and 5UTR regions.

[23174] The complementary binding of VGAM1658 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1658 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1658 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1658 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[23175] It is appreciated that VGAM1658 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1658 host target genes. The mRNA of each one of this plurality of VGAM1658 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1658 RNA, herein designated VGAM RNA, and which when bound by VGAM1658 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1658 host target proteins.

[23176] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM1658 gene, herein designated VGAM GENE, on one or more VGAM1658 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23177] It is yet further appreciated that a function of VGAM1658 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1658 include diagnosis, prevention and treatment of viral infection by Molluscum contagiosum virus. Specific functions, and accordingly utilities, of VGAM1658 correlate with, and may be deduced from, the identity of the host target genes which VGAM1658 binds and inhibits, and the function of these host target genes,

as elaborated hereinbelow.

[23178] Nucleotide sequences of the VGAM1658 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1658 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1658 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1658 are further described hereinbelow with reference to Table 1.

[23179] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1658 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[23180] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1659 (VGAM1659) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[23181] VGAM1659 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene.

The method by which VGAM1659 was detected is described hereinabove with reference to Figs. 2-8.

[23182] VGAM1659 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Molluscum contagiosum virus. VGAM1659 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[23183] VGAM1659 gene, herein designated VGAM GENE, encodes a VGAM1659 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1659 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1659 precursor RNA is designated SEQ ID:1645, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1645 is located at position 13023 relative to the genome of Molluscum contagiosum virus.

[23184] VGAM1659 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1659 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23185] An enzyme complex designated DICER COMPLEX, dices the VGAM1659 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1659 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM1659 RNA is designated SEQ ID:4370, and is provided hereinbelow with reference to the sequence listing part.

[23186] VGAM1659 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1659 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1659 host target RNA, herein designated VGAM HOST TARGET RNA, comprises

three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23187] VGAM1659 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1659 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1659 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1659 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1659 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an

example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23188] The complementary binding of VGAM1659 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1659 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1659 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1659 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[23189] It is appreciated that VGAM1659 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1659 host target genes. The mRNA of each one of this plurality of VGAM1659 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1659 RNA, herein designated VGAM RNA, and which when bound by VGAM1659 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1659 host target proteins.

[23190] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1659 gene, herein designated VGAM GENE, on one or more VGAM1659 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23191] It is yet further appreciated that a function of VGAM1659 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1659 include diagnosis, prevention and treatment of viral infection by Molluscum contagiosum virus. Specific functions, and accordingly utilities, of VGAM1659 correlate with, and may be deduced from, the

identity of the host target genes which VGAM1659 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[23192] Nucleotide sequences of the VGAM1659 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1659 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1659 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1659 are further described hereinbelow with reference to Table 1.

[23193] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1659 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[23194] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1660 (VGAM1660) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[23195] VGAM1660 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1660 was detected is described hereinabove with reference to Figs. 2-8.

[23196] VGAM1660 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Molluscum contagiosum virus. VGAM1660 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[23197] VGAM1660 gene, herein designated VGAM GENE, encodes a VGAM1660 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1660 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1660 precursor RNA is designated SEQ ID:1646, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1646 is located at position 5477 relative to the genome of Molluscum contagiosum virus.

[23198] VGAM1660 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1660 folded precursor RNA, herein designated VGAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23199] An enzyme complex designated DICER COMPLEX, dices the VGAM1660 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1660 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 72%) nucleotide sequence of VGAM1660 RNA is designated SEQ ID:4371, and is provided hereinbelow with reference to the sequence listing part.

[23200] VGAM1660 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1660 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1660 host target RNA,

herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23201] VGAM1660 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1660 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1660 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1660 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1660 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host tar-

get binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23202] The complementary binding of VGAM1660 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1660 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1660 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1660 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[23203] It is appreciated that VGAM1660 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1660 host target genes. The mRNA of each one of this plurality of VGAM1660 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1660 RNA, herein designated VGAM RNA, and which when bound by VGAM1660 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1660 host target proteins.

[23204] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1660 gene, herein designated VGAM GENE, on one or more VGAM1660 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23205] It is yet further appreciated that a function of VGAM1660 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1660 include diagnosis, prevention and treatment of viral infection by Molluscum contagiosum virus. Specific functions, and accordingly utilities, of

VGAM1660 correlate with, and may be deduced from, the identity of the host target genes which VGAM1660 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[23206] Nucleotide sequences of the VGAM1660 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1660 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1660 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1660 are further described hereinbelow with reference to Table 1.

[23207] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1660 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[23208] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1661 (VGAM1661) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the

art.

[23209] VGAM1661 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1661 was detected is described hereinabove with reference to Figs. 2-8.

[23210] VGAM1661 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cercopithecine herpesvirus 7. VGAM1661 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[23211] VGAM1661 gene, herein designated VGAM GENE, encodes a VGAM1661 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1661 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1661 precursor RNA is designated SEQ ID:1647, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1647 is located at position 100245 relative to the genome of Cercopithecine herpesvirus 7.

[23212] VGAM1661 precursor RNA, herein designated VGAM PRE-

CURSOR RNA, folds onto itself, forming VGAM1661 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23213] An enzyme complex designated DICER COMPLEX, dices the VGAM1661 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1661 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM1661 RNA is designated SEQ ID:4372, and is provided hereinbelow with reference to the sequence listing part.

[23214] VGAM1661 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM1661 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1661 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23215] VGAM1661 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1661 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1661 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1661 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1661 host

target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23216] The complementary binding of VGAM1661 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1661 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1661 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1661 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[23217] It is appreciated that VGAM1661 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1661 host target genes. The mRNA of each one of this plurality of VGAM1661 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1661 RNA, herein designated VGAM RNA, and which when bound by VGAM1661 RNA, herein

designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1661 host target proteins.

[23218] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1661 gene, herein designated VGAM GENE, on one or more VGAM1661 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23219] It is yet further appreciated that a function of VGAM1661 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1661 include diagnosis, prevention and

treatment of viral infection by Cercopithecine herpesvirus 7. Specific functions, and accordingly utilities, of VGAM1661 correlate with, and may be deduced from, the identity of the host target genes which VGAM1661 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[23220] Nucleotide sequences of the VGAM1661 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1661 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1661 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1661 are further described hereinbelow with reference to Table 1.

[23221] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1661 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[23222] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1662 (VGAM1662) viral gene, which modulates ex-

pression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[23223] VGAM1662 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1662 was detected is described hereinabove with reference to Figs. 2-8.

[23224] VGAM1662 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cercopithecine herpesvirus 7. VGAM1662 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[23225] VGAM1662 gene, herein designated VGAM GENE, encodes a VGAM1662 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1662 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1662 precursor RNA is designated SEQ ID:1648, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1648 is located at position 99606 relative to the genome of Cercopithecine her-

pesvirus 7.

[23226] VGAM1662 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1662 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23227] An enzyme complex designated DICER COMPLEX, dices the VGAM1662 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1662 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM1662 RNA is designated SEQ ID:4373, and is provided hereinbelow with reference to the sequence listing part.

[23228] VGAM1662 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1662 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1662 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23229] VGAM1662 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1662 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1662 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1662 RNA, herein designated

VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1662 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23230] The complementary binding of VGAM1662 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1662 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1662 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1662 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[23231] It is appreciated that VGAM1662 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1662 host target genes. The mRNA of each one of this plurality of VGAM1662 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM1662 RNA, herein designated VGAM RNA, and which when bound by VGAM1662 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1662 host target proteins.

[23232] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1662 gene, herein designated VGAM GENE, on one or more VGAM1662 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23233] It is yet further appreciated that a function of VGAM1662 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1662 include diagnosis, prevention and treatment of viral infection by Cercopithecine herpesvirus 7. Specific functions, and accordingly utilities, of VGAM1662 correlate with, and may be deduced from, the identity of the host target genes which VGAM1662 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[23234] Nucleotide sequences of the VGAM1662 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1662 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1662 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1662 are further described hereinbelow with reference to Table 1.

[23235] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1662 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[23236] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present

invention, referred to here as Viral Genomic Address Messenger 1663 (VGAM1663) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[23237] VGAM1663 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1663 was detected is described hereinabove with reference to Figs. 2-8.

[23238] VGAM1663 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cercopithecine herpesvirus 7. VGAM1663 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[23239] VGAM1663 gene, herein designated VGAM GENE, encodes a VGAM1663 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1663 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1663 precursor RNA is designated SEQ ID:1649, and is provided hereinbelow with reference to the sequence listing part. Nu-

cleotide sequence SEQ ID:1649 is located at position 98907 relative to the genome of Cercopithecine herpesvirus 7.

[23240] VGAM1663 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1663 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23241] An enzyme complex designated DICER COMPLEX, dices the VGAM1663 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1663 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM1663 RNA is designated SEQ ID:4374, and

is provided hereinbelow with reference to the sequence listing part.

[23242] VGAM1663 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1663 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1663 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23243] VGAM1663 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1663 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1663 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites

shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1663 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1663 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23244] The complementary binding of VGAM1663 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1663 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1663 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1663 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[23245] It is appreciated that VGAM1663 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1663 host target genes. The mRNA of each one of this plurality of VGAM1663 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1663 RNA, herein designated VGAM RNA, and which when bound by VGAM1663 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1663 host target proteins.

[23246] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1663 gene, herein designated VGAM GENE, on one or more VGAM1663 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23247] It is yet further appreciated that a function of VGAM1663 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1663 include diagnosis, prevention and treatment of viral infection by Cercopithecine herpesvirus 7. Specific functions, and accordingly utilities, of VGAM1663 correlate with, and may be deduced from, the identity of the host target genes which VGAM1663 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[23248] Nucleotide sequences of the VGAM1663 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1663 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1663 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1663 are further described hereinbelow with reference to Table 1.

[23249] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1663 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[23250] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1664 (VGAM1664) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[23251] VGAM1664 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1664 was detected is described hereinabove with reference to Figs. 2-8.

[23252] VGAM1664 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cercopithecine herpesvirus 7. VGAM1664 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[23253] VGAM1664 gene, herein designated VGAM GENE, encodes a VGAM1664 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1664 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1664 precur-

sor RNA is designated SEQ ID:1650, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1650 is located at position 105330 relative to the genome of Cercopithecine herpesvirus 7.

[23254] VGAM1664 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1664 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23255] An enzyme complex designated DICER COMPLEX, dices the VGAM1664 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1664 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 42%) nucleotide sequence of VGAM1664 RNA is designated SEQ ID:4375, and is provided hereinbelow with reference to the sequence listing part.

[23256] VGAM1664 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1664 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1664 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23257] VGAM1664 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1664 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1664 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I,

BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1664 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1664 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23258] The complementary binding of VGAM1664 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1664 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1664 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1664 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[23259] It is appreciated that VGAM1664 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM1664 host target genes. The mRNA of each one of this plurality of VGAM1664 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1664 RNA, herein designated VGAM RNA, and which when bound by VGAM1664 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1664 host target proteins.

[23260] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1664 gene, herein designated VGAM GENE, on one or more VGAM1664 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23261] It is yet further appreciated that a function of VGAM1664 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1664 include diagnosis, prevention and treatment of viral infection by Cercopithecine herpesvirus 7. Specific functions, and accordingly utilities, of VGAM1664 correlate with, and may be deduced from, the identity of the host target genes which VGAM1664 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[23262] Nucleotide sequences of the VGAM1664 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1664 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1664 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1664 are further described hereinbelow with reference to Table 1.

[23263] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites

to VGAM1664 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[23264] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1665 (VGAM1665) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[23265] VGAM1665 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1665 was detected is described hereinabove with reference to Figs. 2-8.

[23266] VGAM1665 gene, herein designated VGAM GENE, is a viral gene contained in the genome of infectious spleen and kidney necrosis virus. VGAM1665 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[23267] VGAM1665 gene, herein designated VGAM GENE, encodes a VGAM1665 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1665 precursor RNA, herein designated VGAM PRECURSOR RNA, does not en-

code a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1665 precursor RNA is designated SEQ ID:1651, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1651 is located at position 60134 relative to the genome of infectious spleen and kidney necrosis virus.

[23268] VGAM1665 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1665 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23269] An enzyme complex designated DICER COMPLEX, dices the VGAM1665 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1665 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM1665 RNA is designated SEQ ID:4376, and is provided hereinbelow with reference to the sequence listing part.

[23270] VGAM1665 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1665 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1665 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23271] VGAM1665 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1665 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1665 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host

target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1665 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1665 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23272] The complementary binding of VGAM1665 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1665 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1665 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1665 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[23273] It is appreciated that VGAM1665 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1665 host target genes. The mRNA of each one of this plurality of VGAM1665 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1665 RNA, herein designated VGAM RNA, and which when bound by VGAM1665 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1665 host target proteins.

[23274] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1665 gene, herein designated VGAM GENE, on one or more VGAM1665 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23275] It is yet further appreciated that a function of VGAM1665 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1665 include diagnosis, prevention and treatment of viral infection by infectious spleen and kidney necrosis virus. Specific functions, and accordingly utilities, of VGAM1665 correlate with, and may be deduced from, the identity of the host target genes which VGAM1665 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[23276] Nucleotide sequences of the VGAM1665 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1665 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1665 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1665 are further described hereinbelow with reference to Table 1.

[23277] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1665 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[23278] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1666 (VGAM1666) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[23279] VGAM1666 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1666 was detected is described hereinabove with reference to Figs. 2-8.

[23280] VGAM1666 gene, herein designated VGAM GENE, is a viral gene contained in the genome of infectious spleen and kidney necrosis virus. VGAM1666 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[23281] VGAM1666 gene, herein designated VGAM GENE, encodes a VGAM1666 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and un-

like most ordinary genes, VGAM1666 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1666 precursor RNA is designated SEQ ID:1652, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1652 is located at position 58471 relative to the genome of infectious spleen and kidney necrosis virus.

[23282] VGAM1666 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1666 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23283] An enzyme complex designated DICER COMPLEX, dices the VGAM1666 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1666 RNA, herein designated VGAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 75%) nucleotide sequence of VGAM1666 RNA is designated SEQ ID:4377, and is provided hereinbelow with reference to the sequence listing part.

[23284] VGAM1666 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1666 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1666 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23285] VGAM1666 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1666 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1666 RNA, herein designated

VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1666 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1666 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23286] The complementary binding of VGAM1666 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1666 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1666 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1666 host target protein, herein desig-

nated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[23287] It is appreciated that VGAM1666 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1666 host target genes. The mRNA of each one of this plurality of VGAM1666 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1666 RNA, herein designated VGAM RNA, and which when bound by VGAM1666 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1666 host target proteins.

[23288] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1666 gene, herein designated VGAM GENE, on one or more VGAM1666 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23289] It is yet further appreciated that a function of VGAM1666 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1666 include diagnosis, prevention and treatment of viral infection by infectious spleen and kidney necrosis virus. Specific functions, and accordingly utilities, of VGAM1666 correlate with, and may be deduced from, the identity of the host target genes which VGAM1666 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[23290] Nucleotide sequences of the VGAM1666 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1666 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1666 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1666 are further described hereinbelow with reference to Table 1.

[23291] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1666 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[23292] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1667 (VGAM1667) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[23293] VGAM1667 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1667 was detected is described hereinabove with reference to Figs. 2-8.

[23294] VGAM1667 gene, herein designated VGAM GENE, is a viral gene contained in the genome of infectious spleen and kidney necrosis virus. VGAM1667 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[23295] VGAM1667 gene, herein designated VGAM GENE, encodes

a VGAM1667 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1667 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1667 precursor RNA is designated SEQ ID:1653, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1653 is located at position 52329 relative to the genome of infectious spleen and kidney necrosis virus.

[23296] VGAM1667 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1667 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23297] An enzyme complex designated DICER COMPLEX, dices the VGAM1667 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, into VGAM1667 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM1667 RNA is designated SEQ ID:4378, and is provided hereinbelow with reference to the sequence listing part.

[23298] VGAM1667 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1667 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1667 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23299] VGAM1667 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1667 host target RNA, herein designated VGAM HOST TARGET RNA. This

complementary binding is due to the fact that the nucleotide sequence of VGAM1667 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1667 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1667 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23300] The complementary binding of VGAM1667 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1667 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1667

host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1667 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[23301] It is appreciated that VGAM1667 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1667 host target genes. The mRNA of each one of this plurality of VGAM1667 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1667 RNA, herein designated VGAM RNA, and which when bound by VGAM1667 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1667 host target proteins.

[23302] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1667 gene, herein designated VGAM GENE, on one or more VGAM1667 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23303] It is yet further appreciated that a function of VGAM1667 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1667 include diagnosis, prevention and treatment of viral infection by infectious spleen and kidney necrosis virus. Specific functions, and accordingly utilities, of VGAM1667 correlate with, and may be deduced from, the identity of the host target genes which VGAM1667 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[23304] Nucleotide sequences of the VGAM1667 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1667 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1667 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM1667 are further described hereinbelow with reference to Table 1.

[23305] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1667 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[23306] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1668 (VGAM1668) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[23307] VGAM1668 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1668 was detected is described hereinabove with reference to Figs. 2-8.

[23308] VGAM1668 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human adenovirus D. VGAM1668 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the

human genome.

[23309] VGAM1668 gene, herein designated VGAM GENE, encodes a VGAM1668 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1668 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1668 precursor RNA is designated SEQ ID:1654, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1654 is located at position 20850 relative to the genome of Human adenovirus D.

[23310] VGAM1668 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1668 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23311] An enzyme complex designated DICER COMPLEX, dices

the VGAM1668 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1668 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 70%) nucleotide sequence of VGAM1668 RNA is designated SEQ ID:4379, and is provided hereinbelow with reference to the sequence listing part.

[23312] VGAM1668 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1668 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1668 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23313] VGAM1668 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1668 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1668 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1668 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1668 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23314] The complementary binding of VGAM1668 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1668 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM1668 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1668 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[23315] It is appreciated that VGAM1668 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1668 host target genes. The mRNA of each one of this plurality of VGAM1668 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1668 RNA, herein designated VGAM RNA, and which when bound by VGAM1668 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1668 host target proteins.

[23316] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1668 gene, herein designated VGAM GENE, on one or more VGAM1668 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23317] It is yet further appreciated that a function of VGAM1668 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1668 include diagnosis, prevention and treatment of viral infection by Human adenovirus D. Specific functions, and accordingly utilities, of VGAM1668 correlate with, and may be deduced from, the identity of the host target genes which VGAM1668 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[23318] Nucleotide sequences of the VGAM1668 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1668 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of

VGAM1668 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1668 are further described hereinbelow with reference to Table 1.

[23319] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1668 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[23320] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1669 (VGAM1669) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[23321] VGAM1669 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1669 was detected is described hereinabove with reference to Figs. 2-8.

[23322] VGAM1669 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human adenovirus D. VGAM1669 host target gene, herein designated VGAM

HOST TARGET GENE, is a human gene contained in the human genome.

[23323] VGAM1669 gene, herein designated VGAM GENE, encodes a VGAM1669 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1669 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1669 precursor RNA is designated SEQ ID:1655, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1655 is located at position 18504 relative to the genome of Human adenovirus D.

[23324] VGAM1669 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1669 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23325] An enzyme complex designated DICER COMPLEX, dices the VGAM1669 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1669 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM1669 RNA is designated SEQ ID:4380, and is provided hereinbelow with reference to the sequence listing part.

[23326] VGAM1669 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1669 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1669 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23327] VGAM1669 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites

located in untranslated regions of VGAM1669 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1669 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1669 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1669 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23328] The complementary binding of VGAM1669 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1669 host target RNA, herein designated VGAM

HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1669 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1669 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[23329] It is appreciated that VGAM1669 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1669 host target genes. The mRNA of each one of this plurality of VGAM1669 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1669 RNA, herein designated VGAM RNA, and which when bound by VGAM1669 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1669 host target proteins.

[23330] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1669 gene, herein designated VGAM GENE, on one or more VGAM1669 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove

with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23331] It is yet further appreciated that a function of VGAM1669 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1669 include diagnosis, prevention and treatment of viral infection by Human adenovirus D. Specific functions, and accordingly utilities, of VGAM1669 correlate with, and may be deduced from, the identity of the host target genes which VGAM1669 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[23332] Nucleotide sequences of the VGAM1669 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1669 RNA, herein designated VGAM RNA, and

a schematic representation of the secondary folding of VGAM1669 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1669 are further described hereinbelow with reference to Table 1.

[23333] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1669 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[23334] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1670 (VGAM1670) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[23335] VGAM1670 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1670 was detected is described hereinabove with reference to Figs. 2-8.

[23336] VGAM1670 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human adenovirus D.

VGAM1670 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[23337] VGAM1670 gene, herein designated VGAM GENE, encodes a VGAM1670 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1670 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1670 precursor RNA is designated SEQ ID:1656, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1656 is located at position 16692 relative to the genome of Human adenovirus D.

[23338] VGAM1670 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1670 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[23339] An enzyme complex designated DICER COMPLEX, dices the VGAM1670 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1670 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM1670 RNA is designated SEQ ID:4381, and is provided hereinbelow with reference to the sequence listing part.

[23340] VGAM1670 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1670 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1670 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23341] VGAM1670 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM1670 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1670 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1670 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1670 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23342] The complementary binding of VGAM1670 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM1670 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1670 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1670 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[23343] It is appreciated that VGAM1670 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1670 host target genes. The mRNA of each one of this plurality of VGAM1670 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1670 RNA, herein designated VGAM RNA, and which when bound by VGAM1670 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1670 host target proteins.

[23344] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1670 gene, herein designated VGAM GENE, on one or more VGAM1670 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23345] It is yet further appreciated that a function of VGAM1670 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1670 include diagnosis, prevention and treatment of viral infection by Human adenovirus D. Specific functions, and accordingly utilities, of VGAM1670 correlate with, and may be deduced from, the identity of the host target genes which VGAM1670 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[23346] Nucleotide sequences of the VGAM1670 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

diced VGAM1670 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1670 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1670 are further described hereinbelow with reference to Table 1.

[23347] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1670 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[23348] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1671 (VGAM1671) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[23349] VGAM1671 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1671 was detected is described hereinabove with reference to Figs. 2-8.

[23350] VGAM1671 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of Human adenovirus D. VGAM1671 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[23351] VGAM1671 gene, herein designated VGAM GENE, encodes a VGAM1671 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1671 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1671 precursor RNA is designated SEQ ID:1657, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1657 is located at position 13911 relative to the genome of Human adenovirus D.

[23352] VGAM1671 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1671 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23353] An enzyme complex designated DICER COMPLEX, dices the VGAM1671 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1671 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM1671 RNA is designated SEQ ID:4382, and is provided hereinbelow with reference to the sequence listing part.

[23354] VGAM1671 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1671 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1671 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23355] VGAM1671 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1671 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1671 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1671 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1671 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23356] The complementary binding of VGAM1671 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM1671 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1671 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1671 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[23357] It is appreciated that VGAM1671 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1671 host target genes. The mRNA of each one of this plurality of VGAM1671 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1671 RNA, herein designated VGAM RNA, and which when bound by VGAM1671 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1671 host target proteins.

[23358] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1671 gene, herein designated VGAM GENE, on one or more VGAM1671 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23359] It is yet further appreciated that a function of VGAM1671 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1671 include diagnosis, prevention and treatment of viral infection by Human adenovirus D. Specific functions, and accordingly utilities, of VGAM1671 correlate with, and may be deduced from, the identity of the host target genes which VGAM1671 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[23360] Nucleotide sequences of the VGAM1671 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the diced VGAM1671 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1671 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1671 are further described hereinbelow with reference to Table 1.

[23361] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1671 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[23362] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1672 (VGAM1672) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[23363] VGAM1672 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1672 was detected is described hereinabove with reference to Figs. 2-8.

[23364] VGAM1672 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Tick-borne encephalitis virus. VGAM1672 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[23365] VGAM1672 gene, herein designated VGAM GENE, encodes a VGAM1672 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1672 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1672 precursor RNA is designated SEQ ID:1658, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1658 is located at position 9955 relative to the genome of Tick-borne encephalitis virus.

[23366] VGAM1672 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1672 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23367] An enzyme complex designated DICER COMPLEX, dices the VGAM1672 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1672 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of VGAM1672 RNA is designated SEQ ID:4383, and is provided hereinbelow with reference to the sequence listing part.

[23368] VGAM1672 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1672 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1672 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN COD-

ING and 3UTR respectively.

[23369] VGAM1672 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1672 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1672 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1672 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1672 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23370] The complementary binding of VGAM1672 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1672 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1672 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1672 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[23371] It is appreciated that VGAM1672 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1672 host target genes. The mRNA of each one of this plurality of VGAM1672 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1672 RNA, herein designated VGAM RNA, and which when bound by VGAM1672 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1672 host target proteins.

[23372] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1672 gene, herein designated VGAM GENE, on one

or more VGAM1672 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23373] It is yet further appreciated that a function of VGAM1672 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1672 include diagnosis, prevention and treatment of viral infection by Tick-borne encephalitis virus. Specific functions, and accordingly utilities, of VGAM1672 correlate with, and may be deduced from, the identity of the host target genes which VGAM1672 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[23374] Nucleotide sequences of the VGAM1672 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1672 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1672 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1672 are further described hereinbelow with reference to Table 1.

[23375] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1672 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[23376] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1673 (VGAM1673) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[23377] VGAM1673 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1673 was detected is de-

scribed hereinabove with reference to Figs. 2-8.

[23378] VGAM1673 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Tick-borne encephalitis virus. VGAM1673 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[23379] VGAM1673 gene, herein designated VGAM GENE, encodes a VGAM1673 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1673 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1673 precursor RNA is designated SEQ ID:1659, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1659 is located at position 6145 relative to the genome of Tick-borne encephalitis virus.

[23380] VGAM1673 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1673 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23381] An enzyme complex designated DICER COMPLEX, dices the VGAM1673 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1673 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM1673 RNA is designated SEQ ID:4384, and is provided hereinbelow with reference to the sequence listing part.

[23382] VGAM1673 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1673 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1673 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and

a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23383] VGAM1673 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1673 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1673 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1673 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1673 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both

3UTR and 5UTR regions.

[23384] The complementary binding of VGAM1673 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1673 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1673 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1673 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[23385] It is appreciated that VGAM1673 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1673 host target genes. The mRNA of each one of this plurality of VGAM1673 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1673 RNA, herein designated VGAM RNA, and which when bound by VGAM1673 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1673 host target proteins.

[23386] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM1673 gene, herein designated VGAM GENE, on one or more VGAM1673 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23387] It is yet further appreciated that a function of VGAM1673 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1673 include diagnosis, prevention and treatment of viral infection by Tick-borne encephalitis virus. Specific functions, and accordingly utilities, of VGAM1673 correlate with, and may be deduced from, the identity of the host target genes which VGAM1673 binds and inhibits, and the function of these host target genes,

as elaborated hereinbelow.

[23388] Nucleotide sequences of the VGAM1673 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1673 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1673 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1673 are further described hereinbelow with reference to Table 1.

[23389] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1673 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[23390] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1674 (VGAM1674) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[23391] VGAM1674 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene.

The method by which VGAM1674 was detected is described hereinabove with reference to Figs. 2-8.

[23392] VGAM1674 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Tick-borne encephalitis virus. VGAM1674 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[23393] VGAM1674 gene, herein designated VGAM GENE, encodes a VGAM1674 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1674 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1674 precursor RNA is designated SEQ ID:1660, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1660 is located at position 4389 relative to the genome of Tick-borne encephalitis virus.

[23394] VGAM1674 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1674 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23395] An enzyme complex designated DICER COMPLEX, dices the VGAM1674 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1674 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 56%) nucleotide sequence of VGAM1674 RNA is designated SEQ ID:4385, and is provided hereinbelow with reference to the sequence listing part.

[23396] VGAM1674 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1674 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1674 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding

gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23397] VGAM1674 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1674 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1674 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1674 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1674 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be lo-

cated in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23398] The complementary binding of VGAM1674 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1674 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1674 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1674 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[23399] It is appreciated that VGAM1674 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1674 host target genes. The mRNA of each one of this plurality of VGAM1674 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1674 RNA, herein designated VGAM RNA, and which when bound by VGAM1674 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1674 host target proteins.

[23400] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM1674 gene, herein designated VGAM GENE, on one or more VGAM1674 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23401] It is yet further appreciated that a function of VGAM1674 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1674 include diagnosis, prevention and treatment of viral infection by Tick-borne encephalitis virus. Specific functions, and accordingly utilities, of VGAM1674 correlate with, and may be deduced from, the identity of the host target genes which VGAM1674 binds

and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[23402] Nucleotide sequences of the VGAM1674 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1674 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1674 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1674 are further described hereinbelow with reference to Table 1.

[23403] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1674 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[23404] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1675 (VGAM1675) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[23405] VGAM1675 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1675 was detected is described hereinabove with reference to Figs. 2-8.

[23406] VGAM1675 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Viral hemorrhagic septicemia virus. VGAM1675 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[23407] VGAM1675 gene, herein designated VGAM GENE, encodes a VGAM1675 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1675 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1675 precursor RNA is designated SEQ ID:1661, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1661 is located at position 1531 relative to the genome of Viral hemorrhagic septicemia virus.

[23408] VGAM1675 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1675 folded precursor RNA, herein designated VGAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23409] An enzyme complex designated DICER COMPLEX, dices the VGAM1675 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1675 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM1675 RNA is designated SEQ ID:4386, and is provided hereinbelow with reference to the sequence listing part.

[23410] VGAM1675 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1675 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1675 host target RNA,

herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23411] VGAM1675 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1675 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1675 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1675 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1675 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host tar-

get binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23412] The complementary binding of VGAM1675 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1675 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1675 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1675 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[23413] It is appreciated that VGAM1675 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1675 host target genes. The mRNA of each one of this plurality of VGAM1675 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1675 RNA, herein designated VGAM RNA, and which when bound by VGAM1675 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1675 host target proteins.

[23414] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1675 gene, herein designated VGAM GENE, on one or more VGAM1675 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23415] It is yet further appreciated that a function of VGAM1675 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1675 include diagnosis, prevention and treatment of viral infection by Viral hemorrhagic septicemia virus. Specific functions, and accordingly utilities,

of VGAM1675 correlate with, and may be deduced from, the identity of the host target genes which VGAM1675 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[23416] Nucleotide sequences of the VGAM1675 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1675 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1675 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1675 are further described hereinbelow with reference to Table 1.

[23417] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1675 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[23418] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1676 (VGAM1676) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the

art.

[23419] VGAM1676 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1676 was detected is described hereinabove with reference to Figs. 2-8.

[23420] VGAM1676 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Viral hemorrhagic septicemia virus. VGAM1676 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[23421] VGAM1676 gene, herein designated VGAM GENE, encodes a VGAM1676 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1676 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1676 precursor RNA is designated SEQ ID:1662, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1662 is located at position 7506 relative to the genome of Viral hemorrhagic septicemia virus.

[23422] VGAM1676 precursor RNA, herein designated VGAM PRE-

CURSOR RNA, folds onto itself, forming VGAM1676 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23423] An enzyme complex designated DICER COMPLEX, dices the VGAM1676 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1676 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 51%) nucleotide sequence of VGAM1676 RNA is designated SEQ ID:4387, and is provided hereinbelow with reference to the sequence listing part.

[23424] VGAM1676 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM1676 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1676 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23425] VGAM1676 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1676 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1676 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1676 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1676 host

target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23426] The complementary binding of VGAM1676 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1676 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1676 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1676 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[23427] It is appreciated that VGAM1676 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1676 host target genes. The mRNA of each one of this plurality of VGAM1676 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1676 RNA, herein designated VGAM RNA, and which when bound by VGAM1676 RNA, herein

designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1676 host target proteins.

[23428] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1676 gene, herein designated VGAM GENE, on one or more VGAM1676 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23429] It is yet further appreciated that a function of VGAM1676 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1676 include diagnosis, prevention and

treatment of viral infection by Viral hemorrhagic septicemia virus. Specific functions, and accordingly utilities, of VGAM1676 correlate with, and may be deduced from, the identity of the host target genes which VGAM1676 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[23430] Nucleotide sequences of the VGAM1676 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1676 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1676 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1676 are further described hereinbelow with reference to Table 1.

[23431] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1676 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[23432] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1677 (VGAM1677) viral gene, which modulates ex-

pression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[23433] VGAM1677 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1677 was detected is described hereinabove with reference to Figs. 2-8.

[23434] VGAM1677 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Viral hemorrhagic septicemia virus. VGAM1677 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[23435] VGAM1677 gene, herein designated VGAM GENE, encodes a VGAM1677 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1677 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1677 precursor RNA is designated SEQ ID:1663, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1663 is located at position 5586 relative to the genome of Viral hemorrhagic septicemia

virus.

[23436] VGAM1677 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1677 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23437] An enzyme complex designated DICER COMPLEX, dices the VGAM1677 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1677 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 50%) nucleotide sequence of VGAM1677 RNA is designated SEQ ID:4388, and is provided hereinbelow with reference to the sequence listing part.

[23438] VGAM1677 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1677 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1677 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23439] VGAM1677 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1677 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1677 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1677 RNA, herein designated

VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1677 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23440] The complementary binding of VGAM1677 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1677 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1677 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1677 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[23441] It is appreciated that VGAM1677 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1677 host target genes. The mRNA of each one of this plurality of VGAM1677 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM1677 RNA, herein designated VGAM RNA, and which when bound by VGAM1677 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1677 host target proteins.

[23442] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1677 gene, herein designated VGAM GENE, on one or more VGAM1677 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23443] It is yet further appreciated that a function of VGAM1677 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1677 include diagnosis, prevention and treatment of viral infection by Viral hemorrhagic septicemia virus. Specific functions, and accordingly utilities, of VGAM1677 correlate with, and may be deduced from, the identity of the host target genes which VGAM1677 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[23444] Nucleotide sequences of the VGAM1677 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1677 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1677 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1677 are further described hereinbelow with reference to Table 1.

[23445] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1677 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[23446] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present

invention, referred to here as Viral Genomic Address Messenger 1678 (VGAM1678) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[23447] VGAM1678 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1678 was detected is described hereinabove with reference to Figs. 2-8.

[23448] VGAM1678 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Viral hemorrhagic septicemia virus. VGAM1678 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[23449] VGAM1678 gene, herein designated VGAM GENE, encodes a VGAM1678 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1678 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1678 precursor RNA is designated SEQ ID:1664, and is provided hereinbelow with reference to the sequence listing part. Nu-

cleotide sequence SEQ ID:1664 is located at position 10783 relative to the genome of Viral hemorrhagic septicemia virus.

[23450] VGAM1678 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1678 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23451] An enzyme complex designated DICER COMPLEX, dices the VGAM1678 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1678 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 87%) nucleotide sequence of VGAM1678 RNA is designated SEQ ID:4389, and

is provided hereinbelow with reference to the sequence listing part.

[23452] VGAM1678 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1678 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1678 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23453] VGAM1678 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1678 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1678 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites

shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1678 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1678 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23454] The complementary binding of VGAM1678 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1678 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1678 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1678 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[23455] It is appreciated that VGAM1678 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1678 host target genes. The mRNA of each one of this plurality of VGAM1678 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1678 RNA, herein designated VGAM RNA, and which when bound by VGAM1678 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1678 host target proteins.

[23456] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1678 gene, herein designated VGAM GENE, on one or more VGAM1678 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23457] It is yet further appreciated that a function of VGAM1678 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1678 include diagnosis, prevention and treatment of viral infection by Viral hemorrhagic septicemia virus. Specific functions, and accordingly utilities,

of VGAM1678 correlate with, and may be deduced from, the identity of the host target genes which VGAM1678 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[23458] Nucleotide sequences of the VGAM1678 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1678 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1678 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1678 are further described hereinbelow with reference to Table 1.

[23459] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1678 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[23460] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1679 (VGAM1679) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the

art.

[23461] VGAM1679 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1679 was detected is described hereinabove with reference to Figs. 2-8.

[23462] VGAM1679 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Viral hemorrhagic septicemia virus. VGAM1679 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[23463] VGAM1679 gene, herein designated VGAM GENE, encodes a VGAM1679 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1679 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1679 precursor RNA is designated SEQ ID:1665, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1665 is located at position 1372 relative to the genome of Viral hemorrhagic septicemia virus.

[23464] VGAM1679 precursor RNA, herein designated VGAM PRE-

CURSOR RNA, folds onto itself, forming VGAM1679 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23465] An enzyme complex designated DICER COMPLEX, dices the VGAM1679 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1679 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM1679 RNA is designated SEQ ID:4390, and is provided hereinbelow with reference to the sequence listing part.

[23466] VGAM1679 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM1679 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1679 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23467] VGAM1679 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1679 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1679 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1679 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1679 host

target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23468] The complementary binding of VGAM1679 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1679 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1679 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1679 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[23469] It is appreciated that VGAM1679 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1679 host target genes. The mRNA of each one of this plurality of VGAM1679 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1679 RNA, herein designated VGAM RNA, and which when bound by VGAM1679 RNA, herein

designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1679 host target proteins.

[23470] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1679 gene, herein designated VGAM GENE, on one or more VGAM1679 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23471] It is yet further appreciated that a function of VGAM1679 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1679 include diagnosis, prevention and

treatment of viral infection by Viral hemorrhagic septicemia virus. Specific functions, and accordingly utilities, of VGAM1679 correlate with, and may be deduced from, the identity of the host target genes which VGAM1679 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[23472] Nucleotide sequences of the VGAM1679 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1679 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1679 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1679 are further described hereinbelow with reference to Table 1.

[23473] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1679 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[23474] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1680 (VGAM1680) viral gene, which modulates ex-

pression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[23475] VGAM1680 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1680 was detected is described hereinabove with reference to Figs. 2-8.

[23476] VGAM1680 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Viral hemorrhagic septicemia virus. VGAM1680 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[23477] VGAM1680 gene, herein designated VGAM GENE, encodes a VGAM1680 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1680 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1680 precursor RNA is designated SEQ ID:1666, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1666 is located at position 10244 relative to the genome of Viral hemorrhagic sep-

ticemia virus.

[23478] VGAM1680 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1680 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23479] An enzyme complex designated DICER COMPLEX, dices the VGAM1680 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1680 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM1680 RNA is designated SEQ ID:4391, and is provided hereinbelow with reference to the sequence listing part.

[23480] VGAM1680 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1680 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1680 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23481] VGAM1680 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1680 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1680 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1680 RNA, herein designated

VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1680 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23482] The complementary binding of VGAM1680 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1680 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1680 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1680 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[23483] It is appreciated that VGAM1680 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1680 host target genes. The mRNA of each one of this plurality of VGAM1680 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM1680 RNA, herein designated VGAM RNA, and which when bound by VGAM1680 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1680 host target proteins.

[23484] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1680 gene, herein designated VGAM GENE, on one or more VGAM1680 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23485] It is yet further appreciated that a function of VGAM1680 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1680 include diagnosis, prevention and treatment of viral infection by Viral hemorrhagic septicemia virus. Specific functions, and accordingly utilities, of VGAM1680 correlate with, and may be deduced from, the identity of the host target genes which VGAM1680 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[23486] Nucleotide sequences of the VGAM1680 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1680 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1680 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1680 are further described hereinbelow with reference to Table 1.

[23487] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1680 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[23488] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present

invention, referred to here as Viral Genomic Address Messenger 1681 (VGAM1681) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[23489] VGAM1681 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1681 was detected is described hereinabove with reference to Figs. 2-8.

[23490] VGAM1681 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Vesicular stomatitis Indiana virus. VGAM1681 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[23491] VGAM1681 gene, herein designated VGAM GENE, encodes a VGAM1681 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1681 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1681 precursor RNA is designated SEQ ID:1667, and is provided hereinbelow with reference to the sequence listing part. Nu-

cleotide sequence SEQ ID:1667 is located at position 3549 relative to the genome of Vesicular stomatitis Indiana virus.

[23492] VGAM1681 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1681 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23493] An enzyme complex designated DICER COMPLEX, dices the VGAM1681 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1681 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM1681 RNA is designated SEQ ID:4392, and

is provided hereinbelow with reference to the sequence listing part.

[23494] VGAM1681 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1681 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1681 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23495] VGAM1681 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1681 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1681 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites

shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1681 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1681 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23496] The complementary binding of VGAM1681 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1681 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1681 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1681 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[23497] It is appreciated that VGAM1681 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1681 host target genes. The mRNA of each one of this plurality of VGAM1681 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1681 RNA, herein designated VGAM RNA, and which when bound by VGAM1681 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1681 host target proteins.

[23498] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1681 gene, herein designated VGAM GENE, on one or more VGAM1681 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23499] It is yet further appreciated that a function of VGAM1681 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1681 include diagnosis, prevention and treatment of viral infection by Vesicular stomatitis Indiana virus. Specific functions, and accordingly utilities, of VGAM1681 correlate with, and may be deduced from, the identity of the host target genes which VGAM1681 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[23500] Nucleotide sequences of the VGAM1681 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1681 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1681 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1681 are further described hereinbelow with reference to Table 1.

[23501] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1681 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[23502] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1682 (VGAM1682) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[23503] VGAM1682 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1682 was detected is described hereinabove with reference to Figs. 2-8.

[23504] VGAM1682 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Vesicular stomatitis Indiana virus. VGAM1682 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[23505] VGAM1682 gene, herein designated VGAM GENE, encodes a VGAM1682 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1682 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1682 precur-

sor RNA is designated SEQ ID:1668, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1668 is located at position 10245 relative to the genome of Vesicular stomatitis Indiana virus.

[23506] VGAM1682 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1682 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23507] An enzyme complex designated DICER COMPLEX, dices the VGAM1682 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1682 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 41%) nucleotide sequence of VGAM1682 RNA is designated SEQ ID:4393, and is provided hereinbelow with reference to the sequence listing part.

[23508] VGAM1682 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1682 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1682 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23509] VGAM1682 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1682 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1682 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I,

BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1682 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1682 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23510] The complementary binding of VGAM1682 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1682 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1682 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1682 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[23511] It is appreciated that VGAM1682 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM1682 host target genes. The mRNA of each one of this plurality of VGAM1682 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1682 RNA, herein designated VGAM RNA, and which when bound by VGAM1682 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1682 host target proteins.

[23512] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1682 gene, herein designated VGAM GENE, on one or more VGAM1682 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23513] It is yet further appreciated that a function of VGAM1682 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1682 include diagnosis, prevention and treatment of viral infection by Vesicular stomatitis Indiana virus. Specific functions, and accordingly utilities, of VGAM1682 correlate with, and may be deduced from, the identity of the host target genes which VGAM1682 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[23514] Nucleotide sequences of the VGAM1682 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1682 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1682 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1682 are further described hereinbelow with reference to Table 1.

[23515] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites

to VGAM1682 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[23516] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1683 (VGAM1683) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[23517] VGAM1683 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1683 was detected is described hereinabove with reference to Figs. 2-8.

[23518] VGAM1683 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Vesicular stomatitis Indiana virus. VGAM1683 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[23519] VGAM1683 gene, herein designated VGAM GENE, encodes a VGAM1683 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1683 precursor RNA, herein designated VGAM PRECURSOR RNA, does not en-

code a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1683 precursor RNA is designated SEQ ID:1669, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1669 is located at position 8817 relative to the genome of Vesicular stomatitis Indiana virus.

[23520] VGAM1683 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1683 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23521] An enzyme complex designated DICER COMPLEX, dices the VGAM1683 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1683 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM1683 RNA is designated SEQ ID:4394, and is provided hereinbelow with reference to the sequence listing part.

[23522] VGAM1683 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1683 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1683 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23523] VGAM1683 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1683 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1683 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host

target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1683 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1683 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23524] The complementary binding of VGAM1683 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1683 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1683 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1683 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[23525] It is appreciated that VGAM1683 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1683 host target genes. The mRNA of each one of this plurality of VGAM1683 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1683 RNA, herein designated VGAM RNA, and which when bound by VGAM1683 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1683 host target proteins.

[23526] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1683 gene, herein designated VGAM GENE, on one or more VGAM1683 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23527] It is yet further appreciated that a function of VGAM1683 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1683 include diagnosis, prevention and treatment of viral infection by Vesicular stomatitis Indiana virus. Specific functions, and accordingly utilities, of VGAM1683 correlate with, and may be deduced from, the identity of the host target genes which VGAM1683 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[23528] Nucleotide sequences of the VGAM1683 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1683 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1683 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1683 are further described hereinbelow with reference to Table 1.

[23529] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1683 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[23530] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1684 (VGAM1684) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[23531] VGAM1684 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1684 was detected is described hereinabove with reference to Figs. 2-8.

[23532] VGAM1684 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Vesicular stomatitis Indiana virus. VGAM1684 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[23533] VGAM1684 gene, herein designated VGAM GENE, encodes a VGAM1684 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and un-

like most ordinary genes, VGAM1684 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1684 precursor RNA is designated SEQ ID:1670, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1670 is located at position 5581 relative to the genome of Vesicular stomatitis Indiana virus.

[23534] VGAM1684 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1684 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23535] An enzyme complex designated DICER COMPLEX, dices the VGAM1684 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1684 RNA, herein designated VGAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 68%) nucleotide sequence of VGAM1684 RNA is designated SEQ ID:4395, and is provided hereinbelow with reference to the sequence listing part.

[23536] VGAM1684 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1684 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1684 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23537] VGAM1684 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1684 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1684 RNA, herein designated

VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1684 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1684 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23538] The complementary binding of VGAM1684 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1684 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1684 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1684 host target protein, herein desig-

nated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[23539] It is appreciated that VGAM1684 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1684 host target genes. The mRNA of each one of this plurality of VGAM1684 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1684 RNA, herein designated VGAM RNA, and which when bound by VGAM1684 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1684 host target proteins.

[23540] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1684 gene, herein designated VGAM GENE, on one or more VGAM1684 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23541] It is yet further appreciated that a function of VGAM1684 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1684 include diagnosis, prevention and treatment of viral infection by Vesicular stomatitis Indiana virus. Specific functions, and accordingly utilities, of VGAM1684 correlate with, and may be deduced from, the identity of the host target genes which VGAM1684 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[23542] Nucleotide sequences of the VGAM1684 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1684 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1684 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1684 are further described hereinbelow with reference to Table 1.

[23543] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1684 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[23544] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1685 (VGAM1685) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[23545] VGAM1685 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1685 was detected is described hereinabove with reference to Figs. 2-8.

[23546] VGAM1685 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Vesicular stomatitis Indiana virus. VGAM1685 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[23547] VGAM1685 gene, herein designated VGAM GENE, encodes

a VGAM1685 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1685 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1685 precursor RNA is designated SEQ ID:1671, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1671 is located at position 4965 relative to the genome of Vesicular stomatitis Indiana virus.

[23548] VGAM1685 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1685 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23549] An enzyme complex designated DICER COMPLEX, dices the VGAM1685 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, into VGAM1685 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 61%) nucleotide sequence of VGAM1685 RNA is designated SEQ ID:4396, and is provided hereinbelow with reference to the sequence listing part.

[23550] VGAM1685 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1685 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1685 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23551] VGAM1685 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1685 host target RNA, herein designated VGAM HOST TARGET RNA. This

complementary binding is due to the fact that the nucleotide sequence of VGAM1685 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1685 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1685 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23552] The complementary binding of VGAM1685 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1685 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1685

host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1685 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[23553] It is appreciated that VGAM1685 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1685 host target genes. The mRNA of each one of this plurality of VGAM1685 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1685 RNA, herein designated VGAM RNA, and which when bound by VGAM1685 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1685 host target proteins.

[23554] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1685 gene, herein designated VGAM GENE, on one or more VGAM1685 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23555] It is yet further appreciated that a function of VGAM1685 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1685 include diagnosis, prevention and treatment of viral infection by Vesicular stomatitis Indiana virus. Specific functions, and accordingly utilities, of VGAM1685 correlate with, and may be deduced from, the identity of the host target genes which VGAM1685 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[23556] Nucleotide sequences of the VGAM1685 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1685 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1685 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM1685 are further described hereinbelow with reference to Table 1.

[23557] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1685 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[23558] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1686 (VGAM1686) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[23559] VGAM1686 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1686 was detected is described hereinabove with reference to Figs. 2-8.

[23560] VGAM1686 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Vesicular stomatitis Indiana virus. VGAM1686 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene con-

tained in the human genome.

[23561] VGAM1686 gene, herein designated VGAM GENE, encodes a VGAM1686 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1686 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1686 precursor RNA is designated SEQ ID:1672, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1672 is located at position 2116 relative to the genome of Vesicular stomatitis Indiana virus.

[23562] VGAM1686 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1686 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23563] An enzyme complex designated DICER COMPLEX, dices the VGAM1686 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1686 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 81%) nucleotide sequence of VGAM1686 RNA is designated SEQ ID:4397, and is provided hereinbelow with reference to the sequence listing part.

[23564] VGAM1686 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1686 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1686 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23565] VGAM1686 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites

located in untranslated regions of VGAM1686 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1686 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1686 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1686 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23566] The complementary binding of VGAM1686 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1686 host target RNA, herein designated VGAM

HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1686 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1686 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[23567] It is appreciated that VGAM1686 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1686 host target genes. The mRNA of each one of this plurality of VGAM1686 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1686 RNA, herein designated VGAM RNA, and which when bound by VGAM1686 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1686 host target proteins.

[23568] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1686 gene, herein designated VGAM GENE, on one or more VGAM1686 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove

with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23569] It is yet further appreciated that a function of VGAM1686 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1686 include diagnosis, prevention and treatment of viral infection by Vesicular stomatitis Indiana virus. Specific functions, and accordingly utilities, of VGAM1686 correlate with, and may be deduced from, the identity of the host target genes which VGAM1686 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[23570] Nucleotide sequences of the VGAM1686 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1686 RNA, herein designated VGAM RNA, and

a schematic representation of the secondary folding of VGAM1686 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1686 are further described hereinbelow with reference to Table 1.

[23571] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1686 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[23572] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1687 (VGAM1687) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[23573] VGAM1687 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1687 was detected is described hereinabove with reference to Figs. 2-8.

[23574] VGAM1687 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Chimpanzee cy-

tomegalovirus. VGAM1687 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[23575] VGAM1687 gene, herein designated VGAM GENE, encodes a VGAM1687 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1687 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1687 precursor RNA is designated SEQ ID:1673, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1673 is located at position 126333 relative to the genome of Chimpanzee cytomegalovirus.

[23576] VGAM1687 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1687 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23577] An enzyme complex designated DICER COMPLEX, dices the VGAM1687 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1687 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of VGAM1687 RNA is designated SEQ ID:4398, and is provided hereinbelow with reference to the sequence listing part.

[23578] VGAM1687 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1687 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1687 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23579] VGAM1687 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1687 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1687 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1687 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1687 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23580] The complementary binding of VGAM1687 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM1687 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1687 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1687 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[23581] It is appreciated that VGAM1687 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1687 host target genes. The mRNA of each one of this plurality of VGAM1687 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1687 RNA, herein designated VGAM RNA, and which when bound by VGAM1687 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1687 host target proteins.

[23582] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1687 gene, herein designated VGAM GENE, on one or more VGAM1687 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23583] It is yet further appreciated that a function of VGAM1687 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1687 include diagnosis, prevention and treatment of viral infection by Chimpanzee cytomegalovirus. Specific functions, and accordingly utilities, of VGAM1687 correlate with, and may be deduced from, the identity of the host target genes which VGAM1687 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[23584] Nucleotide sequences of the VGAM1687 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the diced VGAM1687 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1687 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1687 are further described hereinbelow with reference to Table 1.

[23585] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1687 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[23586] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1688 (VGAM1688) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[23587] VGAM1688 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1688 was detected is described hereinabove with reference to Figs. 2-8.

[23588] VGAM1688 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Chimpanzee cytomegalovirus. VGAM1688 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[23589] VGAM1688 gene, herein designated VGAM GENE, encodes a VGAM1688 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1688 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1688 precursor RNA is designated SEQ ID:1674, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1674 is located at position 123345 relative to the genome of Chimpanzee cytomegalovirus.

[23590] VGAM1688 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1688 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23591] An enzyme complex designated DICER COMPLEX, dices the VGAM1688 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1688 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM1688 RNA is designated SEQ ID:4399, and is provided hereinbelow with reference to the sequence listing part.

[23592] VGAM1688 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1688 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1688 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and

a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23593] VGAM1688 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1688 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1688 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1688 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1688 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both

3UTR and 5UTR regions.

[23594] The complementary binding of VGAM1688 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1688 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1688 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1688 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[23595] It is appreciated that VGAM1688 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1688 host target genes. The mRNA of each one of this plurality of VGAM1688 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1688 RNA, herein designated VGAM RNA, and which when bound by VGAM1688 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1688 host target proteins.

[23596] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM1688 gene, herein designated VGAM GENE, on one or more VGAM1688 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23597] It is yet further appreciated that a function of VGAM1688 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1688 include diagnosis, prevention and treatment of viral infection by Chimpanzee cytomegalovirus. Specific functions, and accordingly utilities, of VGAM1688 correlate with, and may be deduced from, the identity of the host target genes which VGAM1688 binds and inhibits, and the function of these

host target genes, as elaborated hereinbelow.

[23598] Nucleotide sequences of the VGAM1688 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1688 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1688 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1688 are further described hereinbelow with reference to Table 1.

[23599] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1688 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[23600] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1689 (VGAM1689) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[23601] VGAM1689 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene.

The method by which VGAM1689 was detected is described hereinabove with reference to Figs. 2-8.

[23602] VGAM1689 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Chimpanzee cytomegalovirus. VGAM1689 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[23603] VGAM1689 gene, herein designated VGAM GENE, encodes a VGAM1689 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1689 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1689 precursor RNA is designated SEQ ID:1675, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1675 is located at position 127857 relative to the genome of Chimpanzee cytomegalovirus.

[23604] VGAM1689 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1689 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23605] An enzyme complex designated DICER COMPLEX, dices the VGAM1689 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1689 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM1689 RNA is designated SEQ ID:4400, and is provided hereinbelow with reference to the sequence listing part.

[23606] VGAM1689 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1689 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1689 host target RNA, herein designated VGAM HOST TARGET RNA, comprises

three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23607] VGAM1689 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1689 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1689 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1689 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1689 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an

example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23608] The complementary binding of VGAM1689 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1689 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1689 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1689 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[23609] It is appreciated that VGAM1689 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1689 host target genes. The mRNA of each one of this plurality of VGAM1689 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1689 RNA, herein designated VGAM RNA, and which when bound by VGAM1689 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1689 host target proteins.

[23610] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1689 gene, herein designated VGAM GENE, on one or more VGAM1689 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23611] It is yet further appreciated that a function of VGAM1689 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1689 include diagnosis, prevention and treatment of viral infection by Chimpanzee cytomegalovirus. Specific functions, and accordingly utilities, of VGAM1689 correlate with, and may be deduced

from, the identity of the host target genes which VGAM1689 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[23612] Nucleotide sequences of the VGAM1689 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1689 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1689 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1689 are further described hereinbelow with reference to Table 1.

[23613] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1689 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[23614] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1690 (VGAM1690) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[23615] VGAM1690 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1690 was detected is described hereinabove with reference to Figs. 2-8.

[23616] VGAM1690 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectocarpus siliculosus virus. VGAM1690 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[23617] VGAM1690 gene, herein designated VGAM GENE, encodes a VGAM1690 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1690 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1690 precursor RNA is designated SEQ ID:1676, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1676 is located at position 49102 relative to the genome of Ectocarpus siliculosus virus.

[23618] VGAM1690 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1690 folded

precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23619] An enzyme complex designated DICER COMPLEX, dices the VGAM1690 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1690 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM1690 RNA is designated SEQ ID:4401, and is provided hereinbelow with reference to the sequence listing part.

[23620] VGAM1690 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1690 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM1690 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23621] VGAM1690 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1690 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1690 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1690 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1690 host target RNA, herein designated VGAM HOST TARGET RNA.

It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23622] The complementary binding of VGAM1690 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1690 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1690 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1690 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[23623] It is appreciated that VGAM1690 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1690 host target genes. The mRNA of each one of this plurality of VGAM1690 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1690 RNA, herein designated VGAM RNA, and which when bound by VGAM1690 RNA, herein designated VGAM RNA, causes inhibition of translation of

respective one or more VGAM1690 host target proteins.

[23624] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1690 gene, herein designated VGAM GENE, on one or more VGAM1690 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23625] It is yet further appreciated that a function of VGAM1690 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1690 include diagnosis, prevention and treatment of viral infection by Ectocarpus siliculosus virus.

Specific functions, and accordingly utilities, of VGAM1690 correlate with, and may be deduced from, the identity of the host target genes which VGAM1690 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[23626] Nucleotide sequences of the VGAM1690 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1690 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1690 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1690 are further described hereinbelow with reference to Table 1.

[23627] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1690 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[23628] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1691 (VGAM1691) viral gene, which modulates expression of respective host target genes thereof, the func-

tion and utility of which host target genes is known in the art.

[23629] VGAM1691 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1691 was detected is described hereinabove with reference to Figs. 2-8.

[23630] VGAM1691 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectocarpus siliculosus virus. VGAM1691 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[23631] VGAM1691 gene, herein designated VGAM GENE, encodes a VGAM1691 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1691 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1691 precursor RNA is designated SEQ ID:1677, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1677 is located at position 46991 relative to the genome of Ectocarpus siliculosus virus.

[23632] VGAM1691 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1691 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23633] An enzyme complex designated DICER COMPLEX, dices the VGAM1691 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1691 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM1691 RNA is designated SEQ ID:4402, and is provided hereinbelow with reference to the sequence listing part.

[23634] VGAM1691 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1691 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1691 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23635] VGAM1691 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1691 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1691 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1691 RNA, herein designated VGAM RNA, may have a different number of host target

binding sites in untranslated regions of a VGAM1691 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23636] The complementary binding of VGAM1691 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1691 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1691 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1691 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[23637] It is appreciated that VGAM1691 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1691 host target genes. The mRNA of each one of this plurality of VGAM1691 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1691 RNA, herein designated VGAM

RNA, and which when bound by VGAM1691 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1691 host target proteins.

[23638] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1691 gene, herein designated VGAM GENE, on one or more VGAM1691 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23639] It is yet further appreciated that a function of VGAM1691 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM1691 include diagnosis, prevention and treatment of viral infection by Ectocarpus siliculosus virus. Specific functions, and accordingly utilities, of VGAM1691 correlate with, and may be deduced from, the identity of the host target genes which VGAM1691 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[23640] Nucleotide sequences of the VGAM1691 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1691 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1691 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1691 are further described hereinbelow with reference to Table 1.

[23641] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1691 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[23642] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Mes-

senger 1692 (VGAM1692) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[23643] VGAM1692 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1692 was detected is described hereinabove with reference to Figs. 2-8.

[23644] VGAM1692 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectocarpus siliculosus virus. VGAM1692 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[23645] VGAM1692 gene, herein designated VGAM GENE, encodes a VGAM1692 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1692 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1692 precursor RNA is designated SEQ ID:1678, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1678 is located at position

52063 relative to the genome of Ectocarpus siliculosus virus.

[23646] VGAM1692 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1692 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23647] An enzyme complex designated DICER COMPLEX, dices the VGAM1692 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1692 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 47%) nucleotide sequence of VGAM1692 RNA is designated SEQ ID:4403, and is provided hereinbelow with reference to the sequence

listing part.

[23648] VGAM1692 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1692 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1692 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23649] VGAM1692 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1692 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1692 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not

meant to be limiting VGAM1692 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1692 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23650] The complementary binding of VGAM1692 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1692 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1692 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1692 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[23651] It is appreciated that VGAM1692 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1692 host target genes. The mRNA of each one of this plurality of VGAM1692 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM1692 RNA, herein designated VGAM RNA, and which when bound by VGAM1692 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1692 host target proteins.

[23652] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1692 gene, herein designated VGAM GENE, on one or more VGAM1692 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23653] It is yet further appreciated that a function of VGAM1692

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1692 include diagnosis, prevention and treatment of viral infection by Ectocarpus siliculosus virus. Specific functions, and accordingly utilities, of VGAM1692 correlate with, and may be deduced from, the identity of the host target genes which VGAM1692 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[23654] Nucleotide sequences of the VGAM1692 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1692 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1692 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1692 are further described hereinbelow with reference to Table 1.

[23655] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1692 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[23656] Fig. 1 further provides a conceptual description of another

novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1693 (VGAM1693) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[23657] VGAM1693 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1693 was detected is described hereinabove with reference to Figs. 2-8.

[23658] VGAM1693 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectocarpus siliculosus virus. VGAM1693 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[23659] VGAM1693 gene, herein designated VGAM GENE, encodes a VGAM1693 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1693 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1693 precursor RNA is designated SEQ ID:1679, and is provided here-

inbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1679 is located at position 54673 relative to the genome of Ectocarpus siliculosus virus.

[23660] VGAM1693 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1693 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23661] An enzyme complex designated DICER COMPLEX, dices the VGAM1693 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1693 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide se-

quence of VGAM1693 RNA is designated SEQ ID:4404, and is provided hereinbelow with reference to the sequence listing part.

[23662] VGAM1693 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1693 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1693 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23663] VGAM1693 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1693 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1693 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is ap-

preciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1693 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1693 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23664] The complementary binding of VGAM1693 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1693 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1693 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1693 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[23665] It is appreciated that VGAM1693 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1693 host target genes. The mRNA of

each one of this plurality of VGAM1693 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1693 RNA, herein designated VGAM RNA, and which when bound by VGAM1693 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1693 host target proteins.

[23666] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1693 gene, herein designated VGAM GENE, on one or more VGAM1693 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science

294,779 (2001)).

[23667] It is yet further appreciated that a function of VGAM1693 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1693 include diagnosis, prevention and treatment of viral infection by Ectocarpus siliculosus virus. Specific functions, and accordingly utilities, of VGAM1693 correlate with, and may be deduced from, the identity of the host target genes which VGAM1693 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[23668] Nucleotide sequences of the VGAM1693 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1693 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1693 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1693 are further described hereinbelow with reference to Table 1.

[23669] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1693 RNA, herein designated VGAM RNA, are de-

scribed hereinbelow with reference to Table 2.

[23670] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1694 (VGAM1694) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[23671] VGAM1694 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1694 was detected is described hereinabove with reference to Figs. 2-8.

[23672] VGAM1694 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectocarpus siliculosus virus. VGAM1694 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[23673] VGAM1694 gene, herein designated VGAM GENE, encodes a VGAM1694 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1694 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly

similar to the nucleotide sequence of VGAM1694 precursor RNA is designated SEQ ID:1680, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1680 is located at position 50970 relative to the genome of Ectocarpus siliculosus virus.

[23674] VGAM1694 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1694 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23675] An enzyme complex designated DICER COMPLEX, dices the VGAM1694 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1694 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM1694 RNA is designated SEQ ID:4405, and is provided hereinbelow with reference to the sequence listing part.

[23676] VGAM1694 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1694 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1694 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23677] VGAM1694 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1694 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1694 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3

such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1694 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1694 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23678] The complementary binding of VGAM1694 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1694 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1694 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1694 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[23679] It is appreciated that VGAM1694 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1694 host target genes. The mRNA of each one of this plurality of VGAM1694 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1694 RNA, herein designated VGAM RNA, and which when bound by VGAM1694 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1694 host target proteins.

[23680] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1694 gene, herein designated VGAM GENE, on one or more VGAM1694 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23681] It is yet further appreciated that a function of VGAM1694 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1694 include diagnosis, prevention and treatment of viral infection by Ectocarpus siliculosus virus. Specific functions, and accordingly utilities, of VGAM1694 correlate with, and may be deduced from, the identity of the host target genes which VGAM1694 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[23682] Nucleotide sequences of the VGAM1694 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1694 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1694 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1694 are further described hereinbelow with reference to Table 1.

[23683] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the

complementarity of each of these host target binding sites to VGAM1694 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[23684] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1695 (VGAM1695) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[23685] VGAM1695 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1695 was detected is described hereinabove with reference to Figs. 2-8.

[23686] VGAM1695 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectocarpus siliculosus virus. VGAM1695 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[23687] VGAM1695 gene, herein designated VGAM GENE, encodes a VGAM1695 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1695 precursor RNA,

herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1695 precursor RNA is designated SEQ ID:1681, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1681 is located at position 51375 relative to the genome of Ectocarpus siliculosus virus.

[23688] VGAM1695 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1695 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23689] An enzyme complex designated DICER COMPLEX, dices the VGAM1695 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1695 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM1695 RNA is designated SEQ ID:4406, and is provided hereinbelow with reference to the sequence listing part.

[23690] VGAM1695 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1695 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1695 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23691] VGAM1695 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1695 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1695 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed

sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1695 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1695 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23692] The complementary binding of VGAM1695 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1695 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1695 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1695 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target

protein is therefore outlined by a broken line.

[23693] It is appreciated that VGAM1695 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1695 host target genes. The mRNA of each one of this plurality of VGAM1695 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1695 RNA, herein designated VGAM RNA, and which when bound by VGAM1695 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1695 host target proteins.

[23694] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1695 gene, herein designated VGAM GENE, on one or more VGAM1695 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23695] It is yet further appreciated that a function of VGAM1695 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1695 include diagnosis, prevention and treatment of viral infection by Ectocarpus siliculosus virus. Specific functions, and accordingly utilities, of VGAM1695 correlate with, and may be deduced from, the identity of the host target genes which VGAM1695 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[23696] Nucleotide sequences of the VGAM1695 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1695 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1695 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1695 are further described hereinbelow with reference to Table 1.

[23697] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1695 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[23698] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1696 (VGAM1696) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[23699] VGAM1696 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1696 was detected is described hereinabove with reference to Figs. 2-8.

[23700] VGAM1696 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectocarpus siliculosus virus. VGAM1696 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[23701] VGAM1696 gene, herein designated VGAM GENE, encodes a VGAM1696 precursor RNA, herein designated VGAM

PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1696 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1696 precursor RNA is designated SEQ ID:1682, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1682 is located at position 52738 relative to the genome of Ectocarpus siliculosus virus.

[23702] VGAM1696 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1696 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23703] An enzyme complex designated DICER COMPLEX, dices the VGAM1696 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1696 RNA,

herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM1696 RNA is designated SEQ ID:4407, and is provided hereinbelow with reference to the sequence listing part.

[23704] VGAM1696 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1696 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1696 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23705] VGAM1696 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1696 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM1696 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1696 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1696 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23706] The complementary binding of VGAM1696 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1696 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1696 host target RNA, herein designated VGAM HOST TARGET

RNA, into VGAM1696 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[23707] It is appreciated that VGAM1696 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1696 host target genes. The mRNA of each one of this plurality of VGAM1696 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1696 RNA, herein designated VGAM RNA, and which when bound by VGAM1696 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1696 host target proteins.

[23708] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1696 gene, herein designated VGAM GENE, on one or more VGAM1696 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23709] It is yet further appreciated that a function of VGAM1696 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1696 include diagnosis, prevention and treatment of viral infection by Ectocarpus siliculosus virus. Specific functions, and accordingly utilities, of VGAM1696 correlate with, and may be deduced from, the identity of the host target genes which VGAM1696 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[23710] Nucleotide sequences of the VGAM1696 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1696 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1696 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1696 are further

described hereinbelow with reference to Table 1.

[23711] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1696 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[23712] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1697 (VGAM1697) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[23713] VGAM1697 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1697 was detected is described hereinabove with reference to Figs. 2-8.

[23714] VGAM1697 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectocarpus siliculosus virus. VGAM1697 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[23715] VGAM1697 gene, herein designated VGAM GENE, encodes a VGAM1697 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1697 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1697 precursor RNA is designated SEQ ID:1683, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1683 is located at position 50957 relative to the genome of Ectocarpus siliculosus virus.

[23716] VGAM1697 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1697 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23717] An enzyme complex designated DICER COMPLEX, dices

the VGAM1697 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1697 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM1697 RNA is designated SEQ ID:4408, and is provided hereinbelow with reference to the sequence listing part.

[23718] VGAM1697 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1697 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1697 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23719] VGAM1697 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1697 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1697 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1697 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1697 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23720] The complementary binding of VGAM1697 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1697 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM1697 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1697 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[23721] It is appreciated that VGAM1697 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1697 host target genes. The mRNA of each one of this plurality of VGAM1697 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1697 RNA, herein designated VGAM RNA, and which when bound by VGAM1697 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1697 host target proteins.

[23722] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1697 gene, herein designated VGAM GENE, on one or more VGAM1697 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23723] It is yet further appreciated that a function of VGAM1697 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1697 include diagnosis, prevention and treatment of viral infection by Ectocarpus siliculosus virus. Specific functions, and accordingly utilities, of VGAM1697 correlate with, and may be deduced from, the identity of the host target genes which VGAM1697 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[23724] Nucleotide sequences of the VGAM1697 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1697 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of

VGAM1697 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1697 are further described hereinbelow with reference to Table 1.

[23725] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1697 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[23726] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1698 (VGAM1698) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[23727] VGAM1698 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1698 was detected is described hereinabove with reference to Figs. 2-8.

[23728] VGAM1698 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectocarpus siliculosus virus. VGAM1698 host target gene, herein designated

VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[23729] VGAM1698 gene, herein designated VGAM GENE, encodes a VGAM1698 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1698 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1698 precursor RNA is designated SEQ ID:1684, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1684 is located at position 52499 relative to the genome of Ectocarpus siliculosus virus.

[23730] VGAM1698 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1698 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[23731] An enzyme complex designated DICER COMPLEX, dices the VGAM1698 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1698 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM1698 RNA is designated SEQ ID:4409, and is provided hereinbelow with reference to the sequence listing part.

[23732] VGAM1698 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1698 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1698 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23733] VGAM1698 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM1698 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1698 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1698 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1698 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23734] The complementary binding of VGAM1698 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM1698 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1698 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1698 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[23735] It is appreciated that VGAM1698 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1698 host target genes. The mRNA of each one of this plurality of VGAM1698 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1698 RNA, herein designated VGAM RNA, and which when bound by VGAM1698 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1698 host target proteins.

[23736] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1698 gene, herein designated VGAM GENE, on one or more VGAM1698 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23737] It is yet further appreciated that a function of VGAM1698 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1698 include diagnosis, prevention and treatment of viral infection by Ectocarpus siliculosus virus. Specific functions, and accordingly utilities, of VGAM1698 correlate with, and may be deduced from, the identity of the host target genes which VGAM1698 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[23738] Nucleotide sequences of the VGAM1698 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

diced VGAM1698 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1698 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1698 are further described hereinbelow with reference to Table 1.

[23739] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1698 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[23740] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1699 (VGAM1699) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[23741] VGAM1699 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1699 was detected is described hereinabove with reference to Figs. 2-8.

[23742] VGAM1699 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of Ectocarpus siliculosus virus. VGAM1699 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[23743] VGAM1699 gene, herein designated VGAM GENE, encodes a VGAM1699 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1699 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1699 precursor RNA is designated SEQ ID:1685, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1685 is located at position 53142 relative to the genome of Ectocarpus siliculosus virus.

[23744] VGAM1699 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1699 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23745] An enzyme complex designated DICER COMPLEX, dices the VGAM1699 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1699 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM1699 RNA is designated SEQ ID:4410, and is provided hereinbelow with reference to the sequence listing part.

[23746] VGAM1699 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1699 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1699 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN COD-

ING and 3UTR respectively.

[23747] VGAM1699 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1699 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1699 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1699 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1699 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23748] The complementary binding of VGAM1699 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1699 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1699 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1699 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[23749] It is appreciated that VGAM1699 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1699 host target genes. The mRNA of each one of this plurality of VGAM1699 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1699 RNA, herein designated VGAM RNA, and which when bound by VGAM1699 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1699 host target proteins.

[23750] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1699 gene, herein designated VGAM GENE, on one

or more VGAM1699 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23751] It is yet further appreciated that a function of VGAM1699 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1699 include diagnosis, prevention and treatment of viral infection by Ectocarpus siliculosus virus. Specific functions, and accordingly utilities, of VGAM1699 correlate with, and may be deduced from, the identity of the host target genes which VGAM1699 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[23752] Nucleotide sequences of the VGAM1699 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1699 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1699 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1699 are further described hereinbelow with reference to Table 1.

[23753] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1699 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[23754] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1700 (VGAM1700) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[23755] VGAM1700 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1700 was detected is de-

scribed hereinabove with reference to Figs. 2-8.

[23756] VGAM1700 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectocarpus siliculosus virus. VGAM1700 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[23757] VGAM1700 gene, herein designated VGAM GENE, encodes a VGAM1700 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1700 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1700 precursor RNA is designated SEQ ID:1686, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1686 is located at position 54256 relative to the genome of Ectocarpus siliculosus virus.

[23758] VGAM1700 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1700 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23759] An enzyme complex designated DICER COMPLEX, dices the VGAM1700 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1700 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 76%) nucleotide sequence of VGAM1700 RNA is designated SEQ ID:4411, and is provided hereinbelow with reference to the sequence listing part.

[23760] VGAM1700 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1700 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1700 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding

gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23761] VGAM1700 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1700 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1700 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1700 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1700 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be lo-

cated in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23762] The complementary binding of VGAM1700 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1700 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1700 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1700 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[23763] It is appreciated that VGAM1700 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1700 host target genes. The mRNA of each one of this plurality of VGAM1700 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1700 RNA, herein designated VGAM RNA, and which when bound by VGAM1700 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1700 host target proteins.

[23764] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM1700 gene, herein designated VGAM GENE, on one or more VGAM1700 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23765] It is yet further appreciated that a function of VGAM1700 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1700 include diagnosis, prevention and treatment of viral infection by Ectocarpus siliculosus virus. Specific functions, and accordingly utilities, of VGAM1700 correlate with, and may be deduced from, the identity of the host target genes which VGAM1700 binds and in-

hibits, and the function of these host target genes, as elaborated hereinbelow.

[23766] Nucleotide sequences of the VGAM1700 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1700 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1700 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1700 are further described hereinbelow with reference to Table 1.

[23767] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1700 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[23768] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1701 (VGAM1701) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[23769] VGAM1701 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1701 was detected is described hereinabove with reference to Figs. 2-8.

[23770] VGAM1701 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectocarpus siliculosus virus. VGAM1701 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[23771] VGAM1701 gene, herein designated VGAM GENE, encodes a VGAM1701 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1701 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1701 precursor RNA is designated SEQ ID:1687, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1687 is located at position 53594 relative to the genome of Ectocarpus siliculosus virus.

[23772] VGAM1701 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1701 folded precursor RNA, herein designated VGAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23773] An enzyme complex designated DICER COMPLEX, dices the VGAM1701 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1701 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM1701 RNA is designated SEQ ID:4412, and is provided hereinbelow with reference to the sequence listing part.

[23774] VGAM1701 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1701 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1701 host target RNA,

herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23775] VGAM1701 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1701 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1701 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1701 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1701 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host tar-

get binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23776] The complementary binding of VGAM1701 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1701 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1701 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1701 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[23777] It is appreciated that VGAM1701 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1701 host target genes. The mRNA of each one of this plurality of VGAM1701 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1701 RNA, herein designated VGAM RNA, and which when bound by VGAM1701 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1701 host target proteins.

[23778] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1701 gene, herein designated VGAM GENE, on one or more VGAM1701 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23779] It is yet further appreciated that a function of VGAM1701 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1701 include diagnosis, prevention and treatment of viral infection by Ectocarpus siliculosus virus. Specific functions, and accordingly utilities, of VGAM1701

correlate with, and may be deduced from, the identity of the host target genes which VGAM1701 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[23780] Nucleotide sequences of the VGAM1701 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1701 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1701 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1701 are further described hereinbelow with reference to Table 1.

[23781] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1701 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[23782] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1702 (VGAM1702) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the

art.

[23783] VGAM1702 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1702 was detected is described hereinabove with reference to Figs. 2-8.

[23784] VGAM1702 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectocarpus siliculosus virus. VGAM1702 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[23785] VGAM1702 gene, herein designated VGAM GENE, encodes a VGAM1702 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1702 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1702 precursor RNA is designated SEQ ID:1688, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1688 is located at position 51117 relative to the genome of Ectocarpus siliculosus virus.

[23786] VGAM1702 precursor RNA, herein designated VGAM PRE-

CURSOR RNA, folds onto itself, forming VGAM1702 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23787] An enzyme complex designated DICER COMPLEX, dices the VGAM1702 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1702 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM1702 RNA is designated SEQ ID:4413, and is provided hereinbelow with reference to the sequence listing part.

[23788] VGAM1702 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM1702 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1702 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23789] VGAM1702 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1702 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1702 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1702 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1702 host

target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23790] The complementary binding of VGAM1702 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1702 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1702 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1702 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[23791] It is appreciated that VGAM1702 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1702 host target genes. The mRNA of each one of this plurality of VGAM1702 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1702 RNA, herein designated VGAM RNA, and which when bound by VGAM1702 RNA, herein

designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1702 host target proteins.

[23792] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1702 gene, herein designated VGAM GENE, on one or more VGAM1702 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23793] It is yet further appreciated that a function of VGAM1702 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1702 include diagnosis, prevention and

treatment of viral infection by Ectocarpus siliculosus virus. Specific functions, and accordingly utilities, of VGAM1702 correlate with, and may be deduced from, the identity of the host target genes which VGAM1702 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[23794] Nucleotide sequences of the VGAM1702 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1702 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1702 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1702 are further described hereinbelow with reference to Table 1.

[23795] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1702 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[23796] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1703 (VGAM1703) viral gene, which modulates ex-

pression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[23797] VGAM1703 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1703 was detected is described hereinabove with reference to Figs. 2-8.

[23798] VGAM1703 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectocarpus siliculosus virus. VGAM1703 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[23799] VGAM1703 gene, herein designated VGAM GENE, encodes a VGAM1703 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1703 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1703 precursor RNA is designated SEQ ID:1689, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1689 is located at position 53714 relative to the genome of Ectocarpus siliculosus

virus.

[23800] VGAM1703 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1703 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23801] An enzyme complex designated DICER COMPLEX, dices the VGAM1703 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1703 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 73%) nucleotide sequence of VGAM1703 RNA is designated SEQ ID:4414, and is provided hereinbelow with reference to the sequence listing part.

[23802] VGAM1703 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1703 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1703 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23803] VGAM1703 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1703 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1703 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1703 RNA, herein designated

VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1703 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23804] The complementary binding of VGAM1703 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1703 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1703 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1703 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[23805] It is appreciated that VGAM1703 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1703 host target genes. The mRNA of each one of this plurality of VGAM1703 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM1703 RNA, herein designated VGAM RNA, and which when bound by VGAM1703 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1703 host target proteins.

[23806] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1703 gene, herein designated VGAM GENE, on one or more VGAM1703 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23807] It is yet further appreciated that a function of VGAM1703 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1703 include diagnosis, prevention and treatment of viral infection by Ectocarpus siliculosus virus. Specific functions, and accordingly utilities, of VGAM1703 correlate with, and may be deduced from, the identity of the host target genes which VGAM1703 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[23808] Nucleotide sequences of the VGAM1703 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1703 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1703 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1703 are further described hereinbelow with reference to Table 1.

[23809] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1703 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[23810] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present

invention, referred to here as Viral Genomic Address Messenger 1704 (VGAM1704) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[23811] VGAM1704 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1704 was detected is described hereinabove with reference to Figs. 2-8.

[23812] VGAM1704 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectocarpus siliculosus virus. VGAM1704 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[23813] VGAM1704 gene, herein designated VGAM GENE, encodes a VGAM1704 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1704 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1704 precursor RNA is designated SEQ ID:1690, and is provided hereinbelow with reference to the sequence listing part. Nu-

cleotide sequence SEQ ID:1690 is located at position 52170 relative to the genome of Ectocarpus siliculosus virus.

[23814] VGAM1704 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1704 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23815] An enzyme complex designated DICER COMPLEX, dices the VGAM1704 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1704 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM1704 RNA is designated SEQ ID:4415, and

is provided hereinbelow with reference to the sequence listing part.

[23816] VGAM1704 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1704 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1704 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23817] VGAM1704 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1704 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1704 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites

shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1704 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1704 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23818] The complementary binding of VGAM1704 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1704 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1704 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1704 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[23819] It is appreciated that VGAM1704 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1704 host target genes. The mRNA of each one of this plurality of VGAM1704 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1704 RNA, herein designated VGAM RNA, and which when bound by VGAM1704 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1704 host target proteins.

[23820] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1704 gene, herein designated VGAM GENE, on one or more VGAM1704 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23821] It is yet further appreciated that a function of VGAM1704 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1704 include diagnosis, prevention and treatment of viral infection by Ectocarpus siliculosus virus. Specific functions, and accordingly utilities, of VGAM1704 correlate with, and may be deduced from, the identity of the host target genes which VGAM1704 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[23822] Nucleotide sequences of the VGAM1704 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1704 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1704 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1704 are further described hereinbelow with reference to Table 1.

[23823] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1704 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[23824] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1705 (VGAM1705) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[23825] VGAM1705 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1705 was detected is described hereinabove with reference to Figs. 2-8.

[23826] VGAM1705 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectocarpus siliculosus virus. VGAM1705 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[23827] VGAM1705 gene, herein designated VGAM GENE, encodes a VGAM1705 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1705 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1705 precur-

sor RNA is designated SEQ ID:1691, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1691 is located at position 51223 relative to the genome of Ectocarpus siliculosus virus.

[23828] VGAM1705 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1705 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23829] An enzyme complex designated DICER COMPLEX, dices the VGAM1705 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1705 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 45%) nucleotide sequence of VGAM1705 RNA is designated SEQ ID:4416, and is provided hereinbelow with reference to the sequence listing part.

[23830] VGAM1705 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1705 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1705 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23831] VGAM1705 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1705 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1705 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I,

BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1705 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1705 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23832] The complementary binding of VGAM1705 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1705 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1705 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1705 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[23833] It is appreciated that VGAM1705 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM1705 host target genes. The mRNA of each one of this plurality of VGAM1705 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1705 RNA, herein designated VGAM RNA, and which when bound by VGAM1705 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1705 host target proteins.

[23834] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1705 gene, herein designated VGAM GENE, on one or more VGAM1705 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23835] It is yet further appreciated that a function of VGAM1705 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1705 include diagnosis, prevention and treatment of viral infection by Ectocarpus siliculosus virus. Specific functions, and accordingly utilities, of VGAM1705 correlate with, and may be deduced from, the identity of the host target genes which VGAM1705 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[23836] Nucleotide sequences of the VGAM1705 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1705 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1705 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1705 are further described hereinbelow with reference to Table 1.

[23837] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites

to VGAM1705 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[23838] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1706 (VGAM1706) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[23839] VGAM1706 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1706 was detected is described hereinabove with reference to Figs. 2-8.

[23840] VGAM1706 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectocarpus siliculosus virus. VGAM1706 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[23841] VGAM1706 gene, herein designated VGAM GENE, encodes a VGAM1706 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1706 precursor RNA, herein designated VGAM PRECURSOR RNA, does not en-

code a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1706 precursor RNA is designated SEQ ID:1692, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1692 is located at position 54780 relative to the genome of Ectocarpus siliculosus virus.

[23842] VGAM1706 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1706 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23843] An enzyme complex designated DICER COMPLEX, dices the VGAM1706 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1706 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM1706 RNA is designated SEQ ID:4417, and is provided hereinbelow with reference to the sequence listing part.

[23844] VGAM1706 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1706 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1706 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23845] VGAM1706 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1706 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1706 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host

target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1706 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1706 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23846] The complementary binding of VGAM1706 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1706 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1706 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1706 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[23847] It is appreciated that VGAM1706 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1706 host target genes. The mRNA of each one of this plurality of VGAM1706 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1706 RNA, herein designated VGAM RNA, and which when bound by VGAM1706 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1706 host target proteins.

[23848] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1706 gene, herein designated VGAM GENE, on one or more VGAM1706 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23849] It is yet further appreciated that a function of VGAM1706 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1706 include diagnosis, prevention and treatment of viral infection by Ectocarpus siliculosus virus. Specific functions, and accordingly utilities, of VGAM1706 correlate with, and may be deduced from, the identity of the host target genes which VGAM1706 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[23850] Nucleotide sequences of the VGAM1706 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1706 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1706 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1706 are further described hereinbelow with reference to Table 1.

[23851] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1706 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[23852] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1707 (VGAM1707) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[23853] VGAM1707 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1707 was detected is described hereinabove with reference to Figs. 2-8.

[23854] VGAM1707 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectocarpus siliculosus virus. VGAM1707 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[23855] VGAM1707 gene, herein designated VGAM GENE, encodes a VGAM1707 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and un-

like most ordinary genes, VGAM1707 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1707 precursor RNA is designated SEQ ID:1693, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1693 is located at position 48576 relative to the genome of Ectocarpus siliculosus virus.

[23856] VGAM1707 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1707 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23857] An enzyme complex designated DICER COMPLEX, dices the VGAM1707 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1707 RNA, herein designated VGAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 61%) nucleotide sequence of VGAM1707 RNA is designated SEQ ID:4418, and is provided hereinbelow with reference to the sequence listing part.

[23858] VGAM1707 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1707 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1707 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23859] VGAM1707 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1707 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1707 RNA, herein designated

VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1707 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1707 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23860] The complementary binding of VGAM1707 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1707 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1707 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1707 host target protein, herein desig-

nated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[23861] It is appreciated that VGAM1707 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1707 host target genes. The mRNA of each one of this plurality of VGAM1707 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1707 RNA, herein designated VGAM RNA, and which when bound by VGAM1707 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1707 host target proteins.

[23862] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1707 gene, herein designated VGAM GENE, on one or more VGAM1707 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23863] It is yet further appreciated that a function of VGAM1707 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1707 include diagnosis, prevention and treatment of viral infection by Ectocarpus siliculosus virus. Specific functions, and accordingly utilities, of VGAM1707 correlate with, and may be deduced from, the identity of the host target genes which VGAM1707 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[23864] Nucleotide sequences of the VGAM1707 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1707 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1707 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1707 are further described hereinbelow with reference to Table 1.

[23865] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1707 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[23866] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1708 (VGAM1708) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[23867] VGAM1708 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1708 was detected is described hereinabove with reference to Figs. 2-8.

[23868] VGAM1708 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Bovine adenovirus B. VGAM1708 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[23869] VGAM1708 gene, herein designated VGAM GENE, encodes

a VGAM1708 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1708 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1708 precursor RNA is designated SEQ ID:1694, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1694 is located at position 17661 relative to the genome of Bovine adenovirus B.

[23870] VGAM1708 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1708 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23871] An enzyme complex designated DICER COMPLEX, dices the VGAM1708 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1708 RNA,

herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 82%) nucleotide sequence of VGAM1708 RNA is designated SEQ ID:4419, and is provided hereinbelow with reference to the sequence listing part.

[23872] VGAM1708 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1708 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1708 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23873] VGAM1708 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1708 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM1708 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1708 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1708 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23874] The complementary binding of VGAM1708 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1708 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1708 host target RNA, herein designated VGAM HOST TARGET

RNA, into VGAM1708 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[23875] It is appreciated that VGAM1708 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1708 host target genes. The mRNA of each one of this plurality of VGAM1708 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1708 RNA, herein designated VGAM RNA, and which when bound by VGAM1708 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1708 host target proteins.

[23876] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1708 gene, herein designated VGAM GENE, on one or more VGAM1708 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23877] It is yet further appreciated that a function of VGAM1708 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1708 include diagnosis, prevention and treatment of viral infection by Bovine adenovirus B. Specific functions, and accordingly utilities, of VGAM1708 correlate with, and may be deduced from, the identity of the host target genes which VGAM1708 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[23878] Nucleotide sequences of the VGAM1708 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1708 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1708 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1708 are further

described hereinbelow with reference to Table 1.

[23879] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1708 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[23880] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1709 (VGAM1709) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[23881] VGAM1709 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1709 was detected is described hereinabove with reference to Figs. 2-8.

[23882] VGAM1709 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Semliki forest virus. VGAM1709 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[23883] VGAM1709 gene, herein designated VGAM GENE, encodes a VGAM1709 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1709 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1709 precursor RNA is designated SEQ ID:1695, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1695 is located at position 4455 relative to the genome of Semliki forest virus.

[23884] VGAM1709 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1709 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23885] An enzyme complex designated DICER COMPLEX, dices the VGAM1709 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, into VGAM1709 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM1709 RNA is designated SEQ ID:4420, and is provided hereinbelow with reference to the sequence listing part.

[23886] VGAM1709 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1709 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1709 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23887] VGAM1709 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1709 host target RNA, herein designated VGAM HOST TARGET RNA. This

complementary binding is due to the fact that the nucleotide sequence of VGAM1709 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1709 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1709 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23888] The complementary binding of VGAM1709 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1709 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1709

host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1709 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[23889] It is appreciated that VGAM1709 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1709 host target genes. The mRNA of each one of this plurality of VGAM1709 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1709 RNA, herein designated VGAM RNA, and which when bound by VGAM1709 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1709 host target proteins.

[23890] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1709 gene, herein designated VGAM GENE, on one or more VGAM1709 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23891] It is yet further appreciated that a function of VGAM1709 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1709 include diagnosis, prevention and treatment of viral infection by Semliki forest virus. Specific functions, and accordingly utilities, of VGAM1709 correlate with, and may be deduced from, the identity of the host target genes which VGAM1709 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[23892] Nucleotide sequences of the VGAM1709 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1709 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1709 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM1709 are further described hereinbelow with reference to Table 1.

[23893] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1709 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[23894] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1710 (VGAM1710) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[23895] VGAM1710 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1710 was detected is described hereinabove with reference to Figs. 2-8.

[23896] VGAM1710 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Semliki forest virus. VGAM1710 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the

human genome.

[23897] VGAM1710 gene, herein designated VGAM GENE, encodes a VGAM1710 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1710 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1710 precursor RNA is designated SEQ ID:1696, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1696 is located at position 7249 relative to the genome of Semliki forest virus.

[23898] VGAM1710 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1710 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23899] An enzyme complex designated DICER COMPLEX, dices

the VGAM1710 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1710 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide sequence of VGAM1710 RNA is designated SEQ ID:4421, and is provided hereinbelow with reference to the sequence listing part.

[23900] VGAM1710 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1710 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1710 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23901] VGAM1710 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1710 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1710 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1710 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1710 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23902] The complementary binding of VGAM1710 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1710 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM1710 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1710 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[23903] It is appreciated that VGAM1710 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1710 host target genes. The mRNA of each one of this plurality of VGAM1710 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1710 RNA, herein designated VGAM RNA, and which when bound by VGAM1710 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1710 host target proteins.

[23904] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1710 gene, herein designated VGAM GENE, on one or more VGAM1710 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23905] It is yet further appreciated that a function of VGAM1710 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1710 include diagnosis, prevention and treatment of viral infection by Semliki forest virus. Specific functions, and accordingly utilities, of VGAM1710 correlate with, and may be deduced from, the identity of the host target genes which VGAM1710 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[23906] Nucleotide sequences of the VGAM1710 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1710 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of

VGAM1710 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1710 are further described hereinbelow with reference to Table 1.

[23907] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1710 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[23908] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1711 (VGAM1711) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[23909] VGAM1711 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1711 was detected is described hereinabove with reference to Figs. 2-8.

[23910] VGAM1711 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Semliki forest virus. VGAM1711 host target gene, herein designated VGAM

HOST TARGET GENE, is a human gene contained in the human genome.

[23911] VGAM1711 gene, herein designated VGAM GENE, encodes a VGAM1711 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1711 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1711 precursor RNA is designated SEQ ID:1697, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1697 is located at position 4081 relative to the genome of Semliki forest virus.

[23912] VGAM1711 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1711 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23913] An enzyme complex designated DICER COMPLEX, dices the VGAM1711 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1711 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM1711 RNA is designated SEQ ID:4422, and is provided hereinbelow with reference to the sequence listing part.

[23914] VGAM1711 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1711 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1711 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23915] VGAM1711 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites

located in untranslated regions of VGAM1711 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1711 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1711 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1711 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23916] The complementary binding of VGAM1711 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1711 host target RNA, herein designated VGAM

HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1711 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1711 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[23917] It is appreciated that VGAM1711 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1711 host target genes. The mRNA of each one of this plurality of VGAM1711 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1711 RNA, herein designated VGAM RNA, and which when bound by VGAM1711 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1711 host target proteins.

[23918] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1711 gene, herein designated VGAM GENE, on one or more VGAM1711 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove

with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23919] It is yet further appreciated that a function of VGAM1711 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1711 include diagnosis, prevention and treatment of viral infection by Semliki forest virus. Specific functions, and accordingly utilities, of VGAM1711 correlate with, and may be deduced from, the identity of the host target genes which VGAM1711 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[23920] Nucleotide sequences of the VGAM1711 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1711 RNA, herein designated VGAM RNA, and

a schematic representation of the secondary folding of VGAM1711 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1711 are further described hereinbelow with reference to Table 1.

[23921] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1711 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[23922] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1712 (VGAM1712) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[23923] VGAM1712 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1712 was detected is described hereinabove with reference to Figs. 2-8.

[23924] VGAM1712 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Sindbis virus.

VGAM1712 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[23925] VGAM1712 gene, herein designated VGAM GENE, encodes a VGAM1712 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1712 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1712 precursor RNA is designated SEQ ID:1698, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1698 is located at position 8817 relative to the genome of Sindbis virus.

[23926] VGAM1712 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1712 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[23927] An enzyme complex designated DICER COMPLEX, dices the VGAM1712 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1712 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM1712 RNA is designated SEQ ID:4423, and is provided hereinbelow with reference to the sequence listing part.

[23928] VGAM1712 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1712 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1712 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23929] VGAM1712 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM1712 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1712 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1712 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1712 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23930] The complementary binding of VGAM1712 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM1712 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1712 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1712 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[23931] It is appreciated that VGAM1712 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1712 host target genes. The mRNA of each one of this plurality of VGAM1712 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1712 RNA, herein designated VGAM RNA, and which when bound by VGAM1712 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1712 host target proteins.

[23932] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1712 gene, herein designated VGAM GENE, on one or more VGAM1712 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23933] It is yet further appreciated that a function of VGAM1712 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1712 include diagnosis, prevention and treatment of viral infection by Sindbis virus. Specific functions, and accordingly utilities, of VGAM1712 correlate with, and may be deduced from, the identity of the host target genes which VGAM1712 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[23934] Nucleotide sequences of the VGAM1712 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

diced VGAM1712 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1712 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1712 are further described hereinbelow with reference to Table 1.

[23935] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1712 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[23936] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1713 (VGAM1713) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[23937] VGAM1713 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1713 was detected is described hereinabove with reference to Figs. 2-8.

[23938] VGAM1713 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of Sindbis virus. VGAM1713 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[23939] VGAM1713 gene, herein designated VGAM GENE, encodes a VGAM1713 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1713 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1713 precursor RNA is designated SEQ ID:1699, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1699 is located at position 8146 relative to the genome of Sindbis virus.

[23940] VGAM1713 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1713 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23941] An enzyme complex designated DICER COMPLEX, dices the VGAM1713 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1713 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM1713 RNA is designated SEQ ID:4424, and is provided hereinbelow with reference to the sequence listing part.

[23942] VGAM1713 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1713 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1713 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23943] VGAM1713 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1713 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1713 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1713 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1713 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23944] The complementary binding of VGAM1713 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM1713 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1713 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1713 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[23945] It is appreciated that VGAM1713 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1713 host target genes. The mRNA of each one of this plurality of VGAM1713 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1713 RNA, herein designated VGAM RNA, and which when bound by VGAM1713 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1713 host target proteins.

[23946] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1713 gene, herein designated VGAM GENE, on one or more VGAM1713 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23947] It is yet further appreciated that a function of VGAM1713 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1713 include diagnosis, prevention and treatment of viral infection by Sindbis virus. Specific functions, and accordingly utilities, of VGAM1713 correlate with, and may be deduced from, the identity of the host target genes which VGAM1713 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[23948] Nucleotide sequences of the VGAM1713 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the diced VGAM1713 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1713 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1713 are further described hereinbelow with reference to Table 1.

[23949] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1713 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[23950] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1714 (VGAM1714) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[23951] VGAM1714 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1714 was detected is described hereinabove with reference to Figs. 2-8.

[23952] VGAM1714 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Sindbis virus. VGAM1714 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[23953] VGAM1714 gene, herein designated VGAM GENE, encodes a VGAM1714 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1714 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1714 precursor RNA is designated SEQ ID:1700, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1700 is located at position 9679 relative to the genome of Sindbis virus.

[23954] VGAM1714 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1714 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23955] An enzyme complex designated DICER COMPLEX, dices the VGAM1714 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1714 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM1714 RNA is designated SEQ ID:4425, and is provided hereinbelow with reference to the sequence listing part.

[23956] VGAM1714 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1714 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1714 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN COD-

ING and 3UTR respectively.

[23957] VGAM1714 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1714 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1714 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1714 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1714 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23958] The complementary binding of VGAM1714 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1714 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1714 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1714 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[23959] It is appreciated that VGAM1714 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1714 host target genes. The mRNA of each one of this plurality of VGAM1714 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1714 RNA, herein designated VGAM RNA, and which when bound by VGAM1714 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1714 host target proteins.

[23960] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1714 gene, herein designated VGAM GENE, on one

or more VGAM1714 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23961] It is yet further appreciated that a function of VGAM1714 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1714 include diagnosis, prevention and treatment of viral infection by Sindbis virus. Specific functions, and accordingly utilities, of VGAM1714 correlate with, and may be deduced from, the identity of the host target genes which VGAM1714 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[23962] Nucleotide sequences of the VGAM1714 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1714 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1714 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1714 are further described hereinbelow with reference to Table 1.

[23963] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1714 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[23964] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1715 (VGAM1715) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[23965] VGAM1715 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1715 was detected is de-

scribed hereinabove with reference to Figs. 2-8.

[23966] VGAM1715 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Sindbis virus. VGAM1715 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[23967] VGAM1715 gene, herein designated VGAM GENE, encodes a VGAM1715 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1715 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1715 precursor RNA is designated SEQ ID:1701, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1701 is located at position 10643 relative to the genome of Sindbis virus.

[23968] VGAM1715 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1715 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23969] An enzyme complex designated DICER COMPLEX, dices the VGAM1715 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1715 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of VGAM1715 RNA is designated SEQ ID:4426, and is provided hereinbelow with reference to the sequence listing part.

[23970] VGAM1715 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1715 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1715 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and

a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23971] VGAM1715 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1715 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1715 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1715 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1715 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both

3UTR and 5UTR regions.

[23972] The complementary binding of VGAM1715 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1715 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1715 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1715 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[23973] It is appreciated that VGAM1715 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1715 host target genes. The mRNA of each one of this plurality of VGAM1715 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1715 RNA, herein designated VGAM RNA, and which when bound by VGAM1715 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1715 host target proteins.

[23974] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM1715 gene, herein designated VGAM GENE, on one or more VGAM1715 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23975] It is yet further appreciated that a function of VGAM1715 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1715 include diagnosis, prevention and treatment of viral infection by Sindbis virus. Specific functions, and accordingly utilities, of VGAM1715 correlate with, and may be deduced from, the identity of the host target genes which VGAM1715 binds and inhibits, and the function of these host target genes, as elaborated herein-

below.

[23976] Nucleotide sequences of the VGAM1715 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1715 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1715 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1715 are further described hereinbelow with reference to Table 1.

[23977] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1715 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[23978] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1716 (VGAM1716) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[23979] VGAM1716 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene.

The method by which VGAM1716 was detected is described hereinabove with reference to Figs. 2-8.

[23980] VGAM1716 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Sindbis virus. VGAM1716 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[23981] VGAM1716 gene, herein designated VGAM GENE, encodes a VGAM1716 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1716 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1716 precursor RNA is designated SEQ ID:1702, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1702 is located at position 8996 relative to the genome of Sindbis virus.

[23982] VGAM1716 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1716 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23983] An enzyme complex designated DICER COMPLEX, dices the VGAM1716 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1716 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 51%) nucleotide sequence of VGAM1716 RNA is designated SEQ ID:4427, and is provided hereinbelow with reference to the sequence listing part.

[23984] VGAM1716 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1716 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1716 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding

gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23985] VGAM1716 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1716 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1716 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1716 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1716 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be lo-

cated in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23986] The complementary binding of VGAM1716 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1716 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1716 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1716 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[23987] It is appreciated that VGAM1716 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1716 host target genes. The mRNA of each one of this plurality of VGAM1716 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1716 RNA, herein designated VGAM RNA, and which when bound by VGAM1716 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1716 host target proteins.

[23988] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM1716 gene, herein designated VGAM GENE, on one or more VGAM1716 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23989] It is yet further appreciated that a function of VGAM1716 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1716 include diagnosis, prevention and treatment of viral infection by Sindbis virus. Specific functions, and accordingly utilities, of VGAM1716 correlate with, and may be deduced from, the identity of the host target genes which VGAM1716 binds and inhibits, and the

function of these host target genes, as elaborated hereinbelow.

[23990] Nucleotide sequences of the VGAM1716 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1716 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1716 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1716 are further described hereinbelow with reference to Table 1.

[23991] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1716 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[23992] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1717 (VGAM1717) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[23993] VGAM1717 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1717 was detected is described hereinabove with reference to Figs. 2-8.

[23994] VGAM1717 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Molluscum contagiosum virus. VGAM1717 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[23995] VGAM1717 gene, herein designated VGAM GENE, encodes a VGAM1717 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1717 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1717 precursor RNA is designated SEQ ID:1703, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1703 is located at position 67026 relative to the genome of Molluscum contagiosum virus.

[23996] VGAM1717 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1717 folded precursor RNA, herein designated VGAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23997] An enzyme complex designated DICER COMPLEX, dices the VGAM1717 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1717 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM1717 RNA is designated SEQ ID:4428, and is provided hereinbelow with reference to the sequence listing part.

[23998] VGAM1717 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1717 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1717 host target RNA,

herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23999] VGAM1717 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1717 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1717 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1717 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1717 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host tar-

get binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24000] The complementary binding of VGAM1717 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1717 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1717 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1717 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[24001] It is appreciated that VGAM1717 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1717 host target genes. The mRNA of each one of this plurality of VGAM1717 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1717 RNA, herein designated VGAM RNA, and which when bound by VGAM1717 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1717 host target proteins.

[24002] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1717 gene, herein designated VGAM GENE, on one or more VGAM1717 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24003] It is yet further appreciated that a function of VGAM1717 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1717 include diagnosis, prevention and treatment of viral infection by Molluscum contagiosum virus. Specific functions, and accordingly utilities, of

VGAM1717 correlate with, and may be deduced from, the identity of the host target genes which VGAM1717 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[24004] Nucleotide sequences of the VGAM1717 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1717 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1717 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1717 are further described hereinbelow with reference to Table 1.

[24005] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1717 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[24006] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1718 (VGAM1718) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the

art.

[24007] VGAM1718 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1718 was detected is described hereinabove with reference to Figs. 2-8.

[24008] VGAM1718 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Molluscum contagiosum virus. VGAM1718 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[24009] VGAM1718 gene, herein designated VGAM GENE, encodes a VGAM1718 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1718 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1718 precursor RNA is designated SEQ ID:1704, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1704 is located at position 64920 relative to the genome of Molluscum contagiosum virus.

[24010] VGAM1718 precursor RNA, herein designated VGAM PRE-

CURSOR RNA, folds onto itself, forming VGAM1718 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24011] An enzyme complex designated DICER COMPLEX, dices the VGAM1718 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1718 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 81%) nucleotide sequence of VGAM1718 RNA is designated SEQ ID:4429, and is provided hereinbelow with reference to the sequence listing part.

[24012] VGAM1718 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM1718 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1718 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24013] VGAM1718 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1718 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1718 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1718 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1718 host

target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24014] The complementary binding of VGAM1718 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1718 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1718 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1718 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[24015] It is appreciated that VGAM1718 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1718 host target genes. The mRNA of each one of this plurality of VGAM1718 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1718 RNA, herein designated VGAM RNA, and which when bound by VGAM1718 RNA, herein

designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1718 host target proteins.

[24016] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1718 gene, herein designated VGAM GENE, on one or more VGAM1718 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24017] It is yet further appreciated that a function of VGAM1718 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1718 include diagnosis, prevention and

treatment of viral infection by Molluscum contagiosum virus. Specific functions, and accordingly utilities, of VGAM1718 correlate with, and may be deduced from, the identity of the host target genes which VGAM1718 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[24018] Nucleotide sequences of the VGAM1718 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1718 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1718 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1718 are further described hereinbelow with reference to Table 1.

[24019] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1718 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[24020] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1719 (VGAM1719) viral gene, which modulates ex-

pression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[24021] VGAM1719 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1719 was detected is described hereinabove with reference to Figs. 2-8.

[24022] VGAM1719 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rat cytomegalovirus. VGAM1719 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[24023] VGAM1719 gene, herein designated VGAM GENE, encodes a VGAM1719 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1719 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1719 precursor RNA is designated SEQ ID:1705, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1705 is located at position 110474 relative to the genome of Rat cytomegalovirus.

[24024] VGAM1719 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1719 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24025] An enzyme complex designated DICER COMPLEX, dices the VGAM1719 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1719 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM1719 RNA is designated SEQ ID:4430, and is provided hereinbelow with reference to the sequence listing part.

[24026] VGAM1719 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1719 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1719 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24027] VGAM1719 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1719 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1719 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1719 RNA, herein designated VGAM RNA, may have a different number of host target

binding sites in untranslated regions of a VGAM1719 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24028] The complementary binding of VGAM1719 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1719 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1719 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1719 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[24029] It is appreciated that VGAM1719 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1719 host target genes. The mRNA of each one of this plurality of VGAM1719 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1719 RNA, herein designated VGAM

RNA, and which when bound by VGAM1719 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1719 host target proteins.

[24030] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1719 gene, herein designated VGAM GENE, on one or more VGAM1719 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24031] It is yet further appreciated that a function of VGAM1719 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM1719 include diagnosis, prevention and treatment of viral infection by Rat cytomegalovirus. Specific functions, and accordingly utilities, of VGAM1719 correlate with, and may be deduced from, the identity of the host target genes which VGAM1719 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[24032] Nucleotide sequences of the VGAM1719 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1719 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1719 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1719 are further described hereinbelow with reference to Table 1.

[24033] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1719 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[24034] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Mes-

senger 1720 (VGAM1720) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[24035] VGAM1720 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1720 was detected is described hereinabove with reference to Figs. 2-8.

[24036] VGAM1720 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rat cytomegalovirus. VGAM1720 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[24037] VGAM1720 gene, herein designated VGAM GENE, encodes a VGAM1720 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1720 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1720 precursor RNA is designated SEQ ID:1706, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1706 is located at position

111844 relative to the genome of Rat cytomegalovirus.

[24038] VGAM1720 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1720 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24039] An enzyme complex designated DICER COMPLEX, dices the VGAM1720 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1720 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM1720 RNA is designated SEQ ID:4431, and is provided hereinbelow with reference to the sequence listing part.

[24040] VGAM1720 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1720 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1720 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24041] VGAM1720 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1720 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1720 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1720 RNA, herein designated

VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1720 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24042] The complementary binding of VGAM1720 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1720 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1720 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1720 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[24043] It is appreciated that VGAM1720 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1720 host target genes. The mRNA of each one of this plurality of VGAM1720 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM1720 RNA, herein designated VGAM RNA, and which when bound by VGAM1720 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1720 host target proteins.

[24044] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1720 gene, herein designated VGAM GENE, on one or more VGAM1720 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24045] It is yet further appreciated that a function of VGAM1720 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1720 include diagnosis, prevention and treatment of viral infection by Rat cytomegalovirus. Specific functions, and accordingly utilities, of VGAM1720 correlate with, and may be deduced from, the identity of the host target genes which VGAM1720 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[24046] Nucleotide sequences of the VGAM1720 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1720 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1720 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1720 are further described hereinbelow with reference to Table 1.

[24047] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1720 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[24048] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present

invention, referred to here as Viral Genomic Address Messenger 1721 (VGAM1721) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[24049] VGAM1721 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1721 was detected is described hereinabove with reference to Figs. 2-8.

[24050] VGAM1721 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Myxoma virus. VGAM1721 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[24051] VGAM1721 gene, herein designated VGAM GENE, encodes a VGAM1721 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1721 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1721 precursor RNA is designated SEQ ID:1707, and is provided hereinbelow with reference to the sequence listing part. Nu-

cleotide sequence SEQ ID:1707 is located at position 8494 relative to the genome of Myxoma virus.

[24052] VGAM1721 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1721 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24053] An enzyme complex designated DICER COMPLEX, dices the VGAM1721 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1721 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM1721 RNA is designated SEQ ID:4432, and is provided hereinbelow with reference to the sequence

listing part.

[24054] VGAM1721 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1721 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1721 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24055] VGAM1721 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1721 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1721 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not

meant to be limiting VGAM1721 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1721 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24056] The complementary binding of VGAM1721 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1721 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1721 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1721 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[24057] It is appreciated that VGAM1721 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1721 host target genes. The mRNA of each one of this plurality of VGAM1721 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM1721 RNA, herein designated VGAM RNA, and which when bound by VGAM1721 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1721 host target proteins.

[24058] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1721 gene, herein designated VGAM GENE, on one or more VGAM1721 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24059] It is yet further appreciated that a function of VGAM1721

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1721 include diagnosis, prevention and treatment of viral infection by Myxoma virus. Specific functions, and accordingly utilities, of VGAM1721 correlate with, and may be deduced from, the identity of the host target genes which VGAM1721 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[24060] Nucleotide sequences of the VGAM1721 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1721 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1721 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1721 are further described hereinbelow with reference to Table 1.

[24061] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1721 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[24062] Fig. 1 further provides a conceptual description of another

novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1722 (VGAM1722) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[24063] VGAM1722 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1722 was detected is described hereinabove with reference to Figs. 2-8.

[24064] VGAM1722 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Myxoma virus. VGAM1722 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[24065] VGAM1722 gene, herein designated VGAM GENE, encodes a VGAM1722 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1722 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1722 precursor RNA is designated SEQ ID:1708, and is provided here-

inbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1708 is located at position 4765 relative to the genome of Myxoma virus.

[24066] VGAM1722 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1722 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24067] An enzyme complex designated DICER COMPLEX, dices the VGAM1722 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1722 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM1722 RNA is designated SEQ ID:4433, and

is provided hereinbelow with reference to the sequence listing part.

[24068] VGAM1722 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1722 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1722 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24069] VGAM1722 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1722 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1722 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites

shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1722 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1722 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24070] The complementary binding of VGAM1722 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1722 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1722 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1722 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[24071] It is appreciated that VGAM1722 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1722 host target genes. The mRNA of each one of this plurality of VGAM1722 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1722 RNA, herein designated VGAM RNA, and which when bound by VGAM1722 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1722 host target proteins.

[24072] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1722 gene, herein designated VGAM GENE, on one or more VGAM1722 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24073] It is yet further appreciated that a function of VGAM1722 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1722 include diagnosis, prevention and treatment of viral infection by Myxoma virus. Specific functions, and accordingly utilities, of VGAM1722 correlate with, and may be deduced from, the identity of the host target genes which VGAM1722 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[24074] Nucleotide sequences of the VGAM1722 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1722 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1722 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1722 are further described hereinbelow with reference to Table 1.

[24075] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1722 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[24076] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1723 (VGAM1723) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[24077] VGAM1723 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1723 was detected is described hereinabove with reference to Figs. 2-8.

[24078] VGAM1723 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Myxoma virus.
VGAM1723 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[24079] VGAM1723 gene, herein designated VGAM GENE, encodes a VGAM1723 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1723 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1723 precur-

sor RNA is designated SEQ ID:1709, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1709 is located at position 4097 relative to the genome of Myxoma virus.

[24080] VGAM1723 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1723 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24081] An enzyme complex designated DICER COMPLEX, dices the VGAM1723 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1723 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide se-

quence of VGAM1723 RNA is designated SEQ ID:4434, and is provided hereinbelow with reference to the sequence listing part.

[24082] VGAM1723 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1723 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1723 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24083] VGAM1723 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1723 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1723 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is ap-

preciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1723 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1723 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24084] The complementary binding of VGAM1723 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1723 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1723 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1723 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[24085] It is appreciated that VGAM1723 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1723 host target genes. The mRNA of

each one of this plurality of VGAM1723 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1723 RNA, herein designated VGAM RNA, and which when bound by VGAM1723 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1723 host target proteins.

[24086] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1723 gene, herein designated VGAM GENE, on one or more VGAM1723 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science

294,779 (2001)).

[24087] It is yet further appreciated that a function of VGAM1723 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1723 include diagnosis, prevention and treatment of viral infection by Myxoma virus. Specific functions, and accordingly utilities, of VGAM1723 correlate with, and may be deduced from, the identity of the host target genes which VGAM1723 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[24088] Nucleotide sequences of the VGAM1723 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1723 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1723 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1723 are further described hereinbelow with reference to Table 1.

[24089] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1723 RNA, herein designated VGAM RNA, are de-

scribed hereinbelow with reference to Table 2.

[24090] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1724 (VGAM1724) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[24091] VGAM1724 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1724 was detected is described hereinabove with reference to Figs. 2-8.

[24092] VGAM1724 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rabies virus. VGAM1724 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[24093] VGAM1724 gene, herein designated VGAM GENE, encodes a VGAM1724 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1724 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1724 precur-

sor RNA is designated SEQ ID:1710, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1710 is located at position 3898 relative to the genome of Rabies virus.

[24094] VGAM1724 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1724 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24095] An enzyme complex designated DICER COMPLEX, dices the VGAM1724 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1724 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide se-

quence of VGAM1724 RNA is designated SEQ ID:4435, and is provided hereinbelow with reference to the sequence listing part.

[24096] VGAM1724 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1724 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1724 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24097] VGAM1724 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1724 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1724 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is ap-

preciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1724 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1724 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24098] The complementary binding of VGAM1724 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1724 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1724 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1724 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[24099] It is appreciated that VGAM1724 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1724 host target genes. The mRNA of

each one of this plurality of VGAM1724 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1724 RNA, herein designated VGAM RNA, and which when bound by VGAM1724 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1724 host target proteins.

[24100] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1724 gene, herein designated VGAM GENE, on one or more VGAM1724 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science

294,779 (2001)).

[24101] It is yet further appreciated that a function of VGAM1724 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1724 include diagnosis, prevention and treatment of viral infection by Rabies virus. Specific functions, and accordingly utilities, of VGAM1724 correlate with, and may be deduced from, the identity of the host target genes which VGAM1724 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[24102] Nucleotide sequences of the VGAM1724 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1724 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1724 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1724 are further described hereinbelow with reference to Table 1.

[24103] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1724 RNA, herein designated VGAM RNA, are de-

scribed hereinbelow with reference to Table 2.

[24104] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1725 (VGAM1725) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[24105] VGAM1725 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1725 was detected is described hereinabove with reference to Figs. 2-8.

[24106] VGAM1725 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rabies virus. VGAM1725 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[24107] VGAM1725 gene, herein designated VGAM GENE, encodes a VGAM1725 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1725 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1725 precur-

sor RNA is designated SEQ ID:1711, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1711 is located at position 8659 relative to the genome of Rabies virus.

[24108] VGAM1725 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1725 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24109] An enzyme complex designated DICER COMPLEX, dices the VGAM1725 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1725 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide se-

quence of VGAM1725 RNA is designated SEQ ID:4436, and is provided hereinbelow with reference to the sequence listing part.

[24110] VGAM1725 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1725 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1725 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24111] VGAM1725 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1725 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1725 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is ap-

preciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1725 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1725 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24112] The complementary binding of VGAM1725 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1725 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1725 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1725 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[24113] It is appreciated that VGAM1725 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1725 host target genes. The mRNA of

each one of this plurality of VGAM1725 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1725 RNA, herein designated VGAM RNA, and which when bound by VGAM1725 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1725 host target proteins.

[24114] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1725 gene, herein designated VGAM GENE, on one or more VGAM1725 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science

294,779 (2001)).

[24115] It is yet further appreciated that a function of VGAM1725 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1725 include diagnosis, prevention and treatment of viral infection by Rabies virus. Specific functions, and accordingly utilities, of VGAM1725 correlate with, and may be deduced from, the identity of the host target genes which VGAM1725 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[24116] Nucleotide sequences of the VGAM1725 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1725 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1725 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1725 are further described hereinbelow with reference to Table 1.

[24117] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1725 RNA, herein designated VGAM RNA, are de-

scribed hereinbelow with reference to Table 2.

[24118] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1726 (VGAM1726) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[24119] VGAM1726 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1726 was detected is described hereinabove with reference to Figs. 2-8.

[24120] VGAM1726 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rabies virus. VGAM1726 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[24121] VGAM1726 gene, herein designated VGAM GENE, encodes a VGAM1726 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1726 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1726 precur-

sor RNA is designated SEQ ID:1712, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1712 is located at position 9658 relative to the genome of Rabies virus.

[24122] VGAM1726 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1726 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24123] An enzyme complex designated DICER COMPLEX, dices the VGAM1726 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1726 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide se-

quence of VGAM1726 RNA is designated SEQ ID:4437, and is provided hereinbelow with reference to the sequence listing part.

[24124] VGAM1726 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1726 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1726 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24125] VGAM1726 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1726 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1726 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is ap-

preciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1726 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1726 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24126] The complementary binding of VGAM1726 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1726 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1726 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1726 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[24127] It is appreciated that VGAM1726 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1726 host target genes. The mRNA of

each one of this plurality of VGAM1726 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1726 RNA, herein designated VGAM RNA, and which when bound by VGAM1726 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1726 host target proteins.

[24128] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1726 gene, herein designated VGAM GENE, on one or more VGAM1726 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science

294,779 (2001)).

[24129] It is yet further appreciated that a function of VGAM1726 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1726 include diagnosis, prevention and treatment of viral infection by Rabies virus. Specific functions, and accordingly utilities, of VGAM1726 correlate with, and may be deduced from, the identity of the host target genes which VGAM1726 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[24130] Nucleotide sequences of the VGAM1726 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1726 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1726 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1726 are further described hereinbelow with reference to Table 1.

[24131] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1726 RNA, herein designated VGAM RNA, are de-

scribed hereinbelow with reference to Table 2.

[24132] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1727 (VGAM1727) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[24133] VGAM1727 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1727 was detected is described hereinabove with reference to Figs. 2-8.

[24134] VGAM1727 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rabies virus. VGAM1727 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[24135] VGAM1727 gene, herein designated VGAM GENE, encodes a VGAM1727 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1727 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1727 precur-

sor RNA is designated SEQ ID:1713, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1713 is located at position 8962 relative to the genome of Rabies virus.

[24136] VGAM1727 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1727 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24137] An enzyme complex designated DICER COMPLEX, dices the VGAM1727 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1727 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide se-

quence of VGAM1727 RNA is designated SEQ ID:4438, and is provided hereinbelow with reference to the sequence listing part.

[24138] VGAM1727 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1727 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1727 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24139] VGAM1727 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1727 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1727 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is ap-

preciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1727 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1727 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24140] The complementary binding of VGAM1727 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1727 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1727 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1727 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[24141] It is appreciated that VGAM1727 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1727 host target genes. The mRNA of

each one of this plurality of VGAM1727 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1727 RNA, herein designated VGAM RNA, and which when bound by VGAM1727 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1727 host target proteins.

[24142] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1727 gene, herein designated VGAM GENE, on one or more VGAM1727 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science

294,779 (2001)).

[24143] It is yet further appreciated that a function of VGAM1727 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1727 include diagnosis, prevention and treatment of viral infection by Rabies virus. Specific functions, and accordingly utilities, of VGAM1727 correlate with, and may be deduced from, the identity of the host target genes which VGAM1727 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[24144] Nucleotide sequences of the VGAM1727 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1727 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1727 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1727 are further described hereinbelow with reference to Table 1.

[24145] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1727 RNA, herein designated VGAM RNA, are de-

scribed hereinbelow with reference to Table 2.

[24146] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1728 (VGAM1728) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[24147] VGAM1728 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1728 was detected is described hereinabove with reference to Figs. 2-8.

[24148] VGAM1728 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rabies virus. VGAM1728 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[24149] VGAM1728 gene, herein designated VGAM GENE, encodes a VGAM1728 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1728 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1728 precur-

sor RNA is designated SEQ ID:1714, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1714 is located at position 4718 relative to the genome of Rabies virus.

[24150] VGAM1728 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1728 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24151] An enzyme complex designated DICER COMPLEX, dices the VGAM1728 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1728 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide se-

quence of VGAM1728 RNA is designated SEQ ID:4439, and is provided hereinbelow with reference to the sequence listing part.

[24152] VGAM1728 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1728 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1728 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24153] VGAM1728 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1728 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1728 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is ap-

preciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1728 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1728 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24154] The complementary binding of VGAM1728 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1728 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1728 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1728 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[24155] It is appreciated that VGAM1728 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1728 host target genes. The mRNA of

each one of this plurality of VGAM1728 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1728 RNA, herein designated VGAM RNA, and which when bound by VGAM1728 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1728 host target proteins.

[24156] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1728 gene, herein designated VGAM GENE, on one or more VGAM1728 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science

294,779 (2001)).

[24157] It is yet further appreciated that a function of VGAM1728 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1728 include diagnosis, prevention and treatment of viral infection by Rabies virus. Specific functions, and accordingly utilities, of VGAM1728 correlate with, and may be deduced from, the identity of the host target genes which VGAM1728 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[24158] Nucleotide sequences of the VGAM1728 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1728 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1728 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1728 are further described hereinbelow with reference to Table 1.

[24159] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1728 RNA, herein designated VGAM RNA, are de-

scribed hereinbelow with reference to Table 2.

[24160] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1729 (VGAM1729) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[24161] VGAM1729 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1729 was detected is described hereinabove with reference to Figs. 2-8.

[24162] VGAM1729 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rabies virus. VGAM1729 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[24163] VGAM1729 gene, herein designated VGAM GENE, encodes a VGAM1729 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1729 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1729 precur-

sor RNA is designated SEQ ID:1715, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1715 is located at position 8293 relative to the genome of Rabies virus.

[24164] VGAM1729 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1729 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24165] An enzyme complex designated DICER COMPLEX, dices the VGAM1729 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1729 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 60%) nucleotide se-

quence of VGAM1729 RNA is designated SEQ ID:4440, and is provided hereinbelow with reference to the sequence listing part.

[24166] VGAM1729 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1729 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1729 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24167] VGAM1729 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1729 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1729 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is ap-

preciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1729 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1729 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24168] The complementary binding of VGAM1729 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1729 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1729 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1729 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[24169] It is appreciated that VGAM1729 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1729 host target genes. The mRNA of

each one of this plurality of VGAM1729 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1729 RNA, herein designated VGAM RNA, and which when bound by VGAM1729 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1729 host target proteins.

[24170] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1729 gene, herein designated VGAM GENE, on one or more VGAM1729 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science

294,779 (2001)).

[24171] It is yet further appreciated that a function of VGAM1729 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1729 include diagnosis, prevention and treatment of viral infection by Rabies virus. Specific functions, and accordingly utilities, of VGAM1729 correlate with, and may be deduced from, the identity of the host target genes which VGAM1729 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[24172] Nucleotide sequences of the VGAM1729 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1729 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1729 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1729 are further described hereinbelow with reference to Table 1.

[24173] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1729 RNA, herein designated VGAM RNA, are de-

scribed hereinbelow with reference to Table 2.

[24174] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1730 (VGAM1730) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[24175] VGAM1730 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1730 was detected is described hereinabove with reference to Figs. 2-8.

[24176] VGAM1730 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rabies virus. VGAM1730 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[24177] VGAM1730 gene, herein designated VGAM GENE, encodes a VGAM1730 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1730 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1730 precur-

sor RNA is designated SEQ ID:1716, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1716 is located at position 6659 relative to the genome of Rabies virus.

[24178] VGAM1730 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1730 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24179] An enzyme complex designated DICER COMPLEX, dices the VGAM1730 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1730 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide se-

quence of VGAM1730 RNA is designated SEQ ID:4441, and is provided hereinbelow with reference to the sequence listing part.

[24180] VGAM1730 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1730 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1730 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24181] VGAM1730 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1730 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1730 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is ap-

preciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1730 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1730 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24182] The complementary binding of VGAM1730 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1730 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1730 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1730 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[24183] It is appreciated that VGAM1730 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1730 host target genes. The mRNA of

each one of this plurality of VGAM1730 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1730 RNA, herein designated VGAM RNA, and which when bound by VGAM1730 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1730 host target proteins.

[24184] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1730 gene, herein designated VGAM GENE, on one or more VGAM1730 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science

294,779 (2001)).

[24185] It is yet further appreciated that a function of VGAM1730 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1730 include diagnosis, prevention and treatment of viral infection by Rabies virus. Specific functions, and accordingly utilities, of VGAM1730 correlate with, and may be deduced from, the identity of the host target genes which VGAM1730 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[24186] Nucleotide sequences of the VGAM1730 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1730 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1730 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1730 are further described hereinbelow with reference to Table 1.

[24187] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1730 RNA, herein designated VGAM RNA, are de-

scribed hereinbelow with reference to Table 2.

[24188] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1731 (VGAM1731) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[24189] VGAM1731 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1731 was detected is described hereinabove with reference to Figs. 2-8.

[24190] VGAM1731 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rabies virus. VGAM1731 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[24191] VGAM1731 gene, herein designated VGAM GENE, encodes a VGAM1731 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1731 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1731 precur-

sor RNA is designated SEQ ID:1717, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1717 is located at position 3422 relative to the genome of Rabies virus.

[24192] VGAM1731 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1731 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24193] An enzyme complex designated DICER COMPLEX, dices the VGAM1731 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1731 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 81%) nucleotide se-

quence of VGAM1731 RNA is designated SEQ ID:4442, and is provided hereinbelow with reference to the sequence listing part.

[24194] VGAM1731 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1731 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1731 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24195] VGAM1731 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1731 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1731 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is ap-

preciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1731 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1731 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24196] The complementary binding of VGAM1731 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1731 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1731 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1731 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[24197] It is appreciated that VGAM1731 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1731 host target genes. The mRNA of

each one of this plurality of VGAM1731 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1731 RNA, herein designated VGAM RNA, and which when bound by VGAM1731 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1731 host target proteins.

[24198] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1731 gene, herein designated VGAM GENE, on one or more VGAM1731 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science

294,779 (2001)).

[24199] It is yet further appreciated that a function of VGAM1731 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1731 include diagnosis, prevention and treatment of viral infection by Rabies virus. Specific functions, and accordingly utilities, of VGAM1731 correlate with, and may be deduced from, the identity of the host target genes which VGAM1731 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[24200] Nucleotide sequences of the VGAM1731 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1731 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1731 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1731 are further described hereinbelow with reference to Table 1.

[24201] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1731 RNA, herein designated VGAM RNA, are de-

scribed hereinbelow with reference to Table 2.

[24202] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1732 (VGAM1732) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[24203] VGAM1732 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1732 was detected is described hereinabove with reference to Figs. 2-8.

[24204] VGAM1732 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rabies virus. VGAM1732 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[24205] VGAM1732 gene, herein designated VGAM GENE, encodes a VGAM1732 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1732 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1732 precur-

sor RNA is designated SEQ ID:1718, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1718 is located at position 9788 relative to the genome of Rabies virus.

[24206] VGAM1732 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1732 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24207] An enzyme complex designated DICER COMPLEX, dices the VGAM1732 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1732 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 47%) nucleotide se-

quence of VGAM1732 RNA is designated SEQ ID:4443, and is provided hereinbelow with reference to the sequence listing part.

[24208] VGAM1732 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1732 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1732 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24209] VGAM1732 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1732 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1732 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is ap-

preciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1732 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1732 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24210] The complementary binding of VGAM1732 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1732 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1732 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1732 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[24211] It is appreciated that VGAM1732 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1732 host target genes. The mRNA of

each one of this plurality of VGAM1732 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1732 RNA, herein designated VGAM RNA, and which when bound by VGAM1732 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1732 host target proteins.

[24212] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1732 gene, herein designated VGAM GENE, on one or more VGAM1732 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science

294,779 (2001)).

[24213] It is yet further appreciated that a function of VGAM1732 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1732 include diagnosis, prevention and treatment of viral infection by Rabies virus. Specific functions, and accordingly utilities, of VGAM1732 correlate with, and may be deduced from, the identity of the host target genes which VGAM1732 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[24214] Nucleotide sequences of the VGAM1732 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1732 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1732 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1732 are further described hereinbelow with reference to Table 1.

[24215] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1732 RNA, herein designated VGAM RNA, are de-

scribed hereinbelow with reference to Table 2.

[24216] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1733 (VGAM1733) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[24217] VGAM1733 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1733 was detected is described hereinabove with reference to Figs. 2-8.

[24218] VGAM1733 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human herpesvirus 3. VGAM1733 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[24219] VGAM1733 gene, herein designated VGAM GENE, encodes a VGAM1733 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1733 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly

similar to the nucleotide sequence of VGAM1733 precursor RNA is designated SEQ ID:1719, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1719 is located at position 40756 relative to the genome of Human herpesvirus 3.

[24220] VGAM1733 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1733 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24221] An enzyme complex designated DICER COMPLEX, dices the VGAM1733 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1733 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 45%) nucleotide sequence of VGAM1733 RNA is designated SEQ ID:4444, and is provided hereinbelow with reference to the sequence listing part.

[24222] VGAM1733 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1733 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1733 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24223] VGAM1733 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1733 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1733 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I,

BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1733 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1733 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24224] The complementary binding of VGAM1733 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1733 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1733 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1733 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[24225] It is appreciated that VGAM1733 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM1733 host target genes. The mRNA of each one of this plurality of VGAM1733 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1733 RNA, herein designated VGAM RNA, and which when bound by VGAM1733 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1733 host target proteins.

[24226] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1733 gene, herein designated VGAM GENE, on one or more VGAM1733 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24227] It is yet further appreciated that a function of VGAM1733 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1733 include diagnosis, prevention and treatment of viral infection by Human herpesvirus 3. Specific functions, and accordingly utilities, of VGAM1733 correlate with, and may be deduced from, the identity of the host target genes which VGAM1733 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[24228] Nucleotide sequences of the VGAM1733 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1733 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1733 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1733 are further described hereinbelow with reference to Table 1.

[24229] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites

to VGAM1733 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[24230] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1734 (VGAM1734) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[24231] VGAM1734 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1734 was detected is described hereinabove with reference to Figs. 2-8.

[24232] VGAM1734 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human herpesvirus 3. VGAM1734 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[24233] VGAM1734 gene, herein designated VGAM GENE, encodes a VGAM1734 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1734 precursor RNA, herein designated VGAM PRECURSOR RNA, does not en-

code a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1734 precursor RNA is designated SEQ ID:1720, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1720 is located at position 35482 relative to the genome of Human herpesvirus 3.

[24234] VGAM1734 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1734 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24235] An enzyme complex designated DICER COMPLEX, dices the VGAM1734 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1734 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide sequence of VGAM1734 RNA is designated SEQ ID:4445, and is provided hereinbelow with reference to the sequence listing part.

[24236] VGAM1734 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1734 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1734 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24237] VGAM1734 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1734 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1734 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3

such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1734 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1734 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24238] The complementary binding of VGAM1734 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1734 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1734 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1734 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[24239] It is appreciated that VGAM1734 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1734 host target genes. The mRNA of each one of this plurality of VGAM1734 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1734 RNA, herein designated VGAM RNA, and which when bound by VGAM1734 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1734 host target proteins.

[24240] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1734 gene, herein designated VGAM GENE, on one or more VGAM1734 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24241] It is yet further appreciated that a function of VGAM1734 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1734 include diagnosis, prevention and treatment of viral infection by Human herpesvirus 3. Specific functions, and accordingly utilities, of VGAM1734 correlate with, and may be deduced from, the identity of the host target genes which VGAM1734 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[24242] Nucleotide sequences of the VGAM1734 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1734 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1734 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1734 are further described hereinbelow with reference to Table 1.

[24243] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the

complementarity of each of these host target binding sites to VGAM1734 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[24244] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1735 (VGAM1735) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[24245] VGAM1735 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1735 was detected is described hereinabove with reference to Figs. 2-8.

[24246] VGAM1735 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human herpesvirus 3. VGAM1735 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[24247] VGAM1735 gene, herein designated VGAM GENE, encodes a VGAM1735 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1735 precursor RNA,

herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1735 precursor RNA is designated SEQ ID:1721, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1721 is located at position 33659 relative to the genome of Human herpesvirus 3.

[24248] VGAM1735 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1735 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24249] An enzyme complex designated DICER COMPLEX, dices the VGAM1735 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1735 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM1735 RNA is designated SEQ ID:4446, and is provided hereinbelow with reference to the sequence listing part.

[24250] VGAM1735 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1735 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1735 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24251] VGAM1735 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1735 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1735 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host

target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1735 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1735 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24252] The complementary binding of VGAM1735 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1735 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1735 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1735 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[24253] It is appreciated that VGAM1735 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1735 host target genes. The mRNA of each one of this plurality of VGAM1735 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1735 RNA, herein designated VGAM RNA, and which when bound by VGAM1735 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1735 host target proteins.

[24254] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1735 gene, herein designated VGAM GENE, on one or more VGAM1735 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24255] It is yet further appreciated that a function of VGAM1735 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1735 include diagnosis, prevention and treatment of viral infection by Human herpesvirus 3. Specific functions, and accordingly utilities, of VGAM1735 correlate with, and may be deduced from, the identity of the host target genes which VGAM1735 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[24256] Nucleotide sequences of the VGAM1735 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1735 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1735 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1735 are further described hereinbelow with reference to Table 1.

[24257] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1735 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[24258] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1736 (VGAM1736) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[24259] VGAM1736 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1736 was detected is described hereinabove with reference to Figs. 2-8.

[24260] VGAM1736 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human herpesvirus 3. VGAM1736 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[24261] VGAM1736 gene, herein designated VGAM GENE, encodes a VGAM1736 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and un-

like most ordinary genes, VGAM1736 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1736 precursor RNA is designated SEQ ID:1722, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1722 is located at position 39181 relative to the genome of Human herpesvirus 3.

[24262] VGAM1736 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1736 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24263] An enzyme complex designated DICER COMPLEX, dices the VGAM1736 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1736 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM1736 RNA is designated SEQ ID:4447, and is provided hereinbelow with reference to the sequence listing part.

[24264] VGAM1736 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1736 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1736 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24265] VGAM1736 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1736 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1736 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed

sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1736 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1736 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24266] The complementary binding of VGAM1736 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1736 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1736 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1736 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target

protein is therefore outlined by a broken line.

[24267] It is appreciated that VGAM1736 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1736 host target genes. The mRNA of each one of this plurality of VGAM1736 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1736 RNA, herein designated VGAM RNA, and which when bound by VGAM1736 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1736 host target proteins.

[24268] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1736 gene, herein designated VGAM GENE, on one or more VGAM1736 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24269] It is yet further appreciated that a function of VGAM1736 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1736 include diagnosis, prevention and treatment of viral infection by Human herpesvirus 3. Specific functions, and accordingly utilities, of VGAM1736 correlate with, and may be deduced from, the identity of the host target genes which VGAM1736 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[24270] Nucleotide sequences of the VGAM1736 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1736 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1736 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1736 are further described hereinbelow with reference to Table 1.

[24271] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1736 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[24272] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1737 (VGAM1737) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[24273] VGAM1737 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1737 was detected is described hereinabove with reference to Figs. 2-8.

[24274] VGAM1737 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human herpesvirus 3. VGAM1737 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[24275] VGAM1737 gene, herein designated VGAM GENE, encodes a VGAM1737 precursor RNA, herein designated VGAM

PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1737 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1737 precursor RNA is designated SEQ ID:1723, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1723 is located at position 32691 relative to the genome of Human herpesvirus 3.

[24276] VGAM1737 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1737 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24277] An enzyme complex designated DICER COMPLEX, dices the VGAM1737 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1737 RNA, herein designated VGAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 56%) nucleotide sequence of VGAM1737 RNA is designated SEQ ID:4448, and is provided hereinbelow with reference to the sequence listing part.

[24278] VGAM1737 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1737 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1737 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24279] VGAM1737 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1737 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1737 RNA, herein designated

VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1737 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1737 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24280] The complementary binding of VGAM1737 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1737 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1737 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1737 host target protein, herein desig-

nated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[24281] It is appreciated that VGAM1737 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1737 host target genes. The mRNA of each one of this plurality of VGAM1737 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1737 RNA, herein designated VGAM RNA, and which when bound by VGAM1737 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1737 host target proteins.

[24282] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1737 gene, herein designated VGAM GENE, on one or more VGAM1737 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24283] It is yet further appreciated that a function of VGAM1737 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1737 include diagnosis, prevention and treatment of viral infection by Human herpesvirus 3. Specific functions, and accordingly utilities, of VGAM1737 correlate with, and may be deduced from, the identity of the host target genes which VGAM1737 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[24284] Nucleotide sequences of the VGAM1737 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1737 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1737 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1737 are further described hereinbelow with reference to Table 1.

[24285] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1737 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[24286] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1738 (VGAM1738) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[24287] VGAM1738 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1738 was detected is described hereinabove with reference to Figs. 2-8.

[24288] VGAM1738 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human herpesvirus 3. VGAM1738 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[24289] VGAM1738 gene, herein designated VGAM GENE, encodes

a VGAM1738 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1738 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1738 precursor RNA is designated SEQ ID:1724, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1724 is located at position 41710 relative to the genome of Human herpesvirus 3.

[24290] VGAM1738 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1738 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24291] An enzyme complex designated DICER COMPLEX, dices the VGAM1738 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1738 RNA,

herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM1738 RNA is designated SEQ ID:4449, and is provided hereinbelow with reference to the sequence listing part.

[24292] VGAM1738 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1738 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1738 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24293] VGAM1738 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1738 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM1738 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1738 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1738 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24294] The complementary binding of VGAM1738 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1738 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1738 host target RNA, herein designated VGAM HOST TARGET

RNA, into VGAM1738 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[24295] It is appreciated that VGAM1738 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1738 host target genes. The mRNA of each one of this plurality of VGAM1738 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1738 RNA, herein designated VGAM RNA, and which when bound by VGAM1738 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1738 host target proteins.

[24296] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1738 gene, herein designated VGAM GENE, on one or more VGAM1738 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24297] It is yet further appreciated that a function of VGAM1738 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1738 include diagnosis, prevention and treatment of viral infection by Human herpesvirus 3. Specific functions, and accordingly utilities, of VGAM1738 correlate with, and may be deduced from, the identity of the host target genes which VGAM1738 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[24298] Nucleotide sequences of the VGAM1738 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1738 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1738 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1738 are further

described hereinbelow with reference to Table 1.

[24299] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1738 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[24300] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1739 (VGAM1739) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[24301] VGAM1739 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1739 was detected is described hereinabove with reference to Figs. 2-8.

[24302] VGAM1739 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human herpesvirus 3. VGAM1739 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[24303] VGAM1739 gene, herein designated VGAM GENE, encodes a VGAM1739 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1739 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1739 precursor RNA is designated SEQ ID:1725, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1725 is located at position 38932 relative to the genome of Human herpesvirus 3.

[24304] VGAM1739 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1739 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24305] An enzyme complex designated DICER COMPLEX, dices the VGAM1739 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, into VGAM1739 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 62%) nucleotide sequence of VGAM1739 RNA is designated SEQ ID:4450, and is provided hereinbelow with reference to the sequence listing part.

[24306] VGAM1739 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1739 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1739 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24307] VGAM1739 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1739 host target RNA, herein designated VGAM HOST TARGET RNA. This

complementary binding is due to the fact that the nucleotide sequence of VGAM1739 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1739 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1739 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24308] The complementary binding of VGAM1739 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1739 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1739

host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1739 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[24309] It is appreciated that VGAM1739 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1739 host target genes. The mRNA of each one of this plurality of VGAM1739 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1739 RNA, herein designated VGAM RNA, and which when bound by VGAM1739 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1739 host target proteins.

[24310] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1739 gene, herein designated VGAM GENE, on one or more VGAM1739 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24311] It is yet further appreciated that a function of VGAM1739 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1739 include diagnosis, prevention and treatment of viral infection by Human herpesvirus 3. Specific functions, and accordingly utilities, of VGAM1739 correlate with, and may be deduced from, the identity of the host target genes which VGAM1739 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[24312] Nucleotide sequences of the VGAM1739 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1739 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1739 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM1739 are further described hereinbelow with reference to Table 1.

[24313] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1739 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[24314] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1740 (VGAM1740) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[24315] VGAM1740 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1740 was detected is described hereinabove with reference to Figs. 2-8.

[24316] VGAM1740 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human herpesvirus 3. VGAM1740 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the

human genome.

[24317] VGAM1740 gene, herein designated VGAM GENE, encodes a VGAM1740 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1740 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1740 precursor RNA is designated SEQ ID:1726, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1726 is located at position 36839 relative to the genome of Human herpesvirus 3.

[24318] VGAM1740 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1740 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24319] An enzyme complex designated DICER COMPLEX, dices

the VGAM1740 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1740 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM1740 RNA is designated SEQ ID:4451, and is provided hereinbelow with reference to the sequence listing part.

[24320] VGAM1740 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1740 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1740 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24321] VGAM1740 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1740 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1740 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1740 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1740 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24322] The complementary binding of VGAM1740 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1740 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM1740 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1740 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[24323] It is appreciated that VGAM1740 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1740 host target genes. The mRNA of each one of this plurality of VGAM1740 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1740 RNA, herein designated VGAM RNA, and which when bound by VGAM1740 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1740 host target proteins.

[24324] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1740 gene, herein designated VGAM GENE, on one or more VGAM1740 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24325] It is yet further appreciated that a function of VGAM1740 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1740 include diagnosis, prevention and treatment of viral infection by Human herpesvirus 3. Specific functions, and accordingly utilities, of VGAM1740 correlate with, and may be deduced from, the identity of the host target genes which VGAM1740 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[24326] Nucleotide sequences of the VGAM1740 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1740 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of

VGAM1740 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1740 are further described hereinbelow with reference to Table 1.

[24327] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1740 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[24328] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1741 (VGAM1741) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[24329] VGAM1741 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1741 was detected is described hereinabove with reference to Figs. 2-8.

[24330] VGAM1741 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cercopithecine herpesvirus 7. VGAM1741 host target gene, herein desig-

nated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[24331] VGAM1741 gene, herein designated VGAM GENE, encodes a VGAM1741 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1741 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1741 precursor RNA is designated SEQ ID:1727, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1727 is located at position 36070 relative to the genome of Cercopithecine herpesvirus 7.

[24332] VGAM1741 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1741 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[24333] An enzyme complex designated DICER COMPLEX, dices the VGAM1741 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1741 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM1741 RNA is designated SEQ ID:4452, and is provided hereinbelow with reference to the sequence listing part.

[24334] VGAM1741 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1741 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1741 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24335] VGAM1741 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM1741 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1741 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1741 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1741 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24336] The complementary binding of VGAM1741 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM1741 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1741 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1741 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[24337] It is appreciated that VGAM1741 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1741 host target genes. The mRNA of each one of this plurality of VGAM1741 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1741 RNA, herein designated VGAM RNA, and which when bound by VGAM1741 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1741 host target proteins.

[24338] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1741 gene, herein designated VGAM GENE, on one or more VGAM1741 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24339] It is yet further appreciated that a function of VGAM1741 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1741 include diagnosis, prevention and treatment of viral infection by Cercopithecine herpesvirus 7. Specific functions, and accordingly utilities, of VGAM1741 correlate with, and may be deduced from, the identity of the host target genes which VGAM1741 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[24340] Nucleotide sequences of the VGAM1741 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

diced VGAM1741 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1741 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1741 are further described hereinbelow with reference to Table 1.

[24341] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1741 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[24342] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1742 (VGAM1742) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[24343] VGAM1742 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1742 was detected is described hereinabove with reference to Figs. 2-8.

[24344] VGAM1742 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of Cercopithecine herpesvirus 7. VGAM1742 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[24345] VGAM1742 gene, herein designated VGAM GENE, encodes a VGAM1742 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1742 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1742 precursor RNA is designated SEQ ID:1728, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1728 is located at position 40735 relative to the genome of Cercopithecine herpesvirus 7.

[24346] VGAM1742 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1742 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24347] An enzyme complex designated DICER COMPLEX, dices the VGAM1742 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1742 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM1742 RNA is designated SEQ ID:4453, and is provided hereinbelow with reference to the sequence listing part.

[24348] VGAM1742 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1742 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1742 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN COD-

ING and 3UTR respectively.

[24349] VGAM1742 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1742 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1742 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1742 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1742 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24350] The complementary binding of VGAM1742 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1742 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1742 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1742 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[24351] It is appreciated that VGAM1742 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1742 host target genes. The mRNA of each one of this plurality of VGAM1742 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1742 RNA, herein designated VGAM RNA, and which when bound by VGAM1742 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1742 host target proteins.

[24352] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1742 gene, herein designated VGAM GENE, on one

or more VGAM1742 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24353] It is yet further appreciated that a function of VGAM1742 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1742 include diagnosis, prevention and treatment of viral infection by Cercopithecine herpesvirus 7. Specific functions, and accordingly utilities, of VGAM1742 correlate with, and may be deduced from, the identity of the host target genes which VGAM1742 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[24354] Nucleotide sequences of the VGAM1742 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1742 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1742 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1742 are further described hereinbelow with reference to Table 1.

[24355] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1742 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[24356] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1743 (VGAM1743) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[24357] VGAM1743 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1743 was detected is de-

scribed hereinabove with reference to Figs. 2-8.

[24358] VGAM1743 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cercopithecine herpesvirus 7. VGAM1743 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[24359] VGAM1743 gene, herein designated VGAM GENE, encodes a VGAM1743 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1743 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1743 precursor RNA is designated SEQ ID:1729, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1729 is located at position 41519 relative to the genome of Cercopithecine herpesvirus 7.

[24360] VGAM1743 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1743 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24361] An enzyme complex designated DICER COMPLEX, dices the VGAM1743 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1743 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 78%) nucleotide sequence of VGAM1743 RNA is designated SEQ ID:4454, and is provided hereinbelow with reference to the sequence listing part.

[24362] VGAM1743 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1743 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1743 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding

gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24363] VGAM1743 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1743 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1743 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1743 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1743 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be lo-

cated in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24364] The complementary binding of VGAM1743 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1743 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1743 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1743 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[24365] It is appreciated that VGAM1743 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1743 host target genes. The mRNA of each one of this plurality of VGAM1743 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1743 RNA, herein designated VGAM RNA, and which when bound by VGAM1743 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1743 host target proteins.

[24366] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM1743 gene, herein designated VGAM GENE, on one or more VGAM1743 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24367] It is yet further appreciated that a function of VGAM1743 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1743 include diagnosis, prevention and treatment of viral infection by Cercopithecine herpesvirus 7. Specific functions, and accordingly utilities, of VGAM1743 correlate with, and may be deduced from, the identity of the host target genes which VGAM1743 binds

and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[24368] Nucleotide sequences of the VGAM1743 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1743 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1743 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1743 are further described hereinbelow with reference to Table 1.

[24369] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1743 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[24370] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1744 (VGAM1744) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[24371] VGAM1744 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1744 was detected is described hereinabove with reference to Figs. 2-8.

[24372] VGAM1744 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cercopithecine herpesvirus 7. VGAM1744 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[24373] VGAM1744 gene, herein designated VGAM GENE, encodes a VGAM1744 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1744 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1744 precursor RNA is designated SEQ ID:1730, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1730 is located at position 38434 relative to the genome of Cercopithecine herpesvirus 7.

[24374] VGAM1744 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1744 folded precursor RNA, herein designated VGAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24375] An enzyme complex designated DICER COMPLEX, dices the VGAM1744 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1744 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM1744 RNA is designated SEQ ID:4455, and is provided hereinbelow with reference to the sequence listing part.

[24376] VGAM1744 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1744 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1744 host target RNA,

herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24377] VGAM1744 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1744 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1744 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1744 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1744 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host tar-

get binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24378] The complementary binding of VGAM1744 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1744 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1744 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1744 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[24379] It is appreciated that VGAM1744 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1744 host target genes. The mRNA of each one of this plurality of VGAM1744 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1744 RNA, herein designated VGAM RNA, and which when bound by VGAM1744 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1744 host target proteins.

[24380] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1744 gene, herein designated VGAM GENE, on one or more VGAM1744 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24381] It is yet further appreciated that a function of VGAM1744 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1744 include diagnosis, prevention and treatment of viral infection by Cercopithecine herpesvirus 7. Specific functions, and accordingly utilities, of

VGAM1744 correlate with, and may be deduced from, the identity of the host target genes which VGAM1744 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[24382] Nucleotide sequences of the VGAM1744 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1744 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1744 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1744 are further described hereinbelow with reference to Table 1.

[24383] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1744 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[24384] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1745 (VGAM1745) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the

art.

[24385] VGAM1745 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1745 was detected is described hereinabove with reference to Figs. 2-8.

[24386] VGAM1745 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cercopithecine herpesvirus 7. VGAM1745 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[24387] VGAM1745 gene, herein designated VGAM GENE, encodes a VGAM1745 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1745 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1745 precursor RNA is designated SEQ ID:1731, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1731 is located at position 37836 relative to the genome of Cercopithecine herpesvirus 7.

[24388] VGAM1745 precursor RNA, herein designated VGAM PRE-

CURSOR RNA, folds onto itself, forming VGAM1745 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24389] An enzyme complex designated DICER COMPLEX, dices the VGAM1745 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1745 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 81%) nucleotide sequence of VGAM1745 RNA is designated SEQ ID:4456, and is provided hereinbelow with reference to the sequence listing part.

[24390] VGAM1745 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM1745 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1745 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24391] VGAM1745 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1745 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1745 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1745 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1745 host

target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24392] The complementary binding of VGAM1745 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1745 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1745 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1745 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[24393] It is appreciated that VGAM1745 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1745 host target genes. The mRNA of each one of this plurality of VGAM1745 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1745 RNA, herein designated VGAM RNA, and which when bound by VGAM1745 RNA, herein

designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1745 host target proteins.

[24394] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1745 gene, herein designated VGAM GENE, on one or more VGAM1745 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24395] It is yet further appreciated that a function of VGAM1745 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1745 include diagnosis, prevention and

treatment of viral infection by Cercopithecine herpesvirus 7. Specific functions, and accordingly utilities, of VGAM1745 correlate with, and may be deduced from, the identity of the host target genes which VGAM1745 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[24396] Nucleotide sequences of the VGAM1745 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1745 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1745 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1745 are further described hereinbelow with reference to Table 1.

[24397] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1745 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[24398] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1746 (VGAM1746) viral gene, which modulates ex-

pression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[24399] VGAM1746 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1746 was detected is described hereinabove with reference to Figs. 2-8.

[24400] VGAM1746 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cercopithecine herpesvirus 7. VGAM1746 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[24401] VGAM1746 gene, herein designated VGAM GENE, encodes a VGAM1746 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1746 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1746 precursor RNA is designated SEQ ID:1732, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1732 is located at position 40845 relative to the genome of Cercopithecine her-

pesvirus 7.

[24402] VGAM1746 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1746 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24403] An enzyme complex designated DICER COMPLEX, dices the VGAM1746 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1746 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 51%) nucleotide sequence of VGAM1746 RNA is designated SEQ ID:4457, and is provided hereinbelow with reference to the sequence listing part.

[24404] VGAM1746 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1746 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1746 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24405] VGAM1746 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1746 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1746 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1746 RNA, herein designated

VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1746 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24406] The complementary binding of VGAM1746 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1746 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1746 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1746 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[24407] It is appreciated that VGAM1746 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1746 host target genes. The mRNA of each one of this plurality of VGAM1746 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM1746 RNA, herein designated VGAM RNA, and which when bound by VGAM1746 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1746 host target proteins.

[24408] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1746 gene, herein designated VGAM GENE, on one or more VGAM1746 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24409] It is yet further appreciated that a function of VGAM1746 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1746 include diagnosis, prevention and treatment of viral infection by Cercopithecine herpesvirus 7. Specific functions, and accordingly utilities, of VGAM1746 correlate with, and may be deduced from, the identity of the host target genes which VGAM1746 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[24410] Nucleotide sequences of the VGAM1746 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1746 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1746 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1746 are further described hereinbelow with reference to Table 1.

[24411] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1746 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[24412] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present

invention, referred to here as Viral Genomic Address Messenger 1747 (VGAM1747) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[24413] VGAM1747 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1747 was detected is described hereinabove with reference to Figs. 2-8.

[24414] VGAM1747 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Camelpox virus. VGAM1747 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[24415] VGAM1747 gene, herein designated VGAM GENE, encodes a VGAM1747 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1747 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1747 precursor RNA is designated SEQ ID:1733, and is provided hereinbelow with reference to the sequence listing part. Nu-

cleotide sequence SEQ ID:1733 is located at position 11942 relative to the genome of Camelpox virus.

[24416] VGAM1747 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1747 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24417] An enzyme complex designated DICER COMPLEX, dices the VGAM1747 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1747 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 61%) nucleotide sequence of VGAM1747 RNA is designated SEQ ID:4458, and is provided hereinbelow with reference to the sequence

listing part.

[24418] VGAM1747 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1747 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1747 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24419] VGAM1747 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1747 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1747 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not

meant to be limiting VGAM1747 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1747 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24420] The complementary binding of VGAM1747 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1747 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1747 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1747 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[24421] It is appreciated that VGAM1747 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1747 host target genes. The mRNA of each one of this plurality of VGAM1747 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM1747 RNA, herein designated VGAM RNA, and which when bound by VGAM1747 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1747 host target proteins.

[24422] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1747 gene, herein designated VGAM GENE, on one or more VGAM1747 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24423] It is yet further appreciated that a function of VGAM1747

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1747 include diagnosis, prevention and treatment of viral infection by Camelpox virus. Specific functions, and accordingly utilities, of VGAM1747 correlate with, and may be deduced from, the identity of the host target genes which VGAM1747 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[24424] Nucleotide sequences of the VGAM1747 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1747 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1747 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1747 are further described hereinbelow with reference to Table 1.

[24425] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1747 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[24426] Fig. 1 further provides a conceptual description of another

novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1748 (VGAM1748) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[24427] VGAM1748 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1748 was detected is described hereinabove with reference to Figs. 2-8.

[24428] VGAM1748 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Camelpox virus. VGAM1748 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[24429] VGAM1748 gene, herein designated VGAM GENE, encodes a VGAM1748 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1748 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1748 precursor RNA is designated SEQ ID:1734, and is provided here-

inbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1734 is located at position 67 relative to the genome of Camelpox virus.

[24430] VGAM1748 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1748 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24431] An enzyme complex designated DICER COMPLEX, dices the VGAM1748 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1748 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM1748 RNA is designated SEQ ID:4459, and

is provided hereinbelow with reference to the sequence listing part.

[24432] VGAM1748 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1748 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1748 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24433] VGAM1748 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1748 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1748 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites

shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1748 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1748 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24434] The complementary binding of VGAM1748 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1748 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1748 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1748 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[24435] It is appreciated that VGAM1748 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1748 host target genes. The mRNA of each one of this plurality of VGAM1748 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1748 RNA, herein designated VGAM RNA, and which when bound by VGAM1748 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1748 host target proteins.

[24436] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1748 gene, herein designated VGAM GENE, on one or more VGAM1748 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24437] It is yet further appreciated that a function of VGAM1748 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1748 include diagnosis, prevention and treatment of viral infection by Camelpox virus. Specific functions, and accordingly utilities, of VGAM1748 correlate with, and may be deduced from, the identity of the host target genes which VGAM1748 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[24438] Nucleotide sequences of the VGAM1748 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1748 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1748 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1748 are further described hereinbelow with reference to Table 1.

[24439] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1748 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[24440] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1749 (VGAM1749) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[24441] VGAM1749 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1749 was detected is described hereinabove with reference to Figs. 2-8.

[24442] VGAM1749 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Camelpox virus. VGAM1749 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[24443] VGAM1749 gene, herein designated VGAM GENE, encodes a VGAM1749 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1749 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1749 precur-

sor RNA is designated SEQ ID:1735, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1735 is located at position 4361 relative to the genome of Camelpox virus.

[24444] VGAM1749 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1749 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24445] An enzyme complex designated DICER COMPLEX, dices the VGAM1749 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1749 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide se-

quence of VGAM1749 RNA is designated SEQ ID:4460, and is provided hereinbelow with reference to the sequence listing part.

[24446] VGAM1749 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1749 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1749 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24447] VGAM1749 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1749 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1749 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is ap-

preciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1749 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1749 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24448] The complementary binding of VGAM1749 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1749 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1749 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1749 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[24449] It is appreciated that VGAM1749 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1749 host target genes. The mRNA of

each one of this plurality of VGAM1749 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1749 RNA, herein designated VGAM RNA, and which when bound by VGAM1749 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1749 host target proteins.

[24450] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1749 gene, herein designated VGAM GENE, on one or more VGAM1749 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science

294,779 (2001)).

[24451] It is yet further appreciated that a function of VGAM1749 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1749 include diagnosis, prevention and treatment of viral infection by Camelpox virus. Specific functions, and accordingly utilities, of VGAM1749 correlate with, and may be deduced from, the identity of the host target genes which VGAM1749 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[24452] Nucleotide sequences of the VGAM1749 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1749 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1749 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1749 are further described hereinbelow with reference to Table 1.

[24453] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1749 RNA, herein designated VGAM RNA, are de-

scribed hereinbelow with reference to Table 2.

[24454] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1750 (VGAM1750) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[24455] VGAM1750 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1750 was detected is described hereinabove with reference to Figs. 2-8.

[24456] VGAM1750 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Camelpox virus. VGAM1750 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[24457] VGAM1750 gene, herein designated VGAM GENE, encodes a VGAM1750 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1750 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly

similar to the nucleotide sequence of VGAM1750 precursor RNA is designated SEQ ID:1736, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1736 is located at position 1194 relative to the genome of Camelpox virus.

[24458] VGAM1750 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1750 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24459] An enzyme complex designated DICER COMPLEX, dices the VGAM1750 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1750 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 41%) nucleotide sequence of VGAM1750 RNA is designated SEQ ID:4461, and is provided hereinbelow with reference to the sequence listing part.

[24460] VGAM1750 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1750 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1750 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24461] VGAM1750 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1750 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1750 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I,

BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1750 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1750 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24462] The complementary binding of VGAM1750 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1750 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1750 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1750 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[24463] It is appreciated that VGAM1750 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM1750 host target genes. The mRNA of each one of this plurality of VGAM1750 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1750 RNA, herein designated VGAM RNA, and which when bound by VGAM1750 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1750 host target proteins.

[24464] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1750 gene, herein designated VGAM GENE, on one or more VGAM1750 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24465] It is yet further appreciated that a function of VGAM1750 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1750 include diagnosis, prevention and treatment of viral infection by Camelpox virus. Specific functions, and accordingly utilities, of VGAM1750 correlate with, and may be deduced from, the identity of the host target genes which VGAM1750 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[24466] Nucleotide sequences of the VGAM1750 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1750 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1750 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1750 are further described hereinbelow with reference to Table 1.

[24467] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites

to VGAM1750 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[24468] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1751 (VGAM1751) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[24469] VGAM1751 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1751 was detected is described hereinabove with reference to Figs. 2-8.

[24470] VGAM1751 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Camelpox virus. VGAM1751 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[24471] VGAM1751 gene, herein designated VGAM GENE, encodes a VGAM1751 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1751 precursor RNA, herein designated VGAM PRECURSOR RNA, does not en-

code a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1751 precursor RNA is designated SEQ ID:1737, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1737 is located at position 58 relative to the genome of Camelpox virus.

[24472] VGAM1751 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1751 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24473] An enzyme complex designated DICER COMPLEX, dices the VGAM1751 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1751 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM1751 RNA is designated SEQ ID:4462, and is provided hereinbelow with reference to the sequence listing part.

[24474] VGAM1751 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1751 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1751 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24475] VGAM1751 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1751 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1751 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1751 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1751 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24476] The complementary binding of VGAM1751 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM1751 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1751 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1751 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[24477] It is appreciated that VGAM1751 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1751 host target genes. The mRNA of each one of this plurality of VGAM1751 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1751 RNA, herein designated VGAM RNA, and which when bound by VGAM1751 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1751 host target proteins.

[24478] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1751 gene, herein designated VGAM GENE, on one or more VGAM1751 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24479] It is yet further appreciated that a function of VGAM1751 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1751 include diagnosis, prevention and treatment of viral infection by Camelpox virus. Specific functions, and accordingly utilities, of VGAM1751 correlate with, and may be deduced from, the identity of the host target genes which VGAM1751 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[24480] Nucleotide sequences of the VGAM1751 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the diced VGAM1751 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1751 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1751 are further described hereinbelow with reference to Table 1.

[24481] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1751 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[24482] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1752 (VGAM1752) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[24483] VGAM1752 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1752 was detected is described hereinabove with reference to Figs. 2-8.

[24484] VGAM1752 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Camelpox virus. VGAM1752 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[24485] VGAM1752 gene, herein designated VGAM GENE, encodes a VGAM1752 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1752 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1752 precursor RNA is designated SEQ ID:1738, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1738 is located at position 2927 relative to the genome of Camelpox virus.

[24486] VGAM1752 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1752 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24487] An enzyme complex designated DICER COMPLEX, dices the VGAM1752 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1752 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM1752 RNA is designated SEQ ID:4463, and is provided hereinbelow with reference to the sequence listing part.

[24488] VGAM1752 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1752 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1752 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN COD-

ING and 3UTR respectively.

[24489] VGAM1752 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1752 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1752 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1752 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1752 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24490] The complementary binding of VGAM1752 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1752 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1752 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1752 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[24491] It is appreciated that VGAM1752 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1752 host target genes. The mRNA of each one of this plurality of VGAM1752 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1752 RNA, herein designated VGAM RNA, and which when bound by VGAM1752 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1752 host target proteins.

[24492] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1752 gene, herein designated VGAM GENE, on one

or more VGAM1752 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24493] It is yet further appreciated that a function of VGAM1752 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1752 include diagnosis, prevention and treatment of viral infection by Camelpox virus. Specific functions, and accordingly utilities, of VGAM1752 correlate with, and may be deduced from, the identity of the host target genes which VGAM1752 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[24494] Nucleotide sequences of the VGAM1752 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1752 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1752 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1752 are further described hereinbelow with reference to Table 1.

[24495] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1752 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[24496] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1753 (VGAM1753) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[24497] VGAM1753 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1753 was detected is de-

scribed hereinabove with reference to Figs. 2-8.

[24498] VGAM1753 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Camelpox virus. VGAM1753 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[24499] VGAM1753 gene, herein designated VGAM GENE, encodes a VGAM1753 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1753 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1753 precursor RNA is designated SEQ ID:1739, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1739 is located at position 2271 relative to the genome of Camelpox virus.

[24500] VGAM1753 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1753 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24501] An enzyme complex designated DICER COMPLEX, dices the VGAM1753 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1753 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM1753 RNA is designated SEQ ID:4464, and is provided hereinbelow with reference to the sequence listing part.

[24502] VGAM1753 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1753 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1753 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and

a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24503] VGAM1753 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1753 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1753 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1753 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1753 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both

3UTR and 5UTR regions.

[24504] The complementary binding of VGAM1753 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1753 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1753 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1753 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[24505] It is appreciated that VGAM1753 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1753 host target genes. The mRNA of each one of this plurality of VGAM1753 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1753 RNA, herein designated VGAM RNA, and which when bound by VGAM1753 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1753 host target proteins.

[24506] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM1753 gene, herein designated VGAM GENE, on one or more VGAM1753 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24507] It is yet further appreciated that a function of VGAM1753 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1753 include diagnosis, prevention and treatment of viral infection by Camelpox virus. Specific functions, and accordingly utilities, of VGAM1753 correlate with, and may be deduced from, the identity of the host target genes which VGAM1753 binds and inhibits, and the function of these host target genes, as elaborated

hereinbelow.

[24508] Nucleotide sequences of the VGAM1753 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1753 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1753 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1753 are further described hereinbelow with reference to Table 1.

[24509] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1753 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[24510] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1754 (VGAM1754) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[24511] VGAM1754 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene.

The method by which VGAM1754 was detected is described hereinabove with reference to Figs. 2-8.

[24512] VGAM1754 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Camelpox virus. VGAM1754 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[24513] VGAM1754 gene, herein designated VGAM GENE, encodes a VGAM1754 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1754 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1754 precursor RNA is designated SEQ ID:1740, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1740 is located at position 9493 relative to the genome of Camelpox virus.

[24514] VGAM1754 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1754 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24515] An enzyme complex designated DICER COMPLEX, dices the VGAM1754 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1754 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 84%) nucleotide sequence of VGAM1754 RNA is designated SEQ ID:4465, and is provided hereinbelow with reference to the sequence listing part.

[24516] VGAM1754 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1754 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1754 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding

gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24517] VGAM1754 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1754 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1754 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1754 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1754 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be lo-

cated in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24518] The complementary binding of VGAM1754 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1754 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1754 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1754 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[24519] It is appreciated that VGAM1754 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1754 host target genes. The mRNA of each one of this plurality of VGAM1754 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1754 RNA, herein designated VGAM RNA, and which when bound by VGAM1754 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1754 host target proteins.

[24520] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM1754 gene, herein designated VGAM GENE, on one or more VGAM1754 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24521] It is yet further appreciated that a function of VGAM1754 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1754 include diagnosis, prevention and treatment of viral infection by Camelpox virus. Specific functions, and accordingly utilities, of VGAM1754 correlate with, and may be deduced from, the identity of the host target genes which VGAM1754 binds and inhibits,

and the function of these host target genes, as elaborated hereinbelow.

[24522] Nucleotide sequences of the VGAM1754 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1754 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1754 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1754 are further described hereinbelow with reference to Table 1.

[24523] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1754 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[24524] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1755 (VGAM1755) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[24525] VGAM1755 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1755 was detected is described hereinabove with reference to Figs. 2-8.

[24526] VGAM1755 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Camelpox virus. VGAM1755 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[24527] VGAM1755 gene, herein designated VGAM GENE, encodes a VGAM1755 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1755 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1755 precursor RNA is designated SEQ ID:1741, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1741 is located at position 5746 relative to the genome of Camelpox virus.

[24528] VGAM1755 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1755 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24529] An enzyme complex designated DICER COMPLEX, dices the VGAM1755 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1755 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM1755 RNA is designated SEQ ID:4466, and is provided hereinbelow with reference to the sequence listing part.

[24530] VGAM1755 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1755 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1755 host target RNA, herein designated VGAM HOST TARGET RNA, comprises

three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24531] VGAM1755 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1755 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1755 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1755 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1755 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an

example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24532] The complementary binding of VGAM1755 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1755 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1755 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1755 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[24533] It is appreciated that VGAM1755 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1755 host target genes. The mRNA of each one of this plurality of VGAM1755 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1755 RNA, herein designated VGAM RNA, and which when bound by VGAM1755 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1755 host target proteins.

[24534] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1755 gene, herein designated VGAM GENE, on one or more VGAM1755 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24535] It is yet further appreciated that a function of VGAM1755 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1755 include diagnosis, prevention and treatment of viral infection by Camelpox virus. Specific functions, and accordingly utilities, of VGAM1755 correlate with, and may be deduced from, the identity of the

host target genes which VGAM1755 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[24536] Nucleotide sequences of the VGAM1755 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1755 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1755 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1755 are further described hereinbelow with reference to Table 1.

[24537] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1755 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[24538] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1756 (VGAM1756) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[24539] VGAM1756 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1756 was detected is described hereinabove with reference to Figs. 2-8.

[24540] VGAM1756 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Camelpox virus. VGAM1756 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[24541] VGAM1756 gene, herein designated VGAM GENE, encodes a VGAM1756 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1756 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1756 precursor RNA is designated SEQ ID:1742, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1742 is located at position 7373 relative to the genome of Camelpox virus.

[24542] VGAM1756 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1756 folded precursor RNA, herein designated VGAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24543] An enzyme complex designated DICER COMPLEX, dices the VGAM1756 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1756 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide sequence of VGAM1756 RNA is designated SEQ ID:4467, and is provided hereinbelow with reference to the sequence listing part.

[24544] VGAM1756 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1756 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1756 host target RNA,

herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24545] VGAM1756 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1756 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1756 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1756 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1756 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host tar-

get binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24546] The complementary binding of VGAM1756 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1756 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1756 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1756 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[24547] It is appreciated that VGAM1756 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1756 host target genes. The mRNA of each one of this plurality of VGAM1756 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1756 RNA, herein designated VGAM RNA, and which when bound by VGAM1756 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1756 host target proteins.

[24548] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1756 gene, herein designated VGAM GENE, on one or more VGAM1756 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24549] It is yet further appreciated that a function of VGAM1756 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1756 include diagnosis, prevention and treatment of viral infection by Camelpox virus. Specific functions, and accordingly utilities, of VGAM1756 corre-

late with, and may be deduced from, the identity of the host target genes which VGAM1756 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[24550] Nucleotide sequences of the VGAM1756 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1756 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1756 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1756 are further described hereinbelow with reference to Table 1.

[24551] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1756 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[24552] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1757 (VGAM1757) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the

art.

[24553] VGAM1757 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1757 was detected is described hereinabove with reference to Figs. 2-8.

[24554] VGAM1757 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Camelpox virus. VGAM1757 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[24555] VGAM1757 gene, herein designated VGAM GENE, encodes a VGAM1757 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1757 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1757 precursor RNA is designated SEQ ID:1743, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1743 is located at position 5203 relative to the genome of Camelpox virus.

[24556] VGAM1757 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1757 folded

precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24557] An enzyme complex designated DICER COMPLEX, dices the VGAM1757 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1757 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 48%) nucleotide sequence of VGAM1757 RNA is designated SEQ ID:4468, and is provided hereinbelow with reference to the sequence listing part.

[24558] VGAM1757 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1757 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM1757 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24559] VGAM1757 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1757 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1757 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1757 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1757 host target RNA, herein designated VGAM HOST TARGET RNA.

It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24560] The complementary binding of VGAM1757 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1757 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1757 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1757 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[24561] It is appreciated that VGAM1757 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1757 host target genes. The mRNA of each one of this plurality of VGAM1757 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1757 RNA, herein designated VGAM RNA, and which when bound by VGAM1757 RNA, herein designated VGAM RNA, causes inhibition of translation of

respective one or more VGAM1757 host target proteins.

[24562] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1757 gene, herein designated VGAM GENE, on one or more VGAM1757 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24563] It is yet further appreciated that a function of VGAM1757 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1757 include diagnosis, prevention and treatment of viral infection by Camelpox virus. Specific

functions, and accordingly utilities, of VGAM1757 correlate with, and may be deduced from, the identity of the host target genes which VGAM1757 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[24564] Nucleotide sequences of the VGAM1757 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1757 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1757 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1757 are further described hereinbelow with reference to Table 1.

[24565] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1757 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[24566] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1758 (VGAM1758) viral gene, which modulates expression of respective host target genes thereof, the func-

tion and utility of which host target genes is known in the art.

[24567] VGAM1758 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1758 was detected is described hereinabove with reference to Figs. 2-8.

[24568] VGAM1758 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Camelpox virus. VGAM1758 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[24569] VGAM1758 gene, herein designated VGAM GENE, encodes a VGAM1758 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1758 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1758 precursor RNA is designated SEQ ID:1744, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1744 is located at position 60 relative to the genome of Camelpox virus.

[24570] VGAM1758 precursor RNA, herein designated VGAM PRE-

CURSOR RNA, folds onto itself, forming VGAM1758 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24571] An enzyme complex designated DICER COMPLEX, dices the VGAM1758 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1758 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM1758 RNA is designated SEQ ID:4469, and is provided hereinbelow with reference to the sequence listing part.

[24572] VGAM1758 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM1758 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1758 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24573] VGAM1758 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1758 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1758 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1758 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1758 host

target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24574] The complementary binding of VGAM1758 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1758 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1758 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1758 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[24575] It is appreciated that VGAM1758 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1758 host target genes. The mRNA of each one of this plurality of VGAM1758 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1758 RNA, herein designated VGAM RNA, and which when bound by VGAM1758 RNA, herein

designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1758 host target proteins.

[24576] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1758 gene, herein designated VGAM GENE, on one or more VGAM1758 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24577] It is yet further appreciated that a function of VGAM1758 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1758 include diagnosis, prevention and

treatment of viral infection by Camelpox virus. Specific functions, and accordingly utilities, of VGAM1758 correlate with, and may be deduced from, the identity of the host target genes which VGAM1758 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[24578] Nucleotide sequences of the VGAM1758 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1758 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1758 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1758 are further described hereinbelow with reference to Table 1.

[24579] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1758 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[24580] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1759 (VGAM1759) viral gene, which modulates ex-

pression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[24581] VGAM1759 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1759 was detected is described hereinabove with reference to Figs. 2-8.

[24582] VGAM1759 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Bovine viral diarrhea virus genotype 2 (BVDV-2). VGAM1759 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[24583] VGAM1759 gene, herein designated VGAM GENE, encodes a VGAM1759 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1759 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1759 precursor RNA is designated SEQ ID:1745, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1745 is located at position 12109 relative to the genome of Bovine viral diarrhea

virus genotype 2 (BVDV-2).

[24584] VGAM1759 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1759 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24585] An enzyme complex designated DICER COMPLEX, dices the VGAM1759 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1759 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 67%) nucleotide sequence of VGAM1759 RNA is designated SEQ ID:4470, and is provided hereinbelow with reference to the sequence listing part.

[24586] VGAM1759 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1759 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1759 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24587] VGAM1759 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1759 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1759 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1759 RNA, herein designated

VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1759 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24588] The complementary binding of VGAM1759 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1759 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1759 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1759 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[24589] It is appreciated that VGAM1759 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1759 host target genes. The mRNA of each one of this plurality of VGAM1759 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM1759 RNA, herein designated VGAM RNA, and which when bound by VGAM1759 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1759 host target proteins.

[24590] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1759 gene, herein designated VGAM GENE, on one or more VGAM1759 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24591] It is yet further appreciated that a function of VGAM1759 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1759 include diagnosis, prevention and treatment of viral infection by Bovine viral diarrhea virus genotype 2 (BVDV-2). Specific functions, and accordingly utilities, of VGAM1759 correlate with, and may be deduced from, the identity of the host target genes which VGAM1759 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[24592] Nucleotide sequences of the VGAM1759 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1759 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1759 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1759 are further described hereinbelow with reference to Table 1.

[24593] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1759 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[24594] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present

invention, referred to here as Viral Genomic Address Messenger 1760 (VGAM1760) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[24595] VGAM1760 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1760 was detected is described hereinabove with reference to Figs. 2-8.

[24596] VGAM1760 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Bovine viral diarrhea virus genotype 2 (BVDV-2). VGAM1760 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[24597] VGAM1760 gene, herein designated VGAM GENE, encodes a VGAM1760 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1760 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1760 precursor RNA is designated SEQ ID:1746, and is provided hereinbelow with reference to the sequence listing part. Nu-

cleotide sequence SEQ ID:1746 is located at position 7567 relative to the genome of Bovine viral diarrhea virus genotype 2 (BVDV-2).

[24598] VGAM1760 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1760 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24599] An enzyme complex designated DICER COMPLEX, dices the VGAM1760 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1760 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 73%) nucleotide sequence of VGAM1760 RNA is designated SEQ ID:4471, and

is provided hereinbelow with reference to the sequence listing part.

[24600] VGAM1760 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1760 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1760 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24601] VGAM1760 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1760 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1760 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites

shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1760 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1760 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24602] The complementary binding of VGAM1760 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1760 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1760 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1760 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[24603] It is appreciated that VGAM1760 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1760 host target genes. The mRNA of each one of this plurality of VGAM1760 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1760 RNA, herein designated VGAM RNA, and which when bound by VGAM1760 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1760 host target proteins.

[24604] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1760 gene, herein designated VGAM GENE, on one or more VGAM1760 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24605] It is yet further appreciated that a function of VGAM1760 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1760 include diagnosis, prevention and treatment of viral infection by Bovine viral diarrhea virus genotype 2 (BVDV-2). Specific functions, and accordingly utilities, of VGAM1760 correlate with, and may be deduced from, the identity of the host target genes which VGAM1760 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[24606] Nucleotide sequences of the VGAM1760 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1760 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1760 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1760 are further described hereinbelow with reference to Table 1.

[24607] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1760 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[24608] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1761 (VGAM1761) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[24609] VGAM1761 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1761 was detected is described hereinabove with reference to Figs. 2-8.

[24610] VGAM1761 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Bovine viral diarrhea virus genotype 2 (BVDV-2). VGAM1761 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[24611] VGAM1761 gene, herein designated VGAM GENE, encodes a VGAM1761 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1761 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1761 precur-

sor RNA is designated SEQ ID:1747, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1747 is located at position 11998 relative to the genome of Bovine viral diarrhea virus genotype 2 (BVDV-2).

[24612] VGAM1761 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1761 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24613] An enzyme complex designated DICER COMPLEX, dices the VGAM1761 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1761 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 44%) nucleotide sequence of VGAM1761 RNA is designated SEQ ID:4472, and is provided hereinbelow with reference to the sequence listing part.

[24614] VGAM1761 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1761 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1761 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24615] VGAM1761 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1761 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1761 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I,

BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1761 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1761 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24616] The complementary binding of VGAM1761 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1761 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1761 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1761 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[24617] It is appreciated that VGAM1761 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM1761 host target genes. The mRNA of each one of this plurality of VGAM1761 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1761 RNA, herein designated VGAM RNA, and which when bound by VGAM1761 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1761 host target proteins.

[24618] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1761 gene, herein designated VGAM GENE, on one or more VGAM1761 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24619] It is yet further appreciated that a function of VGAM1761 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1761 include diagnosis, prevention and treatment of viral infection by Bovine viral diarrhea virus genotype 2 (BVDV-2). Specific functions, and accordingly utilities, of VGAM1761 correlate with, and may be deduced from, the identity of the host target genes which VGAM1761 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[24620] Nucleotide sequences of the VGAM1761 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1761 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1761 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1761 are further described hereinbelow with reference to Table 1.

[24621] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites

to VGAM1761 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[24622] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1762 (VGAM1762) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[24623] VGAM1762 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1762 was detected is described hereinabove with reference to Figs. 2-8.

[24624] VGAM1762 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Bovine viral diarrhea virus genotype 2 (BVDV-2). VGAM1762 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[24625] VGAM1762 gene, herein designated VGAM GENE, encodes a VGAM1762 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1762 precursor RNA, herein designated VGAM PRECURSOR RNA, does not en-

code a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1762 precursor RNA is designated SEQ ID:1748, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1748 is located at position 2442 relative to the genome of Bovine viral diarrhea virus genotype 2 (BVDV-2).

[24626] VGAM1762 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1762 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24627] An enzyme complex designated DICER COMPLEX, dices the VGAM1762 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1762 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 72%) nucleotide sequence of VGAM1762 RNA is designated SEQ ID:4473, and is provided hereinbelow with reference to the sequence listing part.

[24628] VGAM1762 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1762 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1762 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24629] VGAM1762 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1762 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1762 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host

target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1762 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1762 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24630] The complementary binding of VGAM1762 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1762 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1762 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1762 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[24631] It is appreciated that VGAM1762 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1762 host target genes. The mRNA of each one of this plurality of VGAM1762 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1762 RNA, herein designated VGAM RNA, and which when bound by VGAM1762 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1762 host target proteins.

[24632] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1762 gene, herein designated VGAM GENE, on one or more VGAM1762 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24633] It is yet further appreciated that a function of VGAM1762 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1762 include diagnosis, prevention and treatment of viral infection by Bovine viral diarrhea virus genotype 2 (BVDV-2). Specific functions, and accordingly utilities, of VGAM1762 correlate with, and may be deduced from, the identity of the host target genes which VGAM1762 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[24634] Nucleotide sequences of the VGAM1762 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1762 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1762 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1762 are further described hereinbelow with reference to Table 1.

[24635] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1762 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[24636] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1763 (VGAM1763) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[24637] VGAM1763 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1763 was detected is described hereinabove with reference to Figs. 2-8.

[24638] VGAM1763 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Bovine viral diarrhea virus genotype 2 (BVDV-2). VGAM1763 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[24639] VGAM1763 gene, herein designated VGAM GENE, encodes a VGAM1763 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and un-

like most ordinary genes, VGAM1763 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1763 precursor RNA is designated SEQ ID:1749, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1749 is located at position 11479 relative to the genome of Bovine viral diarrhea virus genotype 2 (BVDV-2).

[24640] VGAM1763 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1763 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24641] An enzyme complex designated DICER COMPLEX, dices the VGAM1763 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1763 RNA, herein designated VGAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM1763 RNA is designated SEQ ID:4474, and is provided hereinbelow with reference to the sequence listing part.

[24642] VGAM1763 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1763 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1763 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24643] VGAM1763 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1763 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1763 RNA, herein designated

VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1763 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1763 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24644] The complementary binding of VGAM1763 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1763 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1763 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1763 host target protein, herein desig-

nated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[24645] It is appreciated that VGAM1763 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1763 host target genes. The mRNA of each one of this plurality of VGAM1763 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1763 RNA, herein designated VGAM RNA, and which when bound by VGAM1763 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1763 host target proteins.

[24646] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1763 gene, herein designated VGAM GENE, on one or more VGAM1763 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24647] It is yet further appreciated that a function of VGAM1763 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1763 include diagnosis, prevention and treatment of viral infection by Bovine viral diarrhea virus genotype 2 (BVDV-2). Specific functions, and accordingly utilities, of VGAM1763 correlate with, and may be deduced from, the identity of the host target genes which VGAM1763 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[24648] Nucleotide sequences of the VGAM1763 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1763 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1763 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1763 are further described hereinbelow with reference to Table 1.

[24649] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1763 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[24650] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1764 (VGAM1764) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[24651] VGAM1764 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1764 was detected is described hereinabove with reference to Figs. 2-8.

[24652] VGAM1764 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Bovine viral diarrhea virus genotype 2 (BVDV-2). VGAM1764 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[24653] VGAM1764 gene, herein designated VGAM GENE, encodes

a VGAM1764 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1764 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1764 precursor RNA is designated SEQ ID:1750, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1750 is located at position 3861 relative to the genome of Bovine viral diarrhea virus genotype 2 (BVDV-2).

[24654] VGAM1764 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1764 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24655] An enzyme complex designated DICER COMPLEX, dices the VGAM1764 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, into VGAM1764 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM1764 RNA is designated SEQ ID:4475, and is provided hereinbelow with reference to the sequence listing part.

[24656] VGAM1764 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1764 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1764 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24657] VGAM1764 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1764 host target RNA, herein designated VGAM HOST TARGET RNA. This

complementary binding is due to the fact that the nucleotide sequence of VGAM1764 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1764 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1764 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24658] The complementary binding of VGAM1764 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1764 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1764

host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1764 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[24659] It is appreciated that VGAM1764 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1764 host target genes. The mRNA of each one of this plurality of VGAM1764 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1764 RNA, herein designated VGAM RNA, and which when bound by VGAM1764 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1764 host target proteins.

[24660] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1764 gene, herein designated VGAM GENE, on one or more VGAM1764 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24661] It is yet further appreciated that a function of VGAM1764 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1764 include diagnosis, prevention and treatment of viral infection by Bovine viral diarrhea virus genotype 2 (BVDV-2). Specific functions, and accordingly utilities, of VGAM1764 correlate with, and may be deduced from, the identity of the host target genes which VGAM1764 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[24662] Nucleotide sequences of the VGAM1764 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1764 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1764 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM1764 are further described hereinbelow with reference to Table 1.

[24663] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1764 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[24664] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1765 (VGAM1765) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[24665] VGAM1765 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1765 was detected is described hereinabove with reference to Figs. 2-8.

[24666] VGAM1765 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Bovine viral diarrhea virus genotype 2 (BVDV-2). VGAM1765 host target gene, herein designated VGAM HOST TARGET GENE, is a human

gene contained in the human genome.

[24667] VGAM1765 gene, herein designated VGAM GENE, encodes a VGAM1765 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1765 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1765 precursor RNA is designated SEQ ID:1751, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1751 is located at position 9624 relative to the genome of Bovine viral diarrhea virus genotype 2 (BVDV-2).

[24668] VGAM1765 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1765 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24669] An enzyme complex designated DICER COMPLEX, dices the VGAM1765 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1765 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM1765 RNA is designated SEQ ID:4476, and is provided hereinbelow with reference to the sequence listing part.

[24670] VGAM1765 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1765 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1765 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24671] VGAM1765 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites

located in untranslated regions of VGAM1765 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1765 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1765 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1765 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24672] The complementary binding of VGAM1765 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1765 host target RNA, herein designated VGAM

HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1765 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1765 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[24673] It is appreciated that VGAM1765 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1765 host target genes. The mRNA of each one of this plurality of VGAM1765 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1765 RNA, herein designated VGAM RNA, and which when bound by VGAM1765 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1765 host target proteins.

[24674] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1765 gene, herein designated VGAM GENE, on one or more VGAM1765 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove

with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24675] It is yet further appreciated that a function of VGAM1765 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1765 include diagnosis, prevention and treatment of viral infection by Bovine viral diarrhea virus genotype 2 (BVDV-2). Specific functions, and accordingly utilities, of VGAM1765 correlate with, and may be deduced from, the identity of the host target genes which VGAM1765 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[24676] Nucleotide sequences of the VGAM1765 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1765 RNA, herein designated VGAM RNA, and

a schematic representation of the secondary folding of VGAM1765 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1765 are further described hereinbelow with reference to Table 1.

[24677] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1765 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[24678] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1766 (VGAM1766) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[24679] VGAM1766 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1766 was detected is described hereinabove with reference to Figs. 2-8.

[24680] VGAM1766 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Bovine viral diarrhea

virus genotype 2 (BVDV-2). VGAM1766 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[24681] VGAM1766 gene, herein designated VGAM GENE, encodes a VGAM1766 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1766 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1766 precursor RNA is designated SEQ ID:1752, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1752 is located at position 5325 relative to the genome of Bovine viral diarrhea virus genotype 2 (BVDV-2).

[24682] VGAM1766 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1766 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24683] An enzyme complex designated DICER COMPLEX, dices the VGAM1766 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1766 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM1766 RNA is designated SEQ ID:4477, and is provided hereinbelow with reference to the sequence listing part.

[24684] VGAM1766 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1766 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1766 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24685] VGAM1766 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1766 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1766 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1766 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1766 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24686] The complementary binding of VGAM1766 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM1766 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1766 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1766 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[24687] It is appreciated that VGAM1766 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1766 host target genes. The mRNA of each one of this plurality of VGAM1766 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1766 RNA, herein designated VGAM RNA, and which when bound by VGAM1766 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1766 host target proteins.

[24688] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1766 gene, herein designated VGAM GENE, on one or more VGAM1766 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24689] It is yet further appreciated that a function of VGAM1766 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1766 include diagnosis, prevention and treatment of viral infection by Bovine viral diarrhea virus genotype 2 (BVDV-2). Specific functions, and accordingly utilities, of VGAM1766 correlate with, and may be deduced from, the identity of the host target genes which VGAM1766 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[24690] Nucleotide sequences of the VGAM1766 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the diced VGAM1766 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1766 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1766 are further described hereinbelow with reference to Table 1.

[24691] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1766 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[24692] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1767 (VGAM1767) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[24693] VGAM1767 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1767 was detected is described hereinabove with reference to Figs. 2-8.

[24694] VGAM1767 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rabbit fibroma virus. VGAM1767 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[24695] VGAM1767 gene, herein designated VGAM GENE, encodes a VGAM1767 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1767 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1767 precursor RNA is designated SEQ ID:1753, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1753 is located at position 1407 relative to the genome of Rabbit fibroma virus.

[24696] VGAM1767 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1767 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24697] An enzyme complex designated DICER COMPLEX, dices the VGAM1767 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1767 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM1767 RNA is designated SEQ ID:4478, and is provided hereinbelow with reference to the sequence listing part.

[24698] VGAM1767 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1767 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1767 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN COD-

ING and 3UTR respectively.

[24699] VGAM1767 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1767 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1767 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1767 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1767 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24700] The complementary binding of VGAM1767 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1767 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1767 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1767 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[24701] It is appreciated that VGAM1767 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1767 host target genes. The mRNA of each one of this plurality of VGAM1767 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1767 RNA, herein designated VGAM RNA, and which when bound by VGAM1767 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1767 host target proteins.

[24702] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1767 gene, herein designated VGAM GENE, on one

or more VGAM1767 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24703] It is yet further appreciated that a function of VGAM1767 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1767 include diagnosis, prevention and treatment of viral infection by Rabbit fibroma virus. Specific functions, and accordingly utilities, of VGAM1767 correlate with, and may be deduced from, the identity of the host target genes which VGAM1767 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[24704] Nucleotide sequences of the VGAM1767 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1767 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1767 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1767 are further described hereinbelow with reference to Table 1.

[24705] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1767 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[24706] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1768 (VGAM1768) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[24707] VGAM1768 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1768 was detected is de-

scribed hereinabove with reference to Figs. 2-8.

[24708] VGAM1768 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rabbit fibroma virus. VGAM1768 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[24709] VGAM1768 gene, herein designated VGAM GENE, encodes a VGAM1768 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1768 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1768 precursor RNA is designated SEQ ID:1754, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1754 is located at position 431 relative to the genome of Rabbit fibroma virus.

[24710] VGAM1768 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1768 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24711] An enzyme complex designated DICER COMPLEX, dices the VGAM1768 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1768 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM1768 RNA is designated SEQ ID:4479, and is provided hereinbelow with reference to the sequence listing part.

[24712] VGAM1768 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1768 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1768 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and

a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24713] VGAM1768 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1768 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1768 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1768 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1768 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both

3UTR and 5UTR regions.

[24714] The complementary binding of VGAM1768 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1768 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1768 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1768 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[24715] It is appreciated that VGAM1768 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1768 host target genes. The mRNA of each one of this plurality of VGAM1768 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1768 RNA, herein designated VGAM RNA, and which when bound by VGAM1768 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1768 host target proteins.

[24716] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM1768 gene, herein designated VGAM GENE, on one or more VGAM1768 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24717] It is yet further appreciated that a function of VGAM1768 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1768 include diagnosis, prevention and treatment of viral infection by Rabbit fibroma virus. Specific functions, and accordingly utilities, of VGAM1768 correlate with, and may be deduced from, the identity of the host target genes which VGAM1768 binds and inhibits, and the function of these host target genes, as

elaborated hereinbelow.

[24718] Nucleotide sequences of the VGAM1768 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1768 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1768 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1768 are further described hereinbelow with reference to Table 1.

[24719] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1768 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[24720] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1769 (VGAM1769) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[24721] VGAM1769 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene.

The method by which VGAM1769 was detected is described hereinabove with reference to Figs. 2-8.

[24722] VGAM1769 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rabbit fibroma virus. VGAM1769 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[24723] VGAM1769 gene, herein designated VGAM GENE, encodes a VGAM1769 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1769 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1769 precursor RNA is designated SEQ ID:1755, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1755 is located at position 123 relative to the genome of Rabbit fibroma virus.

[24724] VGAM1769 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1769 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24725] An enzyme complex designated DICER COMPLEX, dices the VGAM1769 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1769 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 84%) nucleotide sequence of VGAM1769 RNA is designated SEQ ID:4480, and is provided hereinbelow with reference to the sequence listing part.

[24726] VGAM1769 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1769 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1769 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding

gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24727] VGAM1769 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1769 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1769 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1769 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1769 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be lo-

cated in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24728] The complementary binding of VGAM1769 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1769 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1769 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1769 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[24729] It is appreciated that VGAM1769 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1769 host target genes. The mRNA of each one of this plurality of VGAM1769 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1769 RNA, herein designated VGAM RNA, and which when bound by VGAM1769 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1769 host target proteins.

[24730] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM1769 gene, herein designated VGAM GENE, on one or more VGAM1769 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24731] It is yet further appreciated that a function of VGAM1769 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1769 include diagnosis, prevention and treatment of viral infection by Rabbit fibroma virus. Specific functions, and accordingly utilities, of VGAM1769 correlate with, and may be deduced from, the identity of the host target genes which VGAM1769 binds and in-

hibits, and the function of these host target genes, as elaborated hereinbelow.

[24732] Nucleotide sequences of the VGAM1769 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1769 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1769 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1769 are further described hereinbelow with reference to Table 1.

[24733] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1769 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[24734] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1770 (VGAM1770) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[24735] VGAM1770 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1770 was detected is described hereinabove with reference to Figs. 2-8.

[24736] VGAM1770 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rabbit fibroma virus. VGAM1770 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[24737] VGAM1770 gene, herein designated VGAM GENE, encodes a VGAM1770 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1770 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1770 precursor RNA is designated SEQ ID:1756, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1756 is located at position 8292 relative to the genome of Rabbit fibroma virus.

[24738] VGAM1770 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1770 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24739] An enzyme complex designated DICER COMPLEX, dices the VGAM1770 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1770 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM1770 RNA is designated SEQ ID:4481, and is provided hereinbelow with reference to the sequence listing part.

[24740] VGAM1770 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1770 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1770 host target RNA, herein designated VGAM HOST TARGET RNA, comprises

three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24741] VGAM1770 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1770 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1770 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1770 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1770 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an

example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24742] The complementary binding of VGAM1770 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1770 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1770 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1770 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[24743] It is appreciated that VGAM1770 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1770 host target genes. The mRNA of each one of this plurality of VGAM1770 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1770 RNA, herein designated VGAM RNA, and which when bound by VGAM1770 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1770 host target proteins.

[24744] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1770 gene, herein designated VGAM GENE, on one or more VGAM1770 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24745] It is yet further appreciated that a function of VGAM1770 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1770 include diagnosis, prevention and treatment of viral infection by Rabbit fibroma virus. Specific functions, and accordingly utilities, of VGAM1770 correlate with, and may be deduced from, the identity of

the host target genes which VGAM1770 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[24746] Nucleotide sequences of the VGAM1770 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1770 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1770 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1770 are further described hereinbelow with reference to Table 1.

[24747] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1770 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[24748] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1771 (VGAM1771) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[24749] VGAM1771 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1771 was detected is described hereinabove with reference to Figs. 2-8.

[24750] VGAM1771 gene, herein designated VGAM GENE, is a viral gene contained in the genome of pestivirus type 1. VGAM1771 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[24751] VGAM1771 gene, herein designated VGAM GENE, encodes a VGAM1771 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1771 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1771 precursor RNA is designated SEQ ID:1757, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1757 is located at position 3477 relative to the genome of pestivirus type 1.

[24752] VGAM1771 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1771 folded precursor RNA, herein designated VGAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24753] An enzyme complex designated DICER COMPLEX, dices the VGAM1771 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1771 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM1771 RNA is designated SEQ ID:4482, and is provided hereinbelow with reference to the sequence listing part.

[24754] VGAM1771 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1771 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1771 host target RNA,

herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24755] VGAM1771 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1771 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1771 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1771 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1771 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host tar-

get binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24756] The complementary binding of VGAM1771 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1771 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1771 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1771 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[24757] It is appreciated that VGAM1771 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1771 host target genes. The mRNA of each one of this plurality of VGAM1771 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1771 RNA, herein designated VGAM RNA, and which when bound by VGAM1771 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1771 host target proteins.

[24758] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1771 gene, herein designated VGAM GENE, on one or more VGAM1771 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24759] It is yet further appreciated that a function of VGAM1771 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1771 include diagnosis, prevention and treatment of viral infection by pestivirus type 1. Specific functions, and accordingly utilities, of VGAM1771 corre-

late with, and may be deduced from, the identity of the host target genes which VGAM1771 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[24760] Nucleotide sequences of the VGAM1771 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1771 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1771 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1771 are further described hereinbelow with reference to Table 1.

[24761] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1771 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[24762] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1772 (VGAM1772) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the

art.

[24763] VGAM1772 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1772 was detected is described hereinabove with reference to Figs. 2-8.

[24764] VGAM1772 gene, herein designated VGAM GENE, is a viral gene contained in the genome of pestivirus type 1. VGAM1772 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[24765] VGAM1772 gene, herein designated VGAM GENE, encodes a VGAM1772 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1772 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1772 precursor RNA is designated SEQ ID:1758, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1758 is located at position 2037 relative to the genome of pestivirus type 1.

[24766] VGAM1772 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1772 folded

precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24767] An enzyme complex designated DICER COMPLEX, dices the VGAM1772 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1772 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 71%) nucleotide sequence of VGAM1772 RNA is designated SEQ ID:4483, and is provided hereinbelow with reference to the sequence listing part.

[24768] VGAM1772 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1772 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM1772 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24769] VGAM1772 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1772 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1772 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1772 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1772 host target RNA, herein designated VGAM HOST TARGET RNA.

It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24770] The complementary binding of VGAM1772 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1772 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1772 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1772 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[24771] It is appreciated that VGAM1772 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1772 host target genes. The mRNA of each one of this plurality of VGAM1772 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1772 RNA, herein designated VGAM RNA, and which when bound by VGAM1772 RNA, herein designated VGAM RNA, causes inhibition of translation of

respective one or more VGAM1772 host target proteins.

[24772] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1772 gene, herein designated VGAM GENE, on one or more VGAM1772 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24773] It is yet further appreciated that a function of VGAM1772 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1772 include diagnosis, prevention and treatment of viral infection by pestivirus type 1. Specific

functions, and accordingly utilities, of VGAM1772 correlate with, and may be deduced from, the identity of the host target genes which VGAM1772 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[24774] Nucleotide sequences of the VGAM1772 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1772 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1772 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1772 are further described hereinbelow with reference to Table 1.

[24775] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1772 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[24776] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1773 (VGAM1773) viral gene, which modulates expression of respective host target genes thereof, the func-

tion and utility of which host target genes is known in the art.

[24777] VGAM1773 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1773 was detected is described hereinabove with reference to Figs. 2-8.

[24778] VGAM1773 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cryphonectria hypovirus 1. VGAM1773 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[24779] VGAM1773 gene, herein designated VGAM GENE, encodes a VGAM1773 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1773 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1773 precursor RNA is designated SEQ ID:1759, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1759 is located at position 6368 relative to the genome of Cryphonectria hypovirus 1.

[24780] VGAM1773 precursor RNA, herein designated VGAM PRE-

CURSOR RNA, folds onto itself, forming VGAM1773 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24781] An enzyme complex designated DICER COMPLEX, dices the VGAM1773 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1773 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM1773 RNA is designated SEQ ID:4484, and is provided hereinbelow with reference to the sequence listing part.

[24782] VGAM1773 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM1773 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1773 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24783] VGAM1773 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1773 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1773 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1773 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1773 host

target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24784] The complementary binding of VGAM1773 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1773 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1773 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1773 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[24785] It is appreciated that VGAM1773 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1773 host target genes. The mRNA of each one of this plurality of VGAM1773 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1773 RNA, herein designated VGAM RNA, and which when bound by VGAM1773 RNA, herein

designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1773 host target proteins.

[24786] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1773 gene, herein designated VGAM GENE, on one or more VGAM1773 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24787] It is yet further appreciated that a function of VGAM1773 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1773 include diagnosis, prevention and

treatment of viral infection by Cryphonectria hypovirus 1. Specific functions, and accordingly utilities, of VGAM1773 correlate with, and may be deduced from, the identity of the host target genes which VGAM1773 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[24788] Nucleotide sequences of the VGAM1773 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1773 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1773 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1773 are further described hereinbelow with reference to Table 1.

[24789] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1773 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[24790] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1774 (VGAM1774) viral gene, which modulates ex-

pression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[24791] VGAM1774 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1774 was detected is described hereinabove with reference to Figs. 2-8.

[24792] VGAM1774 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cryphonectria hypovirus 1. VGAM1774 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[24793] VGAM1774 gene, herein designated VGAM GENE, encodes a VGAM1774 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1774 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1774 precursor RNA is designated SEQ ID:1760, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1760 is located at position 10666 relative to the genome of Cryphonectria hypovirus

1.

[24794] VGAM1774 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1774 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24795] An enzyme complex designated DICER COMPLEX, dices the VGAM1774 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1774 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM1774 RNA is designated SEQ ID:4485, and is provided hereinbelow with reference to the sequence listing part.

[24796] VGAM1774 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1774 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1774 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24797] VGAM1774 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1774 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1774 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1774 RNA, herein designated

VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1774 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24798] The complementary binding of VGAM1774 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1774 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1774 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1774 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[24799] It is appreciated that VGAM1774 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1774 host target genes. The mRNA of each one of this plurality of VGAM1774 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM1774 RNA, herein designated VGAM RNA, and which when bound by VGAM1774 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1774 host target proteins.

[24800] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1774 gene, herein designated VGAM GENE, on one or more VGAM1774 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24801] It is yet further appreciated that a function of VGAM1774 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1774 include diagnosis, prevention and treatment of viral infection by Cryphonectria hypovirus 1. Specific functions, and accordingly utilities, of VGAM1774 correlate with, and may be deduced from, the identity of the host target genes which VGAM1774 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[24802] Nucleotide sequences of the VGAM1774 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1774 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1774 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1774 are further described hereinbelow with reference to Table 1.

[24803] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1774 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[24804] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present

invention, referred to here as Viral Genomic Address Messenger 1775 (VGAM1775) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[24805] VGAM1775 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1775 was detected is described hereinabove with reference to Figs. 2-8.

[24806] VGAM1775 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cryphonectria hypovirus 1. VGAM1775 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[24807] VGAM1775 gene, herein designated VGAM GENE, encodes a VGAM1775 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1775 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1775 precursor RNA is designated SEQ ID:1761, and is provided hereinbelow with reference to the sequence listing part. Nu-

cleotide sequence SEQ ID:1761 is located at position 994 relative to the genome of Cryphonectria hypovirus 1.

[24808] VGAM1775 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1775 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24809] An enzyme complex designated DICER COMPLEX, dices the VGAM1775 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1775 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of VGAM1775 RNA is designated SEQ ID:4486, and is provided hereinbelow with reference to the sequence

listing part.

[24810] VGAM1775 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1775 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1775 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24811] VGAM1775 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1775 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1775 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not

meant to be limiting VGAM1775 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1775 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24812] The complementary binding of VGAM1775 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1775 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1775 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1775 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[24813] It is appreciated that VGAM1775 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1775 host target genes. The mRNA of each one of this plurality of VGAM1775 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM1775 RNA, herein designated VGAM RNA, and which when bound by VGAM1775 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1775 host target proteins.

[24814] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1775 gene, herein designated VGAM GENE, on one or more VGAM1775 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24815] It is yet further appreciated that a function of VGAM1775

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1775 include diagnosis, prevention and treatment of viral infection by Cryphonectria hypovirus 1. Specific functions, and accordingly utilities, of VGAM1775 correlate with, and may be deduced from, the identity of the host target genes which VGAM1775 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[24816] Nucleotide sequences of the VGAM1775 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1775 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1775 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1775 are further described hereinbelow with reference to Table 1.

[24817] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1775 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[24818] Fig. 1 further provides a conceptual description of another

novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1776 (VGAM1776) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[24819] VGAM1776 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1776 was detected is described hereinabove with reference to Figs. 2-8.

[24820] VGAM1776 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cryphonectria hypovirus 1. VGAM1776 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[24821] VGAM1776 gene, herein designated VGAM GENE, encodes a VGAM1776 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1776 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1776 precursor RNA is designated SEQ ID:1762, and is provided here-

inbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1762 is located at position 9833 relative to the genome of Cryphonectria hypovirus 1.

[24822] VGAM1776 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1776 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24823] An enzyme complex designated DICER COMPLEX, dices the VGAM1776 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1776 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 51%) nucleotide sequence of VGAM1776 RNA is designated SEQ ID:4487, and

is provided hereinbelow with reference to the sequence listing part.

[24824] VGAM1776 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1776 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1776 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24825] VGAM1776 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1776 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1776 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites

shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1776 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1776 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24826] The complementary binding of VGAM1776 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1776 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1776 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1776 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[24827] It is appreciated that VGAM1776 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1776 host target genes. The mRNA of each one of this plurality of VGAM1776 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1776 RNA, herein designated VGAM RNA, and which when bound by VGAM1776 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1776 host target proteins.

[24828] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1776 gene, herein designated VGAM GENE, on one or more VGAM1776 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24829] It is yet further appreciated that a function of VGAM1776 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1776 include diagnosis, prevention and treatment of viral infection by Cryphonectria hypovirus 1. Specific functions, and accordingly utilities, of VGAM1776 correlate with, and may be deduced from, the identity of the host target genes which VGAM1776 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[24830] Nucleotide sequences of the VGAM1776 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1776 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1776 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1776 are further described hereinbelow with reference to Table 1.

[24831] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1776 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[24832] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1777 (VGAM1777) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[24833] VGAM1777 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1777 was detected is described hereinabove with reference to Figs. 2-8.

[24834] VGAM1777 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cryphonectria hypovirus 1. VGAM1777 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[24835] VGAM1777 gene, herein designated VGAM GENE, encodes a VGAM1777 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1777 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1777 precur-

sor RNA is designated SEQ ID:1763, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1763 is located at position 7246 relative to the genome of Cryphonectria hypovirus 1.

[24836] VGAM1777 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1777 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24837] An enzyme complex designated DICER COMPLEX, dices the VGAM1777 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1777 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide se-

quence of VGAM1777 RNA is designated SEQ ID:4488, and is provided hereinbelow with reference to the sequence listing part.

[24838] VGAM1777 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1777 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1777 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24839] VGAM1777 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1777 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1777 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is ap-

preciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1777 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1777 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24840] The complementary binding of VGAM1777 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1777 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1777 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1777 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[24841] It is appreciated that VGAM1777 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1777 host target genes. The mRNA of

each one of this plurality of VGAM1777 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1777 RNA, herein designated VGAM RNA, and which when bound by VGAM1777 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1777 host target proteins.

[24842] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1777 gene, herein designated VGAM GENE, on one or more VGAM1777 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science

294,779 (2001)).

[24843] It is yet further appreciated that a function of VGAM1777 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1777 include diagnosis, prevention and treatment of viral infection by Cryphonectria hypovirus 1. Specific functions, and accordingly utilities, of VGAM1777 correlate with, and may be deduced from, the identity of the host target genes which VGAM1777 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[24844] Nucleotide sequences of the VGAM1777 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1777 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1777 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1777 are further described hereinbelow with reference to Table 1.

[24845] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1777 RNA, herein designated VGAM RNA, are de-

scribed hereinbelow with reference to Table 2.

[24846] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1778 (VGAM1778) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[24847] VGAM1778 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1778 was detected is described hereinabove with reference to Figs. 2-8.

[24848] VGAM1778 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cryphonectria hypovirus 1. VGAM1778 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[24849] VGAM1778 gene, herein designated VGAM GENE, encodes a VGAM1778 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1778 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly

similar to the nucleotide sequence of VGAM1778 precursor RNA is designated SEQ ID:1764, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1764 is located at position 3023 relative to the genome of Cryphonectria hypovirus 1.

[24850] VGAM1778 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1778 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24851] An enzyme complex designated DICER COMPLEX, dices the VGAM1778 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1778 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 43%) nucleotide sequence of VGAM1778 RNA is designated SEQ ID:4489, and is provided hereinbelow with reference to the sequence listing part.

[24852] VGAM1778 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1778 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1778 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24853] VGAM1778 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1778 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1778 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I,

BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1778 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1778 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24854] The complementary binding of VGAM1778 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1778 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1778 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1778 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[24855] It is appreciated that VGAM1778 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM1778 host target genes. The mRNA of each one of this plurality of VGAM1778 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1778 RNA, herein designated VGAM RNA, and which when bound by VGAM1778 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1778 host target proteins.

[24856] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1778 gene, herein designated VGAM GENE, on one or more VGAM1778 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24857] It is yet further appreciated that a function of VGAM1778 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1778 include diagnosis, prevention and treatment of viral infection by Cryphonectria hypovirus 1. Specific functions, and accordingly utilities, of VGAM1778 correlate with, and may be deduced from, the identity of the host target genes which VGAM1778 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[24858] Nucleotide sequences of the VGAM1778 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1778 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1778 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1778 are further described hereinbelow with reference to Table 1.

[24859] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites

to VGAM1778 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[24860] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1779 (VGAM1779) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[24861] VGAM1779 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1779 was detected is described hereinabove with reference to Figs. 2-8.

[24862] VGAM1779 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cryphonectria hypovirus 1. VGAM1779 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[24863] VGAM1779 gene, herein designated VGAM GENE, encodes a VGAM1779 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1779 precursor RNA, herein designated VGAM PRECURSOR RNA, does not en-

code a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1779 precursor RNA is designated SEQ ID:1765, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1765 is located at position 4059 relative to the genome of Cryphonectria hypovirus 1.

[24864] VGAM1779 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1779 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24865] An enzyme complex designated DICER COMPLEX, dices the VGAM1779 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1779 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM1779 RNA is designated SEQ ID:4490, and is provided hereinbelow with reference to the sequence listing part.

[24866] VGAM1779 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1779 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1779 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24867] VGAM1779 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1779 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1779 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3

such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1779 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1779 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24868] The complementary binding of VGAM1779 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1779 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1779 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1779 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[24869] It is appreciated that VGAM1779 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1779 host target genes. The mRNA of each one of this plurality of VGAM1779 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1779 RNA, herein designated VGAM RNA, and which when bound by VGAM1779 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1779 host target proteins.

[24870] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1779 gene, herein designated VGAM GENE, on one or more VGAM1779 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24871] It is yet further appreciated that a function of VGAM1779 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1779 include diagnosis, prevention and treatment of viral infection by Cryphonectria hypovirus 1. Specific functions, and accordingly utilities, of VGAM1779 correlate with, and may be deduced from, the identity of the host target genes which VGAM1779 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[24872] Nucleotide sequences of the VGAM1779 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1779 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1779 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1779 are further described hereinbelow with reference to Table 1.

[24873] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the

complementarity of each of these host target binding sites to VGAM1779 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[24874] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1780 (VGAM1780) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[24875] VGAM1780 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1780 was detected is described hereinabove with reference to Figs. 2-8.

[24876] VGAM1780 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cryphonectria hypovirus 1. VGAM1780 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[24877] VGAM1780 gene, herein designated VGAM GENE, encodes a VGAM1780 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1780 precursor RNA,

herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1780 precursor RNA is designated SEQ ID:1766, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1766 is located at position 6807 relative to the genome of Cryphonectria hypovirus 1.

[24878] VGAM1780 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1780 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24879] An enzyme complex designated DICER COMPLEX, dices the VGAM1780 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1780 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 82%) nucleotide sequence of VGAM1780 RNA is designated SEQ ID:4491, and is provided hereinbelow with reference to the sequence listing part.

[24880] VGAM1780 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1780 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1780 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24881] VGAM1780 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1780 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1780 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host

target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1780 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1780 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24882] The complementary binding of VGAM1780 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1780 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1780 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1780 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[24883] It is appreciated that VGAM1780 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1780 host target genes. The mRNA of each one of this plurality of VGAM1780 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1780 RNA, herein designated VGAM RNA, and which when bound by VGAM1780 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1780 host target proteins.

[24884] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1780 gene, herein designated VGAM GENE, on one or more VGAM1780 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24885] It is yet further appreciated that a function of VGAM1780 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1780 include diagnosis, prevention and treatment of viral infection by Cryphonectria hypovirus 1. Specific functions, and accordingly utilities, of VGAM1780 correlate with, and may be deduced from, the identity of the host target genes which VGAM1780 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[24886] Nucleotide sequences of the VGAM1780 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1780 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1780 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1780 are further described hereinbelow with reference to Table 1.

[24887] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1780 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[24888] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1781 (VGAM1781) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[24889] VGAM1781 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1781 was detected is described hereinabove with reference to Figs. 2-8.

[24890] VGAM1781 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cryphonectria hypovirus 1. VGAM1781 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[24891] VGAM1781 gene, herein designated VGAM GENE, encodes a VGAM1781 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and un-

like most ordinary genes, VGAM1781 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1781 precursor RNA is designated SEQ ID:1767, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1767 is located at position 9633 relative to the genome of Cryphonectria hypovirus 1.

[24892] VGAM1781 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1781 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24893] An enzyme complex designated DICER COMPLEX, dices the VGAM1781 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1781 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM1781 RNA is designated SEQ ID:4492, and is provided hereinbelow with reference to the sequence listing part.

[24894] VGAM1781 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1781 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1781 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24895] VGAM1781 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1781 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1781 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed

sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1781 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1781 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24896] The complementary binding of VGAM1781 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1781 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1781 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1781 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target

protein is therefore outlined by a broken line.

[24897] It is appreciated that VGAM1781 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1781 host target genes. The mRNA of each one of this plurality of VGAM1781 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1781 RNA, herein designated VGAM RNA, and which when bound by VGAM1781 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1781 host target proteins.

[24898] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1781 gene, herein designated VGAM GENE, on one or more VGAM1781 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24899] It is yet further appreciated that a function of VGAM1781 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1781 include diagnosis, prevention and treatment of viral infection by Cryphonectria hypovirus 1. Specific functions, and accordingly utilities, of VGAM1781 correlate with, and may be deduced from, the identity of the host target genes which VGAM1781 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[24900] Nucleotide sequences of the VGAM1781 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1781 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1781 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1781 are further described hereinbelow with reference to Table 1.

[24901] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1781 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[24902] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1782 (VGAM1782) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[24903] VGAM1782 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1782 was detected is described hereinabove with reference to Figs. 2-8.

[24904] VGAM1782 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cryphonectria hypovirus 1. VGAM1782 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[24905] VGAM1782 gene, herein designated VGAM GENE, encodes a VGAM1782 precursor RNA, herein designated VGAM

PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1782 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1782 precursor RNA is designated SEQ ID:1768, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1768 is located at position 9154 relative to the genome of Cryphonectria hypovirus 1.

[24906] VGAM1782 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1782 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24907] An enzyme complex designated DICER COMPLEX, dices the VGAM1782 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1782 RNA, herein designated VGAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM1782 RNA is designated SEQ ID:4493, and is provided hereinbelow with reference to the sequence listing part.

[24908] VGAM1782 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1782 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1782 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24909] VGAM1782 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1782 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1782 RNA, herein designated

VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1782 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1782 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24910] The complementary binding of VGAM1782 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1782 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1782 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1782 host target protein, herein desig-

nated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[24911] It is appreciated that VGAM1782 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1782 host target genes. The mRNA of each one of this plurality of VGAM1782 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1782 RNA, herein designated VGAM RNA, and which when bound by VGAM1782 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1782 host target proteins.

[24912] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1782 gene, herein designated VGAM GENE, on one or more VGAM1782 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24913] It is yet further appreciated that a function of VGAM1782 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1782 include diagnosis, prevention and treatment of viral infection by Cryphonectria hypovirus 1. Specific functions, and accordingly utilities, of VGAM1782 correlate with, and may be deduced from, the identity of the host target genes which VGAM1782 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[24914] Nucleotide sequences of the VGAM1782 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1782 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1782 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1782 are further described hereinbelow with reference to Table 1.

[24915] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1782 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[24916] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1783 (VGAM1783) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[24917] VGAM1783 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1783 was detected is described hereinabove with reference to Figs. 2-8.

[24918] VGAM1783 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Fowlpox virus.
VGAM1783 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[24919] VGAM1783 gene, herein designated VGAM GENE, encodes

a VGAM1783 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1783 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1783 precursor RNA is designated SEQ ID:1769, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1769 is located at position 33506 relative to the genome of Fowlpox virus.

[24920] VGAM1783 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1783 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24921] An enzyme complex designated DICER COMPLEX, dices the VGAM1783 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1783 RNA,

herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 55%) nucleotide sequence of VGAM1783 RNA is designated SEQ ID:4494, and is provided hereinbelow with reference to the sequence listing part.

[24922] VGAM1783 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1783 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1783 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24923] VGAM1783 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1783 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM1783 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1783 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1783 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24924] The complementary binding of VGAM1783 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1783 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1783 host target RNA, herein designated VGAM HOST TARGET

RNA, into VGAM1783 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[24925] It is appreciated that VGAM1783 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1783 host target genes. The mRNA of each one of this plurality of VGAM1783 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1783 RNA, herein designated VGAM RNA, and which when bound by VGAM1783 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1783 host target proteins.

[24926] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1783 gene, herein designated VGAM GENE, on one or more VGAM1783 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24927] It is yet further appreciated that a function of VGAM1783 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1783 include diagnosis, prevention and treatment of viral infection by Fowlpox virus. Specific functions, and accordingly utilities, of VGAM1783 correlate with, and may be deduced from, the identity of the host target genes which VGAM1783 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[24928] Nucleotide sequences of the VGAM1783 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1783 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1783 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1783 are further

described hereinbelow with reference to Table 1.

[24929] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1783 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[24930] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1784 (VGAM1784) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[24931] VGAM1784 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1784 was detected is described hereinabove with reference to Figs. 2-8.

[24932] VGAM1784 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Fowlpox virus. VGAM1784 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[24933] VGAM1784 gene, herein designated VGAM GENE, encodes a VGAM1784 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1784 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1784 precursor RNA is designated SEQ ID:1770, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1770 is located at position 43278 relative to the genome of Fowlpox virus.

[24934] VGAM1784 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1784 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24935] An enzyme complex designated DICER COMPLEX, dices the VGAM1784 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, into VGAM1784 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 66%) nucleotide sequence of VGAM1784 RNA is designated SEQ ID:4495, and is provided hereinbelow with reference to the sequence listing part.

[24936] VGAM1784 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1784 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1784 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24937] VGAM1784 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1784 host target RNA, herein designated VGAM HOST TARGET RNA. This

complementary binding is due to the fact that the nucleotide sequence of VGAM1784 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1784 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1784 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24938] The complementary binding of VGAM1784 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1784 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1784

host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1784 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[24939] It is appreciated that VGAM1784 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1784 host target genes. The mRNA of each one of this plurality of VGAM1784 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1784 RNA, herein designated VGAM RNA, and which when bound by VGAM1784 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1784 host target proteins.

[24940] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1784 gene, herein designated VGAM GENE, on one or more VGAM1784 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24941] It is yet further appreciated that a function of VGAM1784 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1784 include diagnosis, prevention and treatment of viral infection by Fowlpox virus. Specific functions, and accordingly utilities, of VGAM1784 correlate with, and may be deduced from, the identity of the host target genes which VGAM1784 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[24942] Nucleotide sequences of the VGAM1784 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1784 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1784 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM1784 are further described hereinbelow with reference to Table 1.

[24943] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1784 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[24944] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1785 (VGAM1785) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[24945] VGAM1785 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1785 was detected is described hereinabove with reference to Figs. 2-8.

[24946] VGAM1785 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Fowlpox virus.
VGAM1785 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the

human genome.

[24947] VGAM1785 gene, herein designated VGAM GENE, encodes a VGAM1785 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1785 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1785 precursor RNA is designated SEQ ID:1771, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1771 is located at position 36138 relative to the genome of Fowlpox virus.

[24948] VGAM1785 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1785 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24949] An enzyme complex designated DICER COMPLEX, dices

the VGAM1785 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1785 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 82%) nucleotide sequence of VGAM1785 RNA is designated SEQ ID:4496, and is provided hereinbelow with reference to the sequence listing part.

[24950] VGAM1785 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1785 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1785 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24951] VGAM1785 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1785 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1785 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1785 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1785 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24952] The complementary binding of VGAM1785 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1785 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM1785 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1785 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[24953] It is appreciated that VGAM1785 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1785 host target genes. The mRNA of each one of this plurality of VGAM1785 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1785 RNA, herein designated VGAM RNA, and which when bound by VGAM1785 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1785 host target proteins.

[24954] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1785 gene, herein designated VGAM GENE, on one or more VGAM1785 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24955] It is yet further appreciated that a function of VGAM1785 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1785 include diagnosis, prevention and treatment of viral infection by Fowlpox virus. Specific functions, and accordingly utilities, of VGAM1785 correlate with, and may be deduced from, the identity of the host target genes which VGAM1785 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[24956] Nucleotide sequences of the VGAM1785 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1785 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of

VGAM1785 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1785 are further described hereinbelow with reference to Table 1.

[24957] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1785 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[24958] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1786 (VGAM1786) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[24959] VGAM1786 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1786 was detected is described hereinabove with reference to Figs. 2-8.

[24960] VGAM1786 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Fowlpox virus. VGAM1786 host target gene, herein designated VGAM

HOST TARGET GENE, is a human gene contained in the human genome.

[24961] VGAM1786 gene, herein designated VGAM GENE, encodes a VGAM1786 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1786 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1786 precursor RNA is designated SEQ ID:1772, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1772 is located at position 36018 relative to the genome of Fowlpox virus.

[24962] VGAM1786 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1786 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24963] An enzyme complex designated DICER COMPLEX, dices the VGAM1786 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1786 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 57%) nucleotide sequence of VGAM1786 RNA is designated SEQ ID:4497, and is provided hereinbelow with reference to the sequence listing part.

[24964] VGAM1786 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1786 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1786 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24965] VGAM1786 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites

located in untranslated regions of VGAM1786 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1786 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1786 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1786 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24966] The complementary binding of VGAM1786 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1786 host target RNA, herein designated VGAM

HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1786 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1786 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[24967] It is appreciated that VGAM1786 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1786 host target genes. The mRNA of each one of this plurality of VGAM1786 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1786 RNA, herein designated VGAM RNA, and which when bound by VGAM1786 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1786 host target proteins.

[24968] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1786 gene, herein designated VGAM GENE, on one or more VGAM1786 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove

with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24969] It is yet further appreciated that a function of VGAM1786 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1786 include diagnosis, prevention and treatment of viral infection by Fowlpox virus. Specific functions, and accordingly utilities, of VGAM1786 correlate with, and may be deduced from, the identity of the host target genes which VGAM1786 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[24970] Nucleotide sequences of the VGAM1786 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1786 RNA, herein designated VGAM RNA, and

a schematic representation of the secondary folding of VGAM1786 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1786 are further described hereinbelow with reference to Table 1.

[24971] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1786 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[24972] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1787 (VGAM1787) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[24973] VGAM1787 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1787 was detected is described hereinabove with reference to Figs. 2-8.

[24974] VGAM1787 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Fowlpox virus.

VGAM1787 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[24975] VGAM1787 gene, herein designated VGAM GENE, encodes a VGAM1787 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1787 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1787 precursor RNA is designated SEQ ID:1773, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1773 is located at position 44889 relative to the genome of Fowlpox virus.

[24976] VGAM1787 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1787 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[24977] An enzyme complex designated DICER COMPLEX, dices the VGAM1787 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1787 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of VGAM1787 RNA is designated SEQ ID:4498, and is provided hereinbelow with reference to the sequence listing part.

[24978] VGAM1787 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1787 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1787 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24979] VGAM1787 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM1787 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1787 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1787 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1787 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24980] The complementary binding of VGAM1787 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM1787 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1787 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1787 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[24981] It is appreciated that VGAM1787 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1787 host target genes. The mRNA of each one of this plurality of VGAM1787 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1787 RNA, herein designated VGAM RNA, and which when bound by VGAM1787 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1787 host target proteins.

[24982] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1787 gene, herein designated VGAM GENE, on one or more VGAM1787 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24983] It is yet further appreciated that a function of VGAM1787 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1787 include diagnosis, prevention and treatment of viral infection by Fowlpox virus. Specific functions, and accordingly utilities, of VGAM1787 correlate with, and may be deduced from, the identity of the host target genes which VGAM1787 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[24984] Nucleotide sequences of the VGAM1787 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

diced VGAM1787 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1787 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1787 are further described hereinbelow with reference to Table 1.

[24985] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1787 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[24986] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1788 (VGAM1788) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[24987] VGAM1788 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1788 was detected is described hereinabove with reference to Figs. 2-8.

[24988] VGAM1788 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of Fowlpox virus. VGAM1788 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[24989] VGAM1788 gene, herein designated VGAM GENE, encodes a VGAM1788 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1788 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1788 precursor RNA is designated SEQ ID:1774, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1774 is located at position 45071 relative to the genome of Fowlpox virus.

[24990] VGAM1788 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1788 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24991] An enzyme complex designated DICER COMPLEX, dices the VGAM1788 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1788 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM1788 RNA is designated SEQ ID:4499, and is provided hereinbelow with reference to the sequence listing part.

[24992] VGAM1788 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1788 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1788 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24993] VGAM1788 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1788 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1788 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1788 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1788 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24994] The complementary binding of VGAM1788 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM1788 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1788 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1788 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[24995] It is appreciated that VGAM1788 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1788 host target genes. The mRNA of each one of this plurality of VGAM1788 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1788 RNA, herein designated VGAM RNA, and which when bound by VGAM1788 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1788 host target proteins.

[24996] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1788 gene, herein designated VGAM GENE, on one or more VGAM1788 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24997] It is yet further appreciated that a function of VGAM1788 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1788 include diagnosis, prevention and treatment of viral infection by Fowlpox virus. Specific functions, and accordingly utilities, of VGAM1788 correlate with, and may be deduced from, the identity of the host target genes which VGAM1788 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[24998] Nucleotide sequences of the VGAM1788 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the diced VGAM1788 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1788 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1788 are further described hereinbelow with reference to Table 1.

[24999] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1788 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[25000] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1789 (VGAM1789) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[25001] VGAM1789 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1789 was detected is described hereinabove with reference to Figs. 2-8.

[25002] VGAM1789 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Fowlpox virus. VGAM1789 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[25003] VGAM1789 gene, herein designated VGAM GENE, encodes a VGAM1789 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1789 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1789 precursor RNA is designated SEQ ID:1775, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1775 is located at position 42299 relative to the genome of Fowlpox virus.

[25004] VGAM1789 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1789 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25005] An enzyme complex designated DICER COMPLEX, dices the VGAM1789 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1789 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM1789 RNA is designated SEQ ID:4500, and is provided hereinbelow with reference to the sequence listing part.

[25006] VGAM1789 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1789 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1789 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN COD-

ING and 3UTR respectively.

[25007] VGAM1789 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1789 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1789 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1789 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1789 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25008] The complementary binding of VGAM1789 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1789 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1789 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1789 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[25009] It is appreciated that VGAM1789 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1789 host target genes. The mRNA of each one of this plurality of VGAM1789 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1789 RNA, herein designated VGAM RNA, and which when bound by VGAM1789 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1789 host target proteins.

[25010] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1789 gene, herein designated VGAM GENE, on one

or more VGAM1789 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25011] It is yet further appreciated that a function of VGAM1789 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1789 include diagnosis, prevention and treatment of viral infection by Fowlpox virus. Specific functions, and accordingly utilities, of VGAM1789 correlate with, and may be deduced from, the identity of the host target genes which VGAM1789 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[25012] Nucleotide sequences of the VGAM1789 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1789 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1789 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1789 are further described hereinbelow with reference to Table 1.

[25013] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1789 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[25014] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1790 (VGAM1790) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[25015] VGAM1790 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1790 was detected is de-

scribed hereinabove with reference to Figs. 2-8.

[25016] VGAM1790 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rana tigrina ranavirus. VGAM1790 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[25017] VGAM1790 gene, herein designated VGAM GENE, encodes a VGAM1790 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1790 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1790 precursor RNA is designated SEQ ID:1776, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1776 is located at position 79077 relative to the genome of Rana tigrina ranavirus.

[25018] VGAM1790 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1790 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25019] An enzyme complex designated DICER COMPLEX, dices the VGAM1790 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1790 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide sequence of VGAM1790 RNA is designated SEQ ID:4501, and is provided hereinbelow with reference to the sequence listing part.

[25020] VGAM1790 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1790 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1790 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and

a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25021] VGAM1790 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1790 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1790 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1790 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1790 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both

3UTR and 5UTR regions.

[25022] The complementary binding of VGAM1790 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1790 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1790 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1790 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[25023] It is appreciated that VGAM1790 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1790 host target genes. The mRNA of each one of this plurality of VGAM1790 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1790 RNA, herein designated VGAM RNA, and which when bound by VGAM1790 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1790 host target proteins.

[25024] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM1790 gene, herein designated VGAM GENE, on one or more VGAM1790 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25025] It is yet further appreciated that a function of VGAM1790 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1790 include diagnosis, prevention and treatment of viral infection by Rana tigrina ranavirus. Specific functions, and accordingly utilities, of VGAM1790 correlate with, and may be deduced from, the identity of the host target genes which VGAM1790 binds and inhibits, and the function of these host target genes, as

elaborated hereinbelow.

[25026] Nucleotide sequences of the VGAM1790 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1790 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1790 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1790 are further described hereinbelow with reference to Table 1.

[25027] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1790 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[25028] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1791 (VGAM1791) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[25029] VGAM1791 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene.

The method by which VGAM1791 was detected is described hereinabove with reference to Figs. 2-8.

[25030] VGAM1791 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rana tigrina ranavirus. VGAM1791 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[25031] VGAM1791 gene, herein designated VGAM GENE, encodes a VGAM1791 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1791 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1791 precursor RNA is designated SEQ ID:1777, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1777 is located at position 85010 relative to the genome of Rana tigrina ranavirus.

[25032] VGAM1791 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1791 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25033] An enzyme complex designated DICER COMPLEX, dices the VGAM1791 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1791 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM1791 RNA is designated SEQ ID:4502, and is provided hereinbelow with reference to the sequence listing part.

[25034] VGAM1791 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1791 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1791 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding

gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25035] VGAM1791 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1791 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1791 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1791 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1791 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be lo-

cated in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25036] The complementary binding of VGAM1791 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1791 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1791 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1791 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[25037] It is appreciated that VGAM1791 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1791 host target genes. The mRNA of each one of this plurality of VGAM1791 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1791 RNA, herein designated VGAM RNA, and which when bound by VGAM1791 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1791 host target proteins.

[25038] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM1791 gene, herein designated VGAM GENE, on one or more VGAM1791 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25039] It is yet further appreciated that a function of VGAM1791 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1791 include diagnosis, prevention and treatment of viral infection by Rana tigrina ranavirus. Specific functions, and accordingly utilities, of VGAM1791 correlate with, and may be deduced from, the identity of the host target genes which VGAM1791 binds and in-

hibits, and the function of these host target genes, as elaborated hereinbelow.

[25040] Nucleotide sequences of the VGAM1791 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1791 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1791 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1791 are further described hereinbelow with reference to Table 1.

[25041] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1791 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[25042] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1792 (VGAM1792) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[25043] VGAM1792 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1792 was detected is described hereinabove with reference to Figs. 2-8.

[25044] VGAM1792 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rana tigrina ranavirus. VGAM1792 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[25045] VGAM1792 gene, herein designated VGAM GENE, encodes a VGAM1792 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1792 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1792 precursor RNA is designated SEQ ID:1778, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1778 is located at position 75405 relative to the genome of Rana tigrina ranavirus.

[25046] VGAM1792 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1792 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25047] An enzyme complex designated DICER COMPLEX, dices the VGAM1792 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1792 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 54%) nucleotide sequence of VGAM1792 RNA is designated SEQ ID:4503, and is provided hereinbelow with reference to the sequence listing part.

[25048] VGAM1792 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1792 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1792 host target RNA, herein designated VGAM HOST TARGET RNA, comprises

three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25049] VGAM1792 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1792 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1792 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1792 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1792 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an

example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25050] The complementary binding of VGAM1792 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1792 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1792 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1792 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[25051] It is appreciated that VGAM1792 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1792 host target genes. The mRNA of each one of this plurality of VGAM1792 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1792 RNA, herein designated VGAM RNA, and which when bound by VGAM1792 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1792 host target proteins.

[25052] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1792 gene, herein designated VGAM GENE, on one or more VGAM1792 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25053] It is yet further appreciated that a function of VGAM1792 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1792 include diagnosis, prevention and treatment of viral infection by Rana tigrina ranavirus. Specific functions, and accordingly utilities, of VGAM1792 correlate with, and may be deduced from, the identity of

the host target genes which VGAM1792 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[25054] Nucleotide sequences of the VGAM1792 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1792 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1792 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1792 are further described hereinbelow with reference to Table 1.

[25055] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1792 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[25056] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1793 (VGAM1793) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[25057] VGAM1793 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1793 was detected is described hereinabove with reference to Figs. 2-8.

[25058] VGAM1793 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rana tigrina ranavirus. VGAM1793 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[25059] VGAM1793 gene, herein designated VGAM GENE, encodes a VGAM1793 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1793 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1793 precursor RNA is designated SEQ ID:1779, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1779 is located at position 85120 relative to the genome of Rana tigrina ranavirus.

[25060] VGAM1793 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1793 folded precursor RNA, herein designated VGAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25061] An enzyme complex designated DICER COMPLEX, dices the VGAM1793 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1793 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of VGAM1793 RNA is designated SEQ ID:4504, and is provided hereinbelow with reference to the sequence listing part.

[25062] VGAM1793 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1793 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1793 host target RNA,

herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25063] VGAM1793 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1793 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1793 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1793 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1793 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host tar-

get binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25064] The complementary binding of VGAM1793 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1793 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1793 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1793 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[25065] It is appreciated that VGAM1793 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1793 host target genes. The mRNA of each one of this plurality of VGAM1793 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1793 RNA, herein designated VGAM RNA, and which when bound by VGAM1793 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1793 host target proteins.

[25066] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1793 gene, herein designated VGAM GENE, on one or more VGAM1793 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25067] It is yet further appreciated that a function of VGAM1793 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1793 include diagnosis, prevention and treatment of viral infection by Rana tigrina ranavirus. Specific functions, and accordingly utilities, of VGAM1793

correlate with, and may be deduced from, the identity of the host target genes which VGAM1793 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[25068] Nucleotide sequences of the VGAM1793 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1793 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1793 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1793 are further described hereinbelow with reference to Table 1.

[25069] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1793 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[25070] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1794 (VGAM1794) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the

art.

[25071] VGAM1794 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1794 was detected is described hereinabove with reference to Figs. 2-8.

[25072] VGAM1794 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rana tigrina ranavirus. VGAM1794 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[25073] VGAM1794 gene, herein designated VGAM GENE, encodes a VGAM1794 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1794 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1794 precursor RNA is designated SEQ ID:1780, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1780 is located at position 84588 relative to the genome of Rana tigrina ranavirus.

[25074] VGAM1794 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1794 folded

precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25075] An enzyme complex designated DICER COMPLEX, dices the VGAM1794 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1794 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM1794 RNA is designated SEQ ID:4505, and is provided hereinbelow with reference to the sequence listing part.

[25076] VGAM1794 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1794 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM1794 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25077] VGAM1794 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1794 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1794 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1794 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1794 host target RNA, herein designated VGAM HOST TARGET RNA.

It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25078] The complementary binding of VGAM1794 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1794 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1794 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1794 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[25079] It is appreciated that VGAM1794 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1794 host target genes. The mRNA of each one of this plurality of VGAM1794 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1794 RNA, herein designated VGAM RNA, and which when bound by VGAM1794 RNA, herein designated VGAM RNA, causes inhibition of translation of

respective one or more VGAM1794 host target proteins.

[25080] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1794 gene, herein designated VGAM GENE, on one or more VGAM1794 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25081] It is yet further appreciated that a function of VGAM1794 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1794 include diagnosis, prevention and treatment of viral infection by Rana tigrina ranavirus. Spe-

cific functions, and accordingly utilities, of VGAM1794 correlate with, and may be deduced from, the identity of the host target genes which VGAM1794 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[25082] Nucleotide sequences of the VGAM1794 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1794 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1794 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1794 are further described hereinbelow with reference to Table 1.

[25083] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1794 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[25084] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1795 (VGAM1795) viral gene, which modulates expression of respective host target genes thereof, the func-

tion and utility of which host target genes is known in the art.

[25085] VGAM1795 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1795 was detected is described hereinabove with reference to Figs. 2-8.

[25086] VGAM1795 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rana tigrina ranavirus. VGAM1795 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[25087] VGAM1795 gene, herein designated VGAM GENE, encodes a VGAM1795 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1795 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1795 precursor RNA is designated SEQ ID:1781, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1781 is located at position 85710 relative to the genome of Rana tigrina ranavirus.

[25088] VGAM1795 precursor RNA, herein designated VGAM PRE-

CURSOR RNA, folds onto itself, forming VGAM1795 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25089] An enzyme complex designated DICER COMPLEX, dices the VGAM1795 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1795 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM1795 RNA is designated SEQ ID:4506, and is provided hereinbelow with reference to the sequence listing part.

[25090] VGAM1795 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM1795 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1795 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25091] VGAM1795 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1795 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1795 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1795 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1795 host

target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25092] The complementary binding of VGAM1795 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1795 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1795 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1795 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[25093] It is appreciated that VGAM1795 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1795 host target genes. The mRNA of each one of this plurality of VGAM1795 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1795 RNA, herein designated VGAM RNA, and which when bound by VGAM1795 RNA, herein

designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1795 host target proteins.

[25094] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1795 gene, herein designated VGAM GENE, on one or more VGAM1795 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25095] It is yet further appreciated that a function of VGAM1795 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1795 include diagnosis, prevention and

treatment of viral infection by Rana tigrina ranavirus. Specific functions, and accordingly utilities, of VGAM1795 correlate with, and may be deduced from, the identity of the host target genes which VGAM1795 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[25096] Nucleotide sequences of the VGAM1795 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1795 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1795 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1795 are further described hereinbelow with reference to Table 1.

[25097] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1795 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[25098] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1796 (VGAM1796) viral gene, which modulates ex-

pression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[25099] VGAM1796 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1796 was detected is described hereinabove with reference to Figs. 2-8.

[25100] VGAM1796 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rana tigrina ranavirus. VGAM1796 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[25101] VGAM1796 gene, herein designated VGAM GENE, encodes a VGAM1796 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1796 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1796 precursor RNA is designated SEQ ID:1782, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1782 is located at position 79650 relative to the genome of Rana tigrina ranavirus.

[25102] VGAM1796 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1796 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25103] An enzyme complex designated DICER COMPLEX, dices the VGAM1796 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1796 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM1796 RNA is designated SEQ ID:4507, and is provided hereinbelow with reference to the sequence listing part.

[25104] VGAM1796 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1796 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1796 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25105] VGAM1796 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1796 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1796 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1796 RNA, herein designated VGAM RNA, may have a different number of host target

binding sites in untranslated regions of a VGAM1796 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25106] The complementary binding of VGAM1796 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1796 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1796 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1796 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[25107] It is appreciated that VGAM1796 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1796 host target genes. The mRNA of each one of this plurality of VGAM1796 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1796 RNA, herein designated VGAM

RNA, and which when bound by VGAM1796 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1796 host target proteins.

[25108] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1796 gene, herein designated VGAM GENE, on one or more VGAM1796 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25109] It is yet further appreciated that a function of VGAM1796 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM1796 include diagnosis, prevention and treatment of viral infection by Rana tigrina ranavirus. Specific functions, and accordingly utilities, of VGAM1796 correlate with, and may be deduced from, the identity of the host target genes which VGAM1796 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[25110] Nucleotide sequences of the VGAM1796 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1796 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1796 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1796 are further described hereinbelow with reference to Table 1.

[25111] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1796 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[25112] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Mes-

senger 1797 (VGAM1797) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[25113] VGAM1797 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1797 was detected is described hereinabove with reference to Figs. 2-8.

[25114] VGAM1797 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rana tigrina ranavirus. VGAM1797 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[25115] VGAM1797 gene, herein designated VGAM GENE, encodes a VGAM1797 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1797 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1797 precursor RNA is designated SEQ ID:1783, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1783 is located at position

82741 relative to the genome of Rana tigrina ranavirus.

[25116] VGAM1797 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1797 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25117] An enzyme complex designated DICER COMPLEX, dices the VGAM1797 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1797 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of VGAM1797 RNA is designated SEQ ID:4508, and is provided hereinbelow with reference to the sequence listing part.

[25118] VGAM1797 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1797 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1797 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25119] VGAM1797 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1797 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1797 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1797 RNA, herein designated

VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1797 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25120] The complementary binding of VGAM1797 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1797 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1797 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1797 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[25121] It is appreciated that VGAM1797 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1797 host target genes. The mRNA of each one of this plurality of VGAM1797 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM1797 RNA, herein designated VGAM RNA, and which when bound by VGAM1797 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1797 host target proteins.

[25122] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1797 gene, herein designated VGAM GENE, on one or more VGAM1797 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25123] It is yet further appreciated that a function of VGAM1797 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1797 include diagnosis, prevention and treatment of viral infection by Rana tigrina ranavirus. Specific functions, and accordingly utilities, of VGAM1797 correlate with, and may be deduced from, the identity of the host target genes which VGAM1797 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[25124] Nucleotide sequences of the VGAM1797 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1797 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1797 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1797 are further described hereinbelow with reference to Table 1.

[25125] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1797 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[25126] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present

invention, referred to here as Viral Genomic Address Messenger 1798 (VGAM1798) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[25127] VGAM1798 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1798 was detected is described hereinabove with reference to Figs. 2-8.

[25128] VGAM1798 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rana tigrina ranavirus. VGAM1798 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[25129] VGAM1798 gene, herein designated VGAM GENE, encodes a VGAM1798 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1798 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1798 precursor RNA is designated SEQ ID:1784, and is provided hereinbelow with reference to the sequence listing part. Nu-

cleotide sequence SEQ ID:1784 is located at position 85493 relative to the genome of Rana tigrina ranavirus.

[25130] VGAM1798 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1798 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25131] An enzyme complex designated DICER COMPLEX, dices the VGAM1798 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1798 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM1798 RNA is designated SEQ ID:4509, and is provided hereinbelow with reference to the sequence

listing part.

[25132] VGAM1798 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1798 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1798 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25133] VGAM1798 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1798 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1798 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not

meant to be limiting VGAM1798 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1798 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25134] The complementary binding of VGAM1798 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1798 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1798 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1798 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[25135] It is appreciated that VGAM1798 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1798 host target genes. The mRNA of each one of this plurality of VGAM1798 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM1798 RNA, herein designated VGAM RNA, and which when bound by VGAM1798 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1798 host target proteins.

[25136] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1798 gene, herein designated VGAM GENE, on one or more VGAM1798 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25137] It is yet further appreciated that a function of VGAM1798

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1798 include diagnosis, prevention and treatment of viral infection by Rana tigrina ranavirus. Specific functions, and accordingly utilities, of VGAM1798 correlate with, and may be deduced from, the identity of the host target genes which VGAM1798 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[25138] Nucleotide sequences of the VGAM1798 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1798 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1798 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1798 are further described hereinbelow with reference to Table 1.

[25139] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1798 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[25140] Fig. 1 further provides a conceptual description of another

novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1799 (VGAM1799) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[25141] VGAM1799 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1799 was detected is described hereinabove with reference to Figs. 2-8.

[25142] VGAM1799 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Tupaia herpesvirus. VGAM1799 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[25143] VGAM1799 gene, herein designated VGAM GENE, encodes a VGAM1799 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1799 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1799 precursor RNA is designated SEQ ID:1785, and is provided here-

inbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1785 is located at position 30160 relative to the genome of Tupaia herpesvirus.

[25144] VGAM1799 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1799 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25145] An enzyme complex designated DICER COMPLEX, dices the VGAM1799 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1799 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM1799 RNA is designated SEQ ID:4510, and

is provided hereinbelow with reference to the sequence listing part.

[25146] VGAM1799 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1799 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1799 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25147] VGAM1799 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1799 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1799 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites

shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1799 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1799 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25148] The complementary binding of VGAM1799 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1799 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1799 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1799 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[25149] It is appreciated that VGAM1799 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1799 host target genes. The mRNA of each one of this plurality of VGAM1799 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1799 RNA, herein designated VGAM RNA, and which when bound by VGAM1799 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1799 host target proteins.

[25150] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1799 gene, herein designated VGAM GENE, on one or more VGAM1799 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25151] It is yet further appreciated that a function of VGAM1799 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1799 include diagnosis, prevention and treatment of viral infection by Tupaia herpesvirus. Specific functions, and accordingly utilities, of VGAM1799 correlate with, and may be deduced from, the identity of the host target genes which VGAM1799 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[25152] Nucleotide sequences of the VGAM1799 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1799 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1799 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1799 are further described hereinbelow with reference to Table 1.

[25153] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1799 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[25154] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1800 (VGAM1800) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[25155] VGAM1800 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1800 was detected is described hereinabove with reference to Figs. 2-8.

[25156] VGAM1800 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Tupaia herpesvirus. VGAM1800 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[25157] VGAM1800 gene, herein designated VGAM GENE, encodes a VGAM1800 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1800 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1800 precur-

sor RNA is designated SEQ ID:1786, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1786 is located at position 23754 relative to the genome of Tupaia herpesvirus.

[25158] VGAM1800 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1800 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25159] An enzyme complex designated DICER COMPLEX, dices the VGAM1800 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1800 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide se-

quence of VGAM1800 RNA is designated SEQ ID:4511, and is provided hereinbelow with reference to the sequence listing part.

[25160] VGAM1800 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1800 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1800 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25161] VGAM1800 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1800 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1800 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is ap-

preciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1800 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1800 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25162] The complementary binding of VGAM1800 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1800 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1800 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1800 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[25163] It is appreciated that VGAM1800 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1800 host target genes. The mRNA of

each one of this plurality of VGAM1800 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1800 RNA, herein designated VGAM RNA, and which when bound by VGAM1800 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1800 host target proteins.

[25164] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1800 gene, herein designated VGAM GENE, on one or more VGAM1800 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science

294,779 (2001)).

[25165] It is yet further appreciated that a function of VGAM1800 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1800 include diagnosis, prevention and treatment of viral infection by Tupaia herpesvirus. Specific functions, and accordingly utilities, of VGAM1800 correlate with, and may be deduced from, the identity of the host target genes which VGAM1800 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[25166] Nucleotide sequences of the VGAM1800 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1800 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1800 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1800 are further described hereinbelow with reference to Table 1.

[25167] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1800 RNA, herein designated VGAM RNA, are de-

scribed hereinbelow with reference to Table 2.

[25168] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1801 (VGAM1801) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[25169] VGAM1801 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1801 was detected is described hereinabove with reference to Figs. 2-8.

[25170] VGAM1801 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Tupaia herpesvirus. VGAM1801 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[25171] VGAM1801 gene, herein designated VGAM GENE, encodes a VGAM1801 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1801 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly

similar to the nucleotide sequence of VGAM1801 precursor RNA is designated SEQ ID:1787, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1787 is located at position 28609 relative to the genome of Tupaia herpesvirus.

[25172] VGAM1801 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1801 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25173] An enzyme complex designated DICER COMPLEX, dices the VGAM1801 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1801 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 45%) nucleotide sequence of VGAM1801 RNA is designated SEQ ID:4512, and is provided hereinbelow with reference to the sequence listing part.

[25174] VGAM1801 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1801 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1801 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25175] VGAM1801 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1801 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1801 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I,

BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1801 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1801 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25176] The complementary binding of VGAM1801 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1801 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1801 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1801 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[25177] It is appreciated that VGAM1801 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM1801 host target genes. The mRNA of each one of this plurality of VGAM1801 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1801 RNA, herein designated VGAM RNA, and which when bound by VGAM1801 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1801 host target proteins.

[25178] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1801 gene, herein designated VGAM GENE, on one or more VGAM1801 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25179] It is yet further appreciated that a function of VGAM1801 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1801 include diagnosis, prevention and treatment of viral infection by Tupaia herpesvirus. Specific functions, and accordingly utilities, of VGAM1801 correlate with, and may be deduced from, the identity of the host target genes which VGAM1801 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[25180] Nucleotide sequences of the VGAM1801 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1801 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1801 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1801 are further described hereinbelow with reference to Table 1.

[25181] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites

to VGAM1801 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[25182] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1802 (VGAM1802) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[25183] VGAM1802 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1802 was detected is described hereinabove with reference to Figs. 2-8.

[25184] VGAM1802 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Tupaia herpesvirus. VGAM1802 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[25185] VGAM1802 gene, herein designated VGAM GENE, encodes a VGAM1802 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1802 precursor RNA, herein designated VGAM PRECURSOR RNA, does not en-

code a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1802 precursor RNA is designated SEQ ID:1788, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1788 is located at position 27372 relative to the genome of Tupaia herpesvirus.

[25186] VGAM1802 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1802 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25187] An enzyme complex designated DICER COMPLEX, dices the VGAM1802 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1802 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM1802 RNA is designated SEQ ID:4513, and is provided hereinbelow with reference to the sequence listing part.

[25188] VGAM1802 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1802 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1802 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25189] VGAM1802 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1802 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1802 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3

such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1802 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1802 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25190] The complementary binding of VGAM1802 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1802 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1802 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1802 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[25191] It is appreciated that VGAM1802 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1802 host target genes. The mRNA of each one of this plurality of VGAM1802 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1802 RNA, herein designated VGAM RNA, and which when bound by VGAM1802 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1802 host target proteins.

[25192] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1802 gene, herein designated VGAM GENE, on one or more VGAM1802 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25193] It is yet further appreciated that a function of VGAM1802 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1802 include diagnosis, prevention and treatment of viral infection by Tupaia herpesvirus. Specific functions, and accordingly utilities, of VGAM1802 correlate with, and may be deduced from, the identity of the host target genes which VGAM1802 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[25194] Nucleotide sequences of the VGAM1802 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1802 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1802 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1802 are further described hereinbelow with reference to Table 1.

[25195] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the

complementarity of each of these host target binding sites to VGAM1802 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[25196] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1803 (VGAM1803) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[25197] VGAM1803 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1803 was detected is described hereinabove with reference to Figs. 2-8.

[25198] VGAM1803 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Tupaia herpesvirus. VGAM1803 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[25199] VGAM1803 gene, herein designated VGAM GENE, encodes a VGAM1803 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1803 precursor RNA,

herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1803 precursor RNA is designated SEQ ID:1789, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1789 is located at position 29560 relative to the genome of Tupaia herpesvirus.

[25200] VGAM1803 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1803 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25201] An enzyme complex designated DICER COMPLEX, dices the VGAM1803 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1803 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM1803 RNA is designated SEQ ID:4514, and is provided hereinbelow with reference to the sequence listing part.

[25202] VGAM1803 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1803 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1803 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25203] VGAM1803 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1803 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1803 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host

target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1803 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1803 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25204] The complementary binding of VGAM1803 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1803 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1803 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1803 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[25205] It is appreciated that VGAM1803 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1803 host target genes. The mRNA of each one of this plurality of VGAM1803 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1803 RNA, herein designated VGAM RNA, and which when bound by VGAM1803 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1803 host target proteins.

[25206] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1803 gene, herein designated VGAM GENE, on one or more VGAM1803 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25207] It is yet further appreciated that a function of VGAM1803 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1803 include diagnosis, prevention and treatment of viral infection by Tupaia herpesvirus. Specific functions, and accordingly utilities, of VGAM1803 correlate with, and may be deduced from, the identity of the host target genes which VGAM1803 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[25208] Nucleotide sequences of the VGAM1803 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1803 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1803 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1803 are further described hereinbelow with reference to Table 1.

[25209] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1803 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[25210] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1804 (VGAM1804) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[25211] VGAM1804 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1804 was detected is described hereinabove with reference to Figs. 2-8.

[25212] VGAM1804 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Tupaia herpesvirus. VGAM1804 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[25213] VGAM1804 gene, herein designated VGAM GENE, encodes a VGAM1804 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and un-

like most ordinary genes, VGAM1804 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1804 precursor RNA is designated SEQ ID:1790, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1790 is located at position 30515 relative to the genome of Tupaia herpesvirus.

[25214] VGAM1804 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1804 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25215] An enzyme complex designated DICER COMPLEX, dices the VGAM1804 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1804 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 70%) nucleotide sequence of VGAM1804 RNA is designated SEQ ID:4515, and is provided hereinbelow with reference to the sequence listing part.

[25216] VGAM1804 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1804 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1804 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25217] VGAM1804 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1804 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1804 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed

sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1804 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1804 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25218] The complementary binding of VGAM1804 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1804 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1804 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1804 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target

protein is therefore outlined by a broken line.

[25219] It is appreciated that VGAM1804 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1804 host target genes. The mRNA of each one of this plurality of VGAM1804 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1804 RNA, herein designated VGAM RNA, and which when bound by VGAM1804 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1804 host target proteins.

[25220] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1804 gene, herein designated VGAM GENE, on one or more VGAM1804 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25221] It is yet further appreciated that a function of VGAM1804 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1804 include diagnosis, prevention and treatment of viral infection by Tupaia herpesvirus. Specific functions, and accordingly utilities, of VGAM1804 correlate with, and may be deduced from, the identity of the host target genes which VGAM1804 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[25222] Nucleotide sequences of the VGAM1804 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1804 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1804 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1804 are further described hereinbelow with reference to Table 1.

[25223] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1804 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[25224] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1805 (VGAM1805) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[25225] VGAM1805 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1805 was detected is described hereinabove with reference to Figs. 2-8.

[25226] VGAM1805 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Tupaia herpesvirus. VGAM1805 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[25227] VGAM1805 gene, herein designated VGAM GENE, encodes a VGAM1805 precursor RNA, herein designated VGAM

PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1805 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1805 precursor RNA is designated SEQ ID:1791, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1791 is located at position 33339 relative to the genome of Tupaia herpesvirus.

[25228] VGAM1805 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1805 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25229] An enzyme complex designated DICER COMPLEX, dices the VGAM1805 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1805 RNA, herein designated VGAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM1805 RNA is designated SEQ ID:4516, and is provided hereinbelow with reference to the sequence listing part.

[25230] VGAM1805 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1805 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1805 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25231] VGAM1805 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1805 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1805 RNA, herein designated

VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1805 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1805 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25232] The complementary binding of VGAM1805 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1805 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1805 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1805 host target protein, herein desig-

nated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[25233] It is appreciated that VGAM1805 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1805 host target genes. The mRNA of each one of this plurality of VGAM1805 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1805 RNA, herein designated VGAM RNA, and which when bound by VGAM1805 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1805 host target proteins.

[25234] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1805 gene, herein designated VGAM GENE, on one or more VGAM1805 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25235] It is yet further appreciated that a function of VGAM1805 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1805 include diagnosis, prevention and treatment of viral infection by Tupaia herpesvirus. Specific functions, and accordingly utilities, of VGAM1805 correlate with, and may be deduced from, the identity of the host target genes which VGAM1805 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[25236] Nucleotide sequences of the VGAM1805 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1805 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1805 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1805 are further described hereinbelow with reference to Table 1.

[25237] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1805 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[25238] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1806 (VGAM1806) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[25239] VGAM1806 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1806 was detected is described hereinabove with reference to Figs. 2-8.

[25240] VGAM1806 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Tupaia herpesvirus. VGAM1806 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[25241] VGAM1806 gene, herein designated VGAM GENE, encodes

a VGAM1806 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1806 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1806 precursor RNA is designated SEQ ID:1792, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1792 is located at position 25245 relative to the genome of Tupaia herpesvirus.

[25242] VGAM1806 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1806 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25243] An enzyme complex designated DICER COMPLEX, dices the VGAM1806 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1806 RNA,

herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM1806 RNA is designated SEQ ID:4517, and is provided hereinbelow with reference to the sequence listing part.

[25244] VGAM1806 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1806 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1806 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25245] VGAM1806 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1806 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM1806 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1806 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1806 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25246] The complementary binding of VGAM1806 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1806 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1806 host target RNA, herein designated VGAM HOST TARGET

RNA, into VGAM1806 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[25247] It is appreciated that VGAM1806 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1806 host target genes. The mRNA of each one of this plurality of VGAM1806 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1806 RNA, herein designated VGAM RNA, and which when bound by VGAM1806 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1806 host target proteins.

[25248] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1806 gene, herein designated VGAM GENE, on one or more VGAM1806 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25249] It is yet further appreciated that a function of VGAM1806 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1806 include diagnosis, prevention and treatment of viral infection by Tupaia herpesvirus. Specific functions, and accordingly utilities, of VGAM1806 correlate with, and may be deduced from, the identity of the host target genes which VGAM1806 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[25250] Nucleotide sequences of the VGAM1806 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1806 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1806 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1806 are further

described hereinbelow with reference to Table 1.

[25251] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1806 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[25252] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1807 (VGAM1807) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[25253] VGAM1807 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1807 was detected is described hereinabove with reference to Figs. 2-8.

[25254] VGAM1807 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rana tigrina ranavirus. VGAM1807 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[25255] VGAM1807 gene, herein designated VGAM GENE, encodes a VGAM1807 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1807 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1807 precursor RNA is designated SEQ ID:1793, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1793 is located at position 16749 relative to the genome of Rana tigrina ranavirus.

[25256] VGAM1807 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1807 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25257] An enzyme complex designated DICER COMPLEX, dices the VGAM1807 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, into VGAM1807 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 49%) nucleotide sequence of VGAM1807 RNA is designated SEQ ID:4518, and is provided hereinbelow with reference to the sequence listing part.

[25258] VGAM1807 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1807 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1807 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25259] VGAM1807 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1807 host target RNA, herein designated VGAM HOST TARGET RNA. This

complementary binding is due to the fact that the nucleotide sequence of VGAM1807 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1807 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1807 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25260] The complementary binding of VGAM1807 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1807 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1807

host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1807 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[25261] It is appreciated that VGAM1807 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1807 host target genes. The mRNA of each one of this plurality of VGAM1807 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1807 RNA, herein designated VGAM RNA, and which when bound by VGAM1807 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1807 host target proteins.

[25262] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1807 gene, herein designated VGAM GENE, on one or more VGAM1807 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25263] It is yet further appreciated that a function of VGAM1807 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1807 include diagnosis, prevention and treatment of viral infection by Rana tigrina ranavirus. Specific functions, and accordingly utilities, of VGAM1807 correlate with, and may be deduced from, the identity of the host target genes which VGAM1807 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[25264] Nucleotide sequences of the VGAM1807 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1807 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1807 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM1807 are further described hereinbelow with reference to Table 1.

[25265] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1807 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[25266] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1808 (VGAM1808) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[25267] VGAM1808 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1808 was detected is described hereinabove with reference to Figs. 2-8.

[25268] VGAM1808 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rana tigrina ranavirus. VGAM1808 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the

human genome.

[25269] VGAM1808 gene, herein designated VGAM GENE, encodes a VGAM1808 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1808 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1808 precursor RNA is designated SEQ ID:1794, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1794 is located at position 27725 relative to the genome of Rana tigrina ranavirus.

[25270] VGAM1808 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1808 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25271] An enzyme complex designated DICER COMPLEX, dices

the VGAM1808 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1808 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 71%) nucleotide sequence of VGAM1808 RNA is designated SEQ ID:4519, and is provided hereinbelow with reference to the sequence listing part.

[25272] VGAM1808 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1808 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1808 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25273] VGAM1808 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1808 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1808 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1808 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1808 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25274] The complementary binding of VGAM1808 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1808 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM1808 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1808 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[25275] It is appreciated that VGAM1808 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1808 host target genes. The mRNA of each one of this plurality of VGAM1808 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1808 RNA, herein designated VGAM RNA, and which when bound by VGAM1808 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1808 host target proteins.

[25276] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1808 gene, herein designated VGAM GENE, on one or more VGAM1808 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25277] It is yet further appreciated that a function of VGAM1808 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1808 include diagnosis, prevention and treatment of viral infection by Rana tigrina ranavirus. Specific functions, and accordingly utilities, of VGAM1808 correlate with, and may be deduced from, the identity of the host target genes which VGAM1808 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[25278] Nucleotide sequences of the VGAM1808 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1808 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of

VGAM1808 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1808 are further described hereinbelow with reference to Table 1.

[25279] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1808 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[25280] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1809 (VGAM1809) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[25281] VGAM1809 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1809 was detected is described hereinabove with reference to Figs. 2-8.

[25282] VGAM1809 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rana tigrina ranavirus. VGAM1809 host target gene, herein designated VGAM

HOST TARGET GENE, is a human gene contained in the human genome.

[25283] VGAM1809 gene, herein designated VGAM GENE, encodes a VGAM1809 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1809 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1809 precursor RNA is designated SEQ ID:1795, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1795 is located at position 28383 relative to the genome of Rana tigrina ranavirus.

[25284] VGAM1809 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1809 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25285] An enzyme complex designated DICER COMPLEX, dices the VGAM1809 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1809 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM1809 RNA is designated SEQ ID:4520, and is provided hereinbelow with reference to the sequence listing part.

[25286] VGAM1809 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1809 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1809 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25287] VGAM1809 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites

located in untranslated regions of VGAM1809 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1809 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1809 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1809 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25288] The complementary binding of VGAM1809 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1809 host target RNA, herein designated VGAM

HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1809 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1809 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[25289] It is appreciated that VGAM1809 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1809 host target genes. The mRNA of each one of this plurality of VGAM1809 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1809 RNA, herein designated VGAM RNA, and which when bound by VGAM1809 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1809 host target proteins.

[25290] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1809 gene, herein designated VGAM GENE, on one or more VGAM1809 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove

with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25291] It is yet further appreciated that a function of VGAM1809 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1809 include diagnosis, prevention and treatment of viral infection by Rana tigrina ranavirus. Specific functions, and accordingly utilities, of VGAM1809 correlate with, and may be deduced from, the identity of the host target genes which VGAM1809 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[25292] Nucleotide sequences of the VGAM1809 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1809 RNA, herein designated VGAM RNA, and

a schematic representation of the secondary folding of VGAM1809 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1809 are further described hereinbelow with reference to Table 1.

[25293] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1809 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[25294] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1810 (VGAM1810) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[25295] VGAM1810 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1810 was detected is described hereinabove with reference to Figs. 2-8.

[25296] VGAM1810 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine herpesvirus 1.

VGAM1810 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[25297] VGAM1810 gene, herein designated VGAM GENE, encodes a VGAM1810 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1810 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1810 precursor RNA is designated SEQ ID:1796, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1796 is located at position 128214 relative to the genome of Equine herpesvirus 1.

[25298] VGAM1810 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1810 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[25299] An enzyme complex designated DICER COMPLEX, dices the VGAM1810 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1810 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 67%) nucleotide sequence of VGAM1810 RNA is designated SEQ ID:4521, and is provided hereinbelow with reference to the sequence listing part.

[25300] VGAM1810 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1810 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1810 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25301] VGAM1810 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM1810 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1810 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1810 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1810 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25302] The complementary binding of VGAM1810 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM1810 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1810 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1810 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[25303] It is appreciated that VGAM1810 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1810 host target genes. The mRNA of each one of this plurality of VGAM1810 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1810 RNA, herein designated VGAM RNA, and which when bound by VGAM1810 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1810 host target proteins.

[25304] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1810 gene, herein designated VGAM GENE, on one or more VGAM1810 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25305] It is yet further appreciated that a function of VGAM1810 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1810 include diagnosis, prevention and treatment of viral infection by Equine herpesvirus 1. Specific functions, and accordingly utilities, of VGAM1810 correlate with, and may be deduced from, the identity of the host target genes which VGAM1810 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[25306] Nucleotide sequences of the VGAM1810 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

diced VGAM1810 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1810 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1810 are further described hereinbelow with reference to Table 1.

[25307] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1810 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[25308] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1811 (VGAM1811) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[25309] VGAM1811 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1811 was detected is described hereinabove with reference to Figs. 2-8.

[25310] VGAM1811 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of Equine herpesvirus 1. VGAM1811 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[25311] VGAM1811 gene, herein designated VGAM GENE, encodes a VGAM1811 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1811 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1811 precursor RNA is designated SEQ ID:1797, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1797 is located at position 132691 relative to the genome of Equine herpesvirus 1.

[25312] VGAM1811 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1811 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25313] An enzyme complex designated DICER COMPLEX, dices the VGAM1811 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1811 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM1811 RNA is designated SEQ ID:4522, and is provided hereinbelow with reference to the sequence listing part.

[25314] VGAM1811 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1811 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1811 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25315] VGAM1811 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1811 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1811 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1811 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1811 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25316] The complementary binding of VGAM1811 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM1811 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1811 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1811 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[25317] It is appreciated that VGAM1811 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1811 host target genes. The mRNA of each one of this plurality of VGAM1811 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1811 RNA, herein designated VGAM RNA, and which when bound by VGAM1811 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1811 host target proteins.

[25318] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1811 gene, herein designated VGAM GENE, on one or more VGAM1811 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25319] It is yet further appreciated that a function of VGAM1811 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1811 include diagnosis, prevention and treatment of viral infection by Equine herpesvirus 1. Specific functions, and accordingly utilities, of VGAM1811 correlate with, and may be deduced from, the identity of the host target genes which VGAM1811 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[25320] Nucleotide sequences of the VGAM1811 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the diced VGAM1811 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1811 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1811 are further described hereinbelow with reference to Table 1.

[25321] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1811 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[25322] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1812 (VGAM1812) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[25323] VGAM1812 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1812 was detected is described hereinabove with reference to Figs. 2-8.

[25324] VGAM1812 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine herpesvirus 1. VGAM1812 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[25325] VGAM1812 gene, herein designated VGAM GENE, encodes a VGAM1812 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1812 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1812 precursor RNA is designated SEQ ID:1798, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1798 is located at position 129486 relative to the genome of Equine herpesvirus 1.

[25326] VGAM1812 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1812 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25327] An enzyme complex designated DICER COMPLEX, dices the VGAM1812 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1812 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM1812 RNA is designated SEQ ID:4523, and is provided hereinbelow with reference to the sequence listing part.

[25328] VGAM1812 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1812 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1812 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN COD-

ING and 3UTR respectively.

[25329] VGAM1812 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1812 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1812 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1812 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1812 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25330] The complementary binding of VGAM1812 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1812 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1812 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1812 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[25331] It is appreciated that VGAM1812 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1812 host target genes. The mRNA of each one of this plurality of VGAM1812 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1812 RNA, herein designated VGAM RNA, and which when bound by VGAM1812 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1812 host target proteins.

[25332] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1812 gene, herein designated VGAM GENE, on one

or more VGAM1812 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25333] It is yet further appreciated that a function of VGAM1812 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1812 include diagnosis, prevention and treatment of viral infection by Equine herpesvirus 1. Specific functions, and accordingly utilities, of VGAM1812 correlate with, and may be deduced from, the identity of the host target genes which VGAM1812 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[25334] Nucleotide sequences of the VGAM1812 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1812 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1812 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1812 are further described hereinbelow with reference to Table 1.

[25335] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1812 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[25336] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1813 (VGAM1813) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[25337] VGAM1813 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1813 was detected is de-

scribed hereinabove with reference to Figs. 2-8.

[25338] VGAM1813 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine herpesvirus 1. VGAM1813 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[25339] VGAM1813 gene, herein designated VGAM GENE, encodes a VGAM1813 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1813 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1813 precursor RNA is designated SEQ ID:1799, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1799 is located at position 137114 relative to the genome of Equine herpesvirus 1.

[25340] VGAM1813 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1813 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25341] An enzyme complex designated DICER COMPLEX, dices the VGAM1813 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1813 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 59%) nucleotide sequence of VGAM1813 RNA is designated SEQ ID:4524, and is provided hereinbelow with reference to the sequence listing part.

[25342] VGAM1813 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1813 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1813 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and

a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25343] VGAM1813 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1813 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1813 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1813 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1813 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both

3UTR and 5UTR regions.

[25344] The complementary binding of VGAM1813 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1813 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1813 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1813 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[25345] It is appreciated that VGAM1813 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1813 host target genes. The mRNA of each one of this plurality of VGAM1813 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1813 RNA, herein designated VGAM RNA, and which when bound by VGAM1813 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1813 host target proteins.

[25346] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM1813 gene, herein designated VGAM GENE, on one or more VGAM1813 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25347] It is yet further appreciated that a function of VGAM1813 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1813 include diagnosis, prevention and treatment of viral infection by Equine herpesvirus 1. Specific functions, and accordingly utilities, of VGAM1813 correlate with, and may be deduced from, the identity of the host target genes which VGAM1813 binds and inhibits, and the function of these host target genes, as

elaborated hereinbelow.

[25348] Nucleotide sequences of the VGAM1813 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1813 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1813 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1813 are further described hereinbelow with reference to Table 1.

[25349] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1813 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[25350] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1814 (VGAM1814) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[25351] VGAM1814 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene.

The method by which VGAM1814 was detected is described hereinabove with reference to Figs. 2-8.

[25352] VGAM1814 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine herpesvirus 1. VGAM1814 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[25353] VGAM1814 gene, herein designated VGAM GENE, encodes a VGAM1814 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1814 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1814 precursor RNA is designated SEQ ID:1800, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1800 is located at position 127841 relative to the genome of Equine herpesvirus 1.

[25354] VGAM1814 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1814 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25355] An enzyme complex designated DICER COMPLEX, dices the VGAM1814 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1814 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 90%) nucleotide sequence of VGAM1814 RNA is designated SEQ ID:4525, and is provided hereinbelow with reference to the sequence listing part.

[25356] VGAM1814 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1814 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1814 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding

gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25357] VGAM1814 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1814 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1814 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1814 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1814 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be lo-

cated in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25358] The complementary binding of VGAM1814 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1814 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1814 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1814 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[25359] It is appreciated that VGAM1814 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1814 host target genes. The mRNA of each one of this plurality of VGAM1814 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1814 RNA, herein designated VGAM RNA, and which when bound by VGAM1814 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1814 host target proteins.

[25360] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM1814 gene, herein designated VGAM GENE, on one or more VGAM1814 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25361] It is yet further appreciated that a function of VGAM1814 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1814 include diagnosis, prevention and treatment of viral infection by Equine herpesvirus 1. Specific functions, and accordingly utilities, of VGAM1814 correlate with, and may be deduced from, the identity of the host target genes which VGAM1814 binds and in-

hibits, and the function of these host target genes, as elaborated hereinbelow.

[25362] Nucleotide sequences of the VGAM1814 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1814 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1814 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1814 are further described hereinbelow with reference to Table 1.

[25363] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1814 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[25364]

[25365] Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1815 (VGAM1815) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[25366] VGAM1815 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1815 was detected is described hereinabove with reference to Figs. 2-8.

[25367] VGAM1815 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine herpesvirus 1. VGAM1815 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[25368] VGAM1815 gene, herein designated VGAM GENE, encodes a VGAM1815 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1815 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1815 precursor RNA is designated SEQ ID:1801, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1801 is located at position 130995 relative to the genome of Equine herpesvirus 1.

[25369] VGAM1815 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1815 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25370] An enzyme complex designated DICER COMPLEX, dices the VGAM1815 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1815 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM1815 RNA is designated SEQ ID:4526, and is provided hereinbelow with reference to the sequence listing part.

[25371] VGAM1815 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1815 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1815 host target RNA, herein designated VGAM HOST TARGET RNA, comprises

three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25372] VGAM1815 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1815 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1815 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1815 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1815 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an

example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25373] The complementary binding of VGAM1815 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1815 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1815 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1815 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[25374] It is appreciated that VGAM1815 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1815 host target genes. The mRNA of each one of this plurality of VGAM1815 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1815 RNA, herein designated VGAM RNA, and which when bound by VGAM1815 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1815 host target proteins.

[25375] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1815 gene, herein designated VGAM GENE, on one or more VGAM1815 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25376] It is yet further appreciated that a function of VGAM1815 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1815 include diagnosis, prevention and treatment of viral infection by Equine herpesvirus 1. Specific functions, and accordingly utilities, of VGAM1815 correlate with, and may be deduced from, the identity of

the host target genes which VGAM1815 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[25377] Nucleotide sequences of the VGAM1815 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1815 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1815 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1815 are further described hereinbelow with reference to Table 1.

[25378] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1815 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[25379] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1816 (VGAM1816) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[25380] VGAM1816 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1816 was detected is described hereinabove with reference to Figs. 2-8.

[25381] VGAM1816 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Camelpox virus. VGAM1816 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[25382] VGAM1816 gene, herein designated VGAM GENE, encodes a VGAM1816 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1816 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1816 precursor RNA is designated SEQ ID:1802, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1802 is located at position 41903 relative to the genome of Camelpox virus.

[25383] VGAM1816 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1816 folded precursor RNA, herein designated VGAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25384] An enzyme complex designated DICER COMPLEX, dices the VGAM1816 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1816 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM1816 RNA is designated SEQ ID:4527, and is provided hereinbelow with reference to the sequence listing part.

[25385] VGAM1816 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1816 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1816 host target RNA,

herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25386] VGAM1816 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1816 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1816 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1816 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1816 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host tar-

get binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25387] The complementary binding of VGAM1816 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1816 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1816 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1816 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[25388] It is appreciated that VGAM1816 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1816 host target genes. The mRNA of each one of this plurality of VGAM1816 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1816 RNA, herein designated VGAM RNA, and which when bound by VGAM1816 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1816 host target proteins.

[25389] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1816 gene, herein designated VGAM GENE, on one or more VGAM1816 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25390] It is yet further appreciated that a function of VGAM1816 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1816 include diagnosis, prevention and treatment of viral infection by Camelpox virus. Specific functions, and accordingly utilities, of VGAM1816 corre-

late with, and may be deduced from, the identity of the host target genes which VGAM1816 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[25391] Nucleotide sequences of the VGAM1816 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1816 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1816 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1816 are further described hereinbelow with reference to Table 1.

[25392] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1816 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[25393] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1817 (VGAM1817) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the

art.

[25394] VGAM1817 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1817 was detected is described hereinabove with reference to Figs. 2-8.

[25395] VGAM1817 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Variola virus. VGAM1817 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[25396] VGAM1817 gene, herein designated VGAM GENE, encodes a VGAM1817 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1817 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1817 precursor RNA is designated SEQ ID:1803, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1803 is located at position 27215 relative to the genome of Variola virus.

[25397] VGAM1817 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1817 folded precursor RNA, herein designated VGAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25398] An enzyme complex designated DICER COMPLEX, dices the VGAM1817 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1817 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 78%) nucleotide sequence of VGAM1817 RNA is designated SEQ ID:4528, and is provided hereinbelow with reference to the sequence listing part.

[25399] VGAM1817 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1817 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1817 host target RNA,

herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25400] VGAM1817 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1817 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1817 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1817 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1817 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host tar-

get binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25401] The complementary binding of VGAM1817 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1817 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1817 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1817 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[25402] It is appreciated that VGAM1817 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1817 host target genes. The mRNA of each one of this plurality of VGAM1817 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1817 RNA, herein designated VGAM RNA, and which when bound by VGAM1817 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1817 host target proteins.

[25403] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1817 gene, herein designated VGAM GENE, on one or more VGAM1817 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25404] It is yet further appreciated that a function of VGAM1817 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1817 include diagnosis, prevention and treatment of viral infection by Variola virus. Specific functions, and accordingly utilities, of VGAM1817 correlate

with, and may be deduced from, the identity of the host target genes which VGAM1817 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[25405] Nucleotide sequences of the VGAM1817 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1817 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1817 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1817 are further described hereinbelow with reference to Table 1.

[25406] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1817 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[25407] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1818 (VGAM1818) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the

art.

[25408] VGAM1818 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1818 was detected is described hereinabove with reference to Figs. 2-8.

[25409] VGAM1818 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Variola virus. VGAM1818 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[25410] VGAM1818 gene, herein designated VGAM GENE, encodes a VGAM1818 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1818 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1818 precursor RNA is designated SEQ ID:1804, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1804 is located at position 28707 relative to the genome of Variola virus.

[25411] VGAM1818 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1818 folded precursor RNA, herein designated VGAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25412] An enzyme complex designated DICER COMPLEX, dices the VGAM1818 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1818 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM1818 RNA is designated SEQ ID:4529, and is provided hereinbelow with reference to the sequence listing part.

[25413] VGAM1818 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1818 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1818 host target RNA,

herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25414] VGAM1818 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1818 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1818 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1818 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1818 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host tar-

get binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25415] The complementary binding of VGAM1818 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1818 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1818 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1818 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[25416] It is appreciated that VGAM1818 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1818 host target genes. The mRNA of each one of this plurality of VGAM1818 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1818 RNA, herein designated VGAM RNA, and which when bound by VGAM1818 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1818 host target proteins.

[25417] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1818 gene, herein designated VGAM GENE, on one or more VGAM1818 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25418] It is yet further appreciated that a function of VGAM1818 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1818 include diagnosis, prevention and treatment of viral infection by Variola virus. Specific functions, and accordingly utilities, of VGAM1818 correlate

with, and may be deduced from, the identity of the host target genes which VGAM1818 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[25419] Nucleotide sequences of the VGAM1818 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1818 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1818 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1818 are further described hereinbelow with reference to Table 1.

[25420] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1818 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[25421] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1819 (VGAM1819) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the

art.

[25422] VGAM1819 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1819 was detected is described hereinabove with reference to Figs. 2-8.

[25423] VGAM1819 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cryphonectria hypovirus. VGAM1819 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[25424] VGAM1819 gene, herein designated VGAM GENE, encodes a VGAM1819 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1819 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1819 precursor RNA is designated SEQ ID:1805, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1805 is located at position 7183 relative to the genome of Cryphonectria hypovirus.

[25425] VGAM1819 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1819 folded

precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25426] An enzyme complex designated DICER COMPLEX, dices the VGAM1819 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1819 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM1819 RNA is designated SEQ ID:4530, and is provided hereinbelow with reference to the sequence listing part.

[25427] VGAM1819 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1819 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM1819 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25428] VGAM1819 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1819 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1819 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1819 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1819 host target RNA, herein designated VGAM HOST TARGET RNA.

It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25429] The complementary binding of VGAM1819 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1819 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1819 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1819 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[25430] It is appreciated that VGAM1819 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1819 host target genes. The mRNA of each one of this plurality of VGAM1819 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1819 RNA, herein designated VGAM RNA, and which when bound by VGAM1819 RNA, herein designated VGAM RNA, causes inhibition of translation of

respective one or more VGAM1819 host target proteins.

[25431] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1819 gene, herein designated VGAM GENE, on one or more VGAM1819 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25432] It is yet further appreciated that a function of VGAM1819 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1819 include diagnosis, prevention and treatment of viral infection by Cryphonectria hypovirus.

Specific functions, and accordingly utilities, of VGAM1819 correlate with, and may be deduced from, the identity of the host target genes which VGAM1819 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[25433] Nucleotide sequences of the VGAM1819 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1819 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1819 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1819 are further described hereinbelow with reference to Table 1.

[25434] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1819 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[25435] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1820 (VGAM1820) viral gene, which modulates expression of respective host target genes thereof, the func-

tion and utility of which host target genes is known in the art.

[25436] VGAM1820 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1820 was detected is described hereinabove with reference to Figs. 2-8.

[25437] VGAM1820 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cryphonectria hypovirus. VGAM1820 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[25438] VGAM1820 gene, herein designated VGAM GENE, encodes a VGAM1820 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1820 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1820 precursor RNA is designated SEQ ID:1806, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1806 is located at position 7825 relative to the genome of Cryphonectria hypovirus.

[25439] VGAM1820 precursor RNA, herein designated VGAM PRE-

CURSOR RNA, folds onto itself, forming VGAM1820 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25440] An enzyme complex designated DICER COMPLEX, dices the VGAM1820 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1820 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of VGAM1820 RNA is designated SEQ ID:4531, and is provided hereinbelow with reference to the sequence listing part.

[25441] VGAM1820 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM1820 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1820 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25442] VGAM1820 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1820 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1820 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1820 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1820 host

target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25443] The complementary binding of VGAM1820 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1820 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1820 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1820 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[25444] It is appreciated that VGAM1820 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1820 host target genes. The mRNA of each one of this plurality of VGAM1820 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1820 RNA, herein designated VGAM RNA, and which when bound by VGAM1820 RNA, herein

designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1820 host target proteins.

[25445] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1820 gene, herein designated VGAM GENE, on one or more VGAM1820 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25446] It is yet further appreciated that a function of VGAM1820 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1820 include diagnosis, prevention and

treatment of viral infection by Cryphonectria hypovirus. Specific functions, and accordingly utilities, of VGAM1820 correlate with, and may be deduced from, the identity of the host target genes which VGAM1820 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[25447] Nucleotide sequences of the VGAM1820 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1820 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1820 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1820 are further described hereinbelow with reference to Table 1.

[25448] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1820 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[25449] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1821 (VGAM1821) viral gene, which modulates ex-

pression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[25450] VGAM1821 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1821 was detected is described hereinabove with reference to Figs. 2-8.

[25451] VGAM1821 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Variola virus. VGAM1821 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[25452] VGAM1821 gene, herein designated VGAM GENE, encodes a VGAM1821 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1821 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1821 precursor RNA is designated SEQ ID:1807, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1807 is located at position 28943 relative to the genome of Variola virus.

[25453] VGAM1821 precursor RNA, herein designated VGAM PRE-

CURSOR RNA, folds onto itself, forming VGAM1821 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25454] An enzyme complex designated DICER COMPLEX, dices the VGAM1821 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1821 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 59%) nucleotide sequence of VGAM1821 RNA is designated SEQ ID:4532, and is provided hereinbelow with reference to the sequence listing part.

[25455] VGAM1821 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM1821 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1821 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25456] VGAM1821 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1821 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1821 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1821 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1821 host

target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25457] The complementary binding of VGAM1821 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1821 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1821 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1821 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[25458] It is appreciated that VGAM1821 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1821 host target genes. The mRNA of each one of this plurality of VGAM1821 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1821 RNA, herein designated VGAM RNA, and which when bound by VGAM1821 RNA, herein

designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1821 host target proteins.

[25459] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1821 gene, herein designated VGAM GENE, on one or more VGAM1821 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25460] It is yet further appreciated that a function of VGAM1821 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1821 include diagnosis, prevention and

treatment of viral infection by Variola virus. Specific functions, and accordingly utilities, of VGAM1821 correlate with, and may be deduced from, the identity of the host target genes which VGAM1821 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[25461] Nucleotide sequences of the VGAM1821 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1821 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1821 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1821 are further described hereinbelow with reference to Table 1.

[25462] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1821 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[25463] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1822 (VGAM1822) viral gene, which modulates ex-

pression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[25464] VGAM1822 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1822 was detected is described hereinabove with reference to Figs. 2-8.

[25465] VGAM1822 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cryphonectria hypovirus. VGAM1822 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[25466] VGAM1822 gene, herein designated VGAM GENE, encodes a VGAM1822 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1822 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1822 precursor RNA is designated SEQ ID:1808, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1808 is located at position 9148 relative to the genome of Cryphonectria hypovirus.

[25467] VGAM1822 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1822 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25468] An enzyme complex designated DICER COMPLEX, dices the VGAM1822 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1822 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM1822 RNA is designated SEQ ID:4533, and is provided hereinbelow with reference to the sequence listing part.

[25469] VGAM1822 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1822 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1822 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25470] VGAM1822 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1822 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1822 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1822 RNA, herein designated VGAM RNA, may have a different number of host target

binding sites in untranslated regions of a VGAM1822 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25471] The complementary binding of VGAM1822 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1822 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1822 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1822 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[25472] It is appreciated that VGAM1822 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1822 host target genes. The mRNA of each one of this plurality of VGAM1822 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1822 RNA, herein designated VGAM

RNA, and which when bound by VGAM1822 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1822 host target proteins.

[25473] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1822 gene, herein designated VGAM GENE, on one or more VGAM1822 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25474] It is yet further appreciated that a function of VGAM1822 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM1822 include diagnosis, prevention and treatment of viral infection by Cryphonectria hypovirus. Specific functions, and accordingly utilities, of VGAM1822 correlate with, and may be deduced from, the identity of the host target genes which VGAM1822 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[25475] Nucleotide sequences of the VGAM1822 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1822 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1822 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1822 are further described hereinbelow with reference to Table 1.

[25476] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1822 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[25477] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Mes-

senger 1823 (VGAM1823) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[25478] VGAM1823 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1823 was detected is described hereinabove with reference to Figs. 2-8.

[25479] VGAM1823 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cryphonectria hypovirus. VGAM1823 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[25480] VGAM1823 gene, herein designated VGAM GENE, encodes a VGAM1823 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1823 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1823 precursor RNA is designated SEQ ID:1809, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1809 is located at position 3317

relative to the genome of Cryphonectria hypovirus.

[25481] VGAM1823 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1823 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25482] An enzyme complex designated DICER COMPLEX, dices the VGAM1823 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1823 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 73%) nucleotide sequence of VGAM1823 RNA is designated SEQ ID:4534, and is provided hereinbelow with reference to the sequence listing part.

[25483] VGAM1823 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1823 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1823 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25484] VGAM1823 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1823 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1823 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1823 RNA, herein designated

VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1823 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25485] The complementary binding of VGAM1823 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1823 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1823 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1823 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[25486] It is appreciated that VGAM1823 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1823 host target genes. The mRNA of each one of this plurality of VGAM1823 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM1823 RNA, herein designated VGAM RNA, and which when bound by VGAM1823 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1823 host target proteins.

[25487] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1823 gene, herein designated VGAM GENE, on one or more VGAM1823 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25488] It is yet further appreciated that a function of VGAM1823 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1823 include diagnosis, prevention and treatment of viral infection by Cryphonectria hypovirus. Specific functions, and accordingly utilities, of VGAM1823 correlate with, and may be deduced from, the identity of the host target genes which VGAM1823 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[25489] Nucleotide sequences of the VGAM1823 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1823 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1823 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1823 are further described hereinbelow with reference to Table 1.

[25490] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1823 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[25491] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present

invention, referred to here as Viral Genomic Address Messenger 1824 (VGAM1824) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[25492] VGAM1824 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1824 was detected is described hereinabove with reference to Figs. 2-8.

[25493] VGAM1824 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cryphonectria hypovirus. VGAM1824 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[25494] VGAM1824 gene, herein designated VGAM GENE, encodes a VGAM1824 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1824 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1824 precursor RNA is designated SEQ ID:1810, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1810 is located at position 3901 relative to the genome of Cryphonectria hypovirus.

[25495] VGAM1824 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1824 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25496] An enzyme complex designated DICER COMPLEX, dices the VGAM1824 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, into VGAM1824 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 73%) nucleotide sequence of VGAM1824 RNA is designated SEQ ID:4535, and is provided hereinbelow with reference to the sequence listing part.

[25497] VGAM1824 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1824 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1824 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25498] VGAM1824 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1824 host target RNA, herein designated VGAM HOST TARGET RNA. This

complementary binding is due to the fact that the nucleotide sequence of VGAM1824 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1824 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1824 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25499] The complementary binding of VGAM1824 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1824 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1824

host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1824 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[25500] It is appreciated that VGAM1824 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1824 host target genes. The mRNA of each one of this plurality of VGAM1824 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1824 RNA, herein designated VGAM RNA, and which when bound by VGAM1824 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1824 host target proteins.

[25501] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1824 gene, herein designated VGAM GENE, on one or more VGAM1824 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25502] It is yet further appreciated that a function of VGAM1824 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1824 include diagnosis, prevention and treatment of viral infection by Cryphonectria hypovirus. Specific functions, and accordingly utilities, of VGAM1824 correlate with, and may be deduced from, the identity of the host target genes which VGAM1824 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[25503] Nucleotide sequences of the VGAM1824 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1824 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1824 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM1824 are further described hereinbelow with reference to Table 1.

[25504] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1824 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[25505] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1825 (VGAM1825) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[25506] VGAM1825 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1825 was detected is described hereinabove with reference to Figs. 2-8.

[25507] VGAM1825 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Vaccinia virus.
VGAM1825 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the

human genome.

[25508] VGAM1825 gene, herein designated VGAM GENE, encodes a VGAM1825 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1825 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1825 precursor RNA is designated SEQ ID:1811, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1811 is located at position 34526 relative to the genome of Vaccinia virus.

[25509] VGAM1825 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1825 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25510] An enzyme complex designated DICER COMPLEX, dices

the VGAM1825 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1825 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 66%) nucleotide sequence of VGAM1825 RNA is designated SEQ ID:4536, and is provided hereinbelow with reference to the sequence listing part.

[25511] VGAM1825 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1825 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1825 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25512] VGAM1825 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1825 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1825 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1825 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1825 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25513] The complementary binding of VGAM1825 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1825 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM1825 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1825 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[25514] It is appreciated that VGAM1825 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1825 host target genes. The mRNA of each one of this plurality of VGAM1825 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1825 RNA, herein designated VGAM RNA, and which when bound by VGAM1825 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1825 host target proteins.

[25515] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1825 gene, herein designated VGAM GENE, on one or more VGAM1825 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25516] It is yet further appreciated that a function of VGAM1825 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1825 include diagnosis, prevention and treatment of viral infection by Vaccinia virus. Specific functions, and accordingly utilities, of VGAM1825 correlate with, and may be deduced from, the identity of the host target genes which VGAM1825 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[25517] Nucleotide sequences of the VGAM1825 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1825 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of

VGAM1825 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1825 are further described hereinbelow with reference to Table 1.

[25518] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1825 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[25519] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1826 (VGAM1826) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[25520] VGAM1826 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1826 was detected is described hereinabove with reference to Figs. 2-8.

[25521] VGAM1826 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Variola virus. VGAM1826 host target gene, herein designated VGAM HOST TARGET

GENE, is a human gene contained in the human genome.

[25522] VGAM1826 gene, herein designated VGAM GENE, encodes a VGAM1826 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1826 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1826 precursor RNA is designated SEQ ID:1812, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1812 is located at position 29285 relative to the genome of Variola virus.

[25523] VGAM1826 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1826 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25524] An enzyme complex designated DICER COMPLEX, dices

the VGAM1826 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1826 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM1826 RNA is designated SEQ ID:4537, and is provided hereinbelow with reference to the sequence listing part.

[25525] VGAM1826 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1826 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1826 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25526] VGAM1826 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1826 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1826 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1826 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1826 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25527] The complementary binding of VGAM1826 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1826 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM1826 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1826 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[25528] It is appreciated that VGAM1826 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1826 host target genes. The mRNA of each one of this plurality of VGAM1826 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1826 RNA, herein designated VGAM RNA, and which when bound by VGAM1826 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1826 host target proteins.

[25529] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1826 gene, herein designated VGAM GENE, on one or more VGAM1826 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25530] It is yet further appreciated that a function of VGAM1826 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1826 include diagnosis, prevention and treatment of viral infection by Variola virus. Specific functions, and accordingly utilities, of VGAM1826 correlate with, and may be deduced from, the identity of the host target genes which VGAM1826 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[25531] Nucleotide sequences of the VGAM1826 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1826 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of

VGAM1826 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1826 are further described hereinbelow with reference to Table 1.

[25532] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1826 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[25533] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1827 (VGAM1827) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[25534] VGAM1827 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1827 was detected is described hereinabove with reference to Figs. 2-8.

[25535] VGAM1827 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rabbit fibroma virus. VGAM1827 host target gene, herein designated VGAM

HOST TARGET GENE, is a human gene contained in the human genome.

[25536] VGAM1827 gene, herein designated VGAM GENE, encodes a VGAM1827 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1827 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1827 precursor RNA is designated SEQ ID:1813, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1813 is located at position 144104 relative to the genome of Rabbit fibroma virus.

[25537] VGAM1827 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1827 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25538] An enzyme complex designated DICER COMPLEX, dices the VGAM1827 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1827 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM1827 RNA is designated SEQ ID:4538, and is provided hereinbelow with reference to the sequence listing part.

[25539] VGAM1827 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1827 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1827 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25540] VGAM1827 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites

located in untranslated regions of VGAM1827 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1827 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1827 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1827 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25541] The complementary binding of VGAM1827 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1827 host target RNA, herein designated VGAM

HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1827 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1827 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[25542] It is appreciated that VGAM1827 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1827 host target genes. The mRNA of each one of this plurality of VGAM1827 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1827 RNA, herein designated VGAM RNA, and which when bound by VGAM1827 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1827 host target proteins.

[25543] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1827 gene, herein designated VGAM GENE, on one or more VGAM1827 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove

with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25544] It is yet further appreciated that a function of VGAM1827 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1827 include diagnosis, prevention and treatment of viral infection by Rabbit fibroma virus. Specific functions, and accordingly utilities, of VGAM1827 correlate with, and may be deduced from, the identity of the host target genes which VGAM1827 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[25545] Nucleotide sequences of the VGAM1827 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1827 RNA, herein designated VGAM RNA, and

a schematic representation of the secondary folding of VGAM1827 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1827 are further described hereinbelow with reference to Table 1.

[25546] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1827 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[25547] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1828 (VGAM1828) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[25548] VGAM1828 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1828 was detected is described hereinabove with reference to Figs. 2-8.

[25549] VGAM1828 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rabbit fibroma virus.

VGAM1828 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[25550] VGAM1828 gene, herein designated VGAM GENE, encodes a VGAM1828 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1828 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1828 precursor RNA is designated SEQ ID:1814, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1814 is located at position 140535 relative to the genome of Rabbit fibroma virus.

[25551] VGAM1828 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1828 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[25552] An enzyme complex designated DICER COMPLEX, dices the VGAM1828 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1828 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM1828 RNA is designated SEQ ID:4539, and is provided hereinbelow with reference to the sequence listing part.

[25553] VGAM1828 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1828 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1828 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25554] VGAM1828 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM1828 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1828 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1828 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1828 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25555] The complementary binding of VGAM1828 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM1828 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1828 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1828 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[25556] It is appreciated that VGAM1828 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1828 host target genes. The mRNA of each one of this plurality of VGAM1828 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1828 RNA, herein designated VGAM RNA, and which when bound by VGAM1828 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1828 host target proteins.

[25557] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1828 gene, herein designated VGAM GENE, on one or more VGAM1828 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25558] It is yet further appreciated that a function of VGAM1828 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1828 include diagnosis, prevention and treatment of viral infection by Rabbit fibroma virus. Specific functions, and accordingly utilities, of VGAM1828 correlate with, and may be deduced from, the identity of the host target genes which VGAM1828 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[25559] Nucleotide sequences of the VGAM1828 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

diced VGAM1828 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1828 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1828 are further described hereinbelow with reference to Table 1.

[25560] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1828 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[25561] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1829 (VGAM1829) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[25562] VGAM1829 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1829 was detected is described hereinabove with reference to Figs. 2-8.

[25563] VGAM1829 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of Rabbit fibroma virus. VGAM1829 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[25564] VGAM1829 gene, herein designated VGAM GENE, encodes a VGAM1829 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1829 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1829 precursor RNA is designated SEQ ID:1815, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1815 is located at position 140030 relative to the genome of Rabbit fibroma virus.

[25565] VGAM1829 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1829 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25566] An enzyme complex designated DICER COMPLEX, dices the VGAM1829 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1829 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM1829 RNA is designated SEQ ID:4540, and is provided hereinbelow with reference to the sequence listing part.

[25567] VGAM1829 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1829 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1829 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25568] VGAM1829 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1829 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1829 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1829 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1829 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25569] The complementary binding of VGAM1829 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM1829 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1829 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1829 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[25570] It is appreciated that VGAM1829 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1829 host target genes. The mRNA of each one of this plurality of VGAM1829 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1829 RNA, herein designated VGAM RNA, and which when bound by VGAM1829 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1829 host target proteins.

[25571] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1829 gene, herein designated VGAM GENE, on one or more VGAM1829 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25572] It is yet further appreciated that a function of VGAM1829 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1829 include diagnosis, prevention and treatment of viral infection by Rabbit fibroma virus. Specific functions, and accordingly utilities, of VGAM1829 correlate with, and may be deduced from, the identity of the host target genes which VGAM1829 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[25573] Nucleotide sequences of the VGAM1829 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the diced VGAM1829 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1829 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1829 are further described hereinbelow with reference to Table 1.

[25574] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1829 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[25575] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1830 (VGAM1830) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[25576] VGAM1830 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1830 was detected is described hereinabove with reference to Figs. 2-8.

[25577] VGAM1830 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Camelpox virus. VGAM1830 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[25578] VGAM1830 gene, herein designated VGAM GENE, encodes a VGAM1830 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1830 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1830 precursor RNA is designated SEQ ID:1816, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1816 is located at position 40729 relative to the genome of Camelpox virus.

[25579] VGAM1830 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1830 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25580] An enzyme complex designated DICER COMPLEX, dices the VGAM1830 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1830 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM1830 RNA is designated SEQ ID:4541, and is provided hereinbelow with reference to the sequence listing part.

[25581] VGAM1830 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1830 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1830 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN COD-

ING and 3UTR respectively.

[25582] VGAM1830 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1830 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1830 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1830 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1830 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25583] The complementary binding of VGAM1830 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1830 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1830 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1830 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[25584] It is appreciated that VGAM1830 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1830 host target genes. The mRNA of each one of this plurality of VGAM1830 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1830 RNA, herein designated VGAM RNA, and which when bound by VGAM1830 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1830 host target proteins.

[25585] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1830 gene, herein designated VGAM GENE, on one

or more VGAM1830 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25586] It is yet further appreciated that a function of VGAM1830 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1830 include diagnosis, prevention and treatment of viral infection by Camelpox virus. Specific functions, and accordingly utilities, of VGAM1830 correlate with, and may be deduced from, the identity of the host target genes which VGAM1830 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[25587] Nucleotide sequences of the VGAM1830 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1830 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1830 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1830 are further described hereinbelow with reference to Table 1.

[25588] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1830 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[25589] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1831 (VGAM1831) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[25590] VGAM1831 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1831 was detected is de-

scribed hereinabove with reference to Figs. 2-8.

[25591] VGAM1831 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Camelpox virus. VGAM1831 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[25592] VGAM1831 gene, herein designated VGAM GENE, encodes a VGAM1831 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1831 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1831 precursor RNA is designated SEQ ID:1817, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1817 is located at position 40965 relative to the genome of Camelpox virus.

[25593] VGAM1831 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1831 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25594] An enzyme complex designated DICER COMPLEX, dices the VGAM1831 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1831 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 61%) nucleotide sequence of VGAM1831 RNA is designated SEQ ID:4542, and is provided hereinbelow with reference to the sequence listing part.

[25595] VGAM1831 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1831 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1831 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and

a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25596] VGAM1831 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1831 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1831 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1831 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1831 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both

3UTR and 5UTR regions.

[25597] The complementary binding of VGAM1831 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1831 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1831 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1831 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[25598] It is appreciated that VGAM1831 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1831 host target genes. The mRNA of each one of this plurality of VGAM1831 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1831 RNA, herein designated VGAM RNA, and which when bound by VGAM1831 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1831 host target proteins.

[25599] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM1831 gene, herein designated VGAM GENE, on one or more VGAM1831 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25600] It is yet further appreciated that a function of VGAM1831 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1831 include diagnosis, prevention and treatment of viral infection by Camelpox virus. Specific functions, and accordingly utilities, of VGAM1831 correlate with, and may be deduced from, the identity of the host target genes which VGAM1831 binds and inhibits, and the function of these host target genes, as elaborated

hereinbelow.

[25601] Nucleotide sequences of the VGAM1831 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1831 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1831 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1831 are further described hereinbelow with reference to Table 1.

[25602] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1831 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[25603] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1832 (VGAM1832) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[25604] VGAM1832 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene.

The method by which VGAM1832 was detected is described hereinabove with reference to Figs. 2-8.

[25605] VGAM1832 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Camelpox virus. VGAM1832 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[25606] VGAM1832 gene, herein designated VGAM GENE, encodes a VGAM1832 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1832 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1832 precursor RNA is designated SEQ ID:1818, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1818 is located at position 38937 relative to the genome of Camelpox virus.

[25607] VGAM1832 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1832 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25608] An enzyme complex designated DICER COMPLEX, dices the VGAM1832 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1832 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 48%) nucleotide sequence of VGAM1832 RNA is designated SEQ ID:4543, and is provided hereinbelow with reference to the sequence listing part.

[25609] VGAM1832 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1832 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1832 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding

gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25610] VGAM1832 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1832 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1832 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1832 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1832 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be lo-

cated in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25611] The complementary binding of VGAM1832 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1832 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1832 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1832 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[25612] It is appreciated that VGAM1832 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1832 host target genes. The mRNA of each one of this plurality of VGAM1832 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1832 RNA, herein designated VGAM RNA, and which when bound by VGAM1832 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1832 host target proteins.

[25613] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM1832 gene, herein designated VGAM GENE, on one or more VGAM1832 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25614] It is yet further appreciated that a function of VGAM1832 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1832 include diagnosis, prevention and treatment of viral infection by Camelpox virus. Specific functions, and accordingly utilities, of VGAM1832 correlate with, and may be deduced from, the identity of the host target genes which VGAM1832 binds and inhibits,

and the function of these host target genes, as elaborated hereinbelow.

[25615] Nucleotide sequences of the VGAM1832 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1832 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1832 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1832 are further described hereinbelow with reference to Table 1.

[25616] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1832 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[25617] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1833 (VGAM1833) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[25618] VGAM1833 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1833 was detected is described hereinabove with reference to Figs. 2-8.

[25619] VGAM1833 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Camelpox virus. VGAM1833 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[25620] VGAM1833 gene, herein designated VGAM GENE, encodes a VGAM1833 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1833 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1833 precursor RNA is designated SEQ ID:1819, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1819 is located at position 38839 relative to the genome of Camelpox virus.

[25621] VGAM1833 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1833 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25622] An enzyme complex designated DICER COMPLEX, dices the VGAM1833 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1833 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM1833 RNA is designated SEQ ID:4544, and is provided hereinbelow with reference to the sequence listing part.

[25623] VGAM1833 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1833 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1833 host target RNA, herein designated VGAM HOST TARGET RNA, comprises

three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25624] VGAM1833 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1833 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1833 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1833 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1833 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an

example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25625] The complementary binding of VGAM1833 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1833 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1833 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1833 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[25626] It is appreciated that VGAM1833 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1833 host target genes. The mRNA of each one of this plurality of VGAM1833 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1833 RNA, herein designated VGAM RNA, and which when bound by VGAM1833 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1833 host target proteins.

[25627] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1833 gene, herein designated VGAM GENE, on one or more VGAM1833 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25628] It is yet further appreciated that a function of VGAM1833 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1833 include diagnosis, prevention and treatment of viral infection by Camelpox virus. Specific functions, and accordingly utilities, of VGAM1833 correlate with, and may be deduced from, the identity of the

host target genes which VGAM1833 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[25629] Nucleotide sequences of the VGAM1833 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1833 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1833 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1833 are further described hereinbelow with reference to Table 1.

[25630] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1833 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[25631] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1834 (VGAM1834) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[25632] VGAM1834 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1834 was detected is described hereinabove with reference to Figs. 2-8.

[25633] VGAM1834 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Camelpox virus. VGAM1834 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[25634] VGAM1834 gene, herein designated VGAM GENE, encodes a VGAM1834 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1834 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1834 precursor RNA is designated SEQ ID:1820, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1820 is located at position 36702 relative to the genome of Camelpox virus.

[25635] VGAM1834 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1834 folded precursor RNA, herein designated VGAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25636] An enzyme complex designated DICER COMPLEX, dices the VGAM1834 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1834 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM1834 RNA is designated SEQ ID:4545, and is provided hereinbelow with reference to the sequence listing part.

[25637] VGAM1834 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1834 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1834 host target RNA,

herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25638] VGAM1834 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1834 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1834 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1834 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1834 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host tar-

get binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25639] The complementary binding of VGAM1834 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1834 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1834 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1834 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[25640] It is appreciated that VGAM1834 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1834 host target genes. The mRNA of each one of this plurality of VGAM1834 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1834 RNA, herein designated VGAM RNA, and which when bound by VGAM1834 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1834 host target proteins.

[25641] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1834 gene, herein designated VGAM GENE, on one or more VGAM1834 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25642] It is yet further appreciated that a function of VGAM1834 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1834 include diagnosis, prevention and treatment of viral infection by Camelpox virus. Specific functions, and accordingly utilities, of VGAM1834 corre-

late with, and may be deduced from, the identity of the host target genes which VGAM1834 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[25643] Nucleotide sequences of the VGAM1834 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1834 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1834 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1834 are further described hereinbelow with reference to Table 1.

[25644] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1834 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[25645] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1835 (VGAM1835) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the

art.

[25646] VGAM1835 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1835 was detected is described hereinabove with reference to Figs. 2-8.

[25647] VGAM1835 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Fowlpox virus. VGAM1835 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[25648] VGAM1835 gene, herein designated VGAM GENE, encodes a VGAM1835 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1835 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1835 precursor RNA is designated SEQ ID:1821, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1821 is located at position 136546 relative to the genome of Fowlpox virus.

[25649] VGAM1835 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1835 folded

precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25650] An enzyme complex designated DICER COMPLEX, dices the VGAM1835 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1835 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM1835 RNA is designated SEQ ID:4546, and is provided hereinbelow with reference to the sequence listing part.

[25651] VGAM1835 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1835 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM1835 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25652] VGAM1835 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1835 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1835 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1835 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1835 host target RNA, herein designated VGAM HOST TARGET RNA.

It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25653] The complementary binding of VGAM1835 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1835 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1835 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1835 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[25654] It is appreciated that VGAM1835 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1835 host target genes. The mRNA of each one of this plurality of VGAM1835 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1835 RNA, herein designated VGAM RNA, and which when bound by VGAM1835 RNA, herein designated VGAM RNA, causes inhibition of translation of

respective one or more VGAM1835 host target proteins.

[25655] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1835 gene, herein designated VGAM GENE, on one or more VGAM1835 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25656] It is yet further appreciated that a function of VGAM1835 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1835 include diagnosis, prevention and treatment of viral infection by Fowlpox virus. Specific

functions, and accordingly utilities, of VGAM1835 correlate with, and may be deduced from, the identity of the host target genes which VGAM1835 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[25657] Nucleotide sequences of the VGAM1835 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1835 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1835 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1835 are further described hereinbelow with reference to Table 1.

[25658] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1835 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[25659] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1836 (VGAM1836) viral gene, which modulates expression of respective host target genes thereof, the func-

tion and utility of which host target genes is known in the art.

[25660] VGAM1836 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1836 was detected is described hereinabove with reference to Figs. 2-8.

[25661] VGAM1836 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Fowlpox virus. VGAM1836 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[25662] VGAM1836 gene, herein designated VGAM GENE, encodes a VGAM1836 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1836 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1836 precursor RNA is designated SEQ ID:1822, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1822 is located at position 140071 relative to the genome of Fowlpox virus.

[25663] VGAM1836 precursor RNA, herein designated VGAM PRE-

CURSOR RNA, folds onto itself, forming VGAM1836 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25664] An enzyme complex designated DICER COMPLEX, dices the VGAM1836 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1836 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM1836 RNA is designated SEQ ID:4547, and is provided hereinbelow with reference to the sequence listing part.

[25665] VGAM1836 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM1836 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1836 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25666] VGAM1836 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1836 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1836 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1836 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1836 host

target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25667] The complementary binding of VGAM1836 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1836 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1836 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1836 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[25668] It is appreciated that VGAM1836 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1836 host target genes. The mRNA of each one of this plurality of VGAM1836 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1836 RNA, herein designated VGAM RNA, and which when bound by VGAM1836 RNA, herein

designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1836 host target proteins.

[25669] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1836 gene, herein designated VGAM GENE, on one or more VGAM1836 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25670] It is yet further appreciated that a function of VGAM1836 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1836 include diagnosis, prevention and

treatment of viral infection by Fowlpox virus. Specific functions, and accordingly utilities, of VGAM1836 correlate with, and may be deduced from, the identity of the host target genes which VGAM1836 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[25671] Nucleotide sequences of the VGAM1836 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1836 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1836 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1836 are further described hereinbelow with reference to Table 1.

[25672] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1836 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[25673] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1837 (VGAM1837) viral gene, which modulates ex-

pression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[25674] VGAM1837 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1837 was detected is described hereinabove with reference to Figs. 2-8.

[25675] VGAM1837 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Fowlpox virus. VGAM1837 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[25676] VGAM1837 gene, herein designated VGAM GENE, encodes a VGAM1837 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1837 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1837 precursor RNA is designated SEQ ID:1823, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1823 is located at position 133890 relative to the genome of Fowlpox virus.

[25677] VGAM1837 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1837 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25678] An enzyme complex designated DICER COMPLEX, dices the VGAM1837 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1837 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM1837 RNA is designated SEQ ID:4548, and is provided hereinbelow with reference to the sequence listing part.

[25679] VGAM1837 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1837 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1837 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25680] VGAM1837 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1837 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1837 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1837 RNA, herein designated VGAM RNA, may have a different number of host target

binding sites in untranslated regions of a VGAM1837 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25681] The complementary binding of VGAM1837 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1837 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1837 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1837 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[25682] It is appreciated that VGAM1837 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1837 host target genes. The mRNA of each one of this plurality of VGAM1837 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1837 RNA, herein designated VGAM

RNA, and which when bound by VGAM1837 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1837 host target proteins.

[25683] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1837 gene, herein designated VGAM GENE, on one or more VGAM1837 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25684] It is yet further appreciated that a function of VGAM1837 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM1837 include diagnosis, prevention and treatment of viral infection by Fowlpox virus. Specific functions, and accordingly utilities, of VGAM1837 correlate with, and may be deduced from, the identity of the host target genes which VGAM1837 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[25685] Nucleotide sequences of the VGAM1837 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1837 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1837 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1837 are further described hereinbelow with reference to Table 1.

[25686] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1837 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[25687] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Mes-

senger 1838 (VGAM1838) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[25688] VGAM1838 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1838 was detected is described hereinabove with reference to Figs. 2-8.

[25689] VGAM1838 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Fowlpox virus. VGAM1838 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[25690] VGAM1838 gene, herein designated VGAM GENE, encodes a VGAM1838 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1838 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1838 precursor RNA is designated SEQ ID:1824, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1824 is located at position

131052 relative to the genome of Fowlpox virus.

[25691] VGAM1838 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1838 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25692] An enzyme complex designated DICER COMPLEX, dices the VGAM1838 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1838 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 50%) nucleotide sequence of VGAM1838 RNA is designated SEQ ID:4549, and is provided hereinbelow with reference to the sequence listing part.

[25693] VGAM1838 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1838 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1838 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25694] VGAM1838 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1838 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1838 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1838 RNA, herein designated

VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1838 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25695] The complementary binding of VGAM1838 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1838 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1838 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1838 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[25696] It is appreciated that VGAM1838 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1838 host target genes. The mRNA of each one of this plurality of VGAM1838 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM1838 RNA, herein designated VGAM RNA, and which when bound by VGAM1838 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1838 host target proteins.

[25697] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1838 gene, herein designated VGAM GENE, on one or more VGAM1838 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25698] It is yet further appreciated that a function of VGAM1838 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1838 include diagnosis, prevention and treatment of viral infection by Fowlpox virus. Specific functions, and accordingly utilities, of VGAM1838 correlate with, and may be deduced from, the identity of the host target genes which VGAM1838 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[25699] Nucleotide sequences of the VGAM1838 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1838 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1838 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1838 are further described hereinbelow with reference to Table 1.

[25700] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1838 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[25701] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present

invention, referred to here as Viral Genomic Address Messenger 1839 (VGAM1839) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[25702] VGAM1839 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1839 was detected is described hereinabove with reference to Figs. 2-8.

[25703] VGAM1839 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Fowlpox virus.
VGAM1839 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[25704] VGAM1839 gene, herein designated VGAM GENE, encodes a VGAM1839 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1839 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1839 precursor RNA is designated SEQ ID:1825, and is provided hereinbelow with reference to the sequence listing part. Nu-

cleotide sequence SEQ ID:1825 is located at position 139769 relative to the genome of Fowlpox virus.

[25705] VGAM1839 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1839 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25706] An enzyme complex designated DICER COMPLEX, dices the VGAM1839 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1839 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM1839 RNA is designated SEQ ID:4550, and is provided hereinbelow with reference to the sequence

listing part.

[25707] VGAM1839 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1839 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1839 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25708] VGAM1839 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1839 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1839 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not

meant to be limiting VGAM1839 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1839 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25709] The complementary binding of VGAM1839 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1839 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1839 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1839 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[25710] It is appreciated that VGAM1839 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1839 host target genes. The mRNA of each one of this plurality of VGAM1839 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM1839 RNA, herein designated VGAM RNA, and which when bound by VGAM1839 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1839 host target proteins.

[25711] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1839 gene, herein designated VGAM GENE, on one or more VGAM1839 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25712] It is yet further appreciated that a function of VGAM1839

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1839 include diagnosis, prevention and treatment of viral infection by Fowlpox virus. Specific functions, and accordingly utilities, of VGAM1839 correlate with, and may be deduced from, the identity of the host target genes which VGAM1839 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[25713] Nucleotide sequences of the VGAM1839 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1839 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1839 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1839 are further described hereinbelow with reference to Table 1.

[25714] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1839 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[25715] Fig. 1 further provides a conceptual description of another

novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1840 (VGAM1840) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[25716] VGAM1840 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1840 was detected is described hereinabove with reference to Figs. 2-8.

[25717] VGAM1840 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cowpea mottle virus. VGAM1840 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[25718] VGAM1840 gene, herein designated VGAM GENE, encodes a VGAM1840 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1840 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1840 precursor RNA is designated SEQ ID:1826, and is provided here-

inbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1826 is located at position 998 relative to the genome of Cowpea mottle virus.

[25719] VGAM1840 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1840 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25720] An enzyme complex designated DICER COMPLEX, dices the VGAM1840 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1840 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM1840 RNA is designated SEQ ID:4551, and

is provided hereinbelow with reference to the sequence listing part.

[25721] VGAM1840 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1840 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1840 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25722] VGAM1840 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1840 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1840 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites

shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1840 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1840 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25723] The complementary binding of VGAM1840 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1840 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1840 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1840 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[25724] It is appreciated that VGAM1840 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1840 host target genes. The mRNA of each one of this plurality of VGAM1840 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1840 RNA, herein designated VGAM RNA, and which when bound by VGAM1840 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1840 host target proteins.

[25725] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1840 gene, herein designated VGAM GENE, on one or more VGAM1840 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25726] It is yet further appreciated that a function of VGAM1840 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1840 include diagnosis, prevention and treatment of viral infection by Cowpea mottle virus. Specific functions, and accordingly utilities, of VGAM1840 correlate with, and may be deduced from, the identity of the host target genes which VGAM1840 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[25727] Nucleotide sequences of the VGAM1840 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1840 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1840 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1840 are further described hereinbelow with reference to Table 1.

[25728] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1840 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[25729] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1841 (VGAM1841) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[25730] VGAM1841 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1841 was detected is described hereinabove with reference to Figs. 2-8.

[25731] VGAM1841 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cowpea mottle virus. VGAM1841 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[25732] VGAM1841 gene, herein designated VGAM GENE, encodes a VGAM1841 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1841 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1841 precur-

sor RNA is designated SEQ ID:1827, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1827 is located at position 695 relative to the genome of Cowpea mottle virus.

[25733] VGAM1841 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1841 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25734] An enzyme complex designated DICER COMPLEX, dices the VGAM1841 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1841 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 81%) nucleotide se-

quence of VGAM1841 RNA is designated SEQ ID:4552, and is provided hereinbelow with reference to the sequence listing part.

[25735] VGAM1841 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1841 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1841 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25736] VGAM1841 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1841 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1841 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is ap-

preciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1841 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1841 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25737] The complementary binding of VGAM1841 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1841 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1841 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1841 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[25738] It is appreciated that VGAM1841 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1841 host target genes. The mRNA of

each one of this plurality of VGAM1841 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1841 RNA, herein designated VGAM RNA, and which when bound by VGAM1841 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1841 host target proteins.

[25739] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1841 gene, herein designated VGAM GENE, on one or more VGAM1841 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science

294,779 (2001)).

[25740] It is yet further appreciated that a function of VGAM1841 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1841 include diagnosis, prevention and treatment of viral infection by Cowpea mottle virus. Specific functions, and accordingly utilities, of VGAM1841 correlate with, and may be deduced from, the identity of the host target genes which VGAM1841 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[25741] Nucleotide sequences of the VGAM1841 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1841 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1841 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1841 are further described hereinbelow with reference to Table 1.

[25742] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1841 RNA, herein designated VGAM RNA, are de-

scribed hereinbelow with reference to Table 2.

[25743] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1842 (VGAM1842) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[25744] VGAM1842 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1842 was detected is described hereinabove with reference to Figs. 2-8.

[25745] VGAM1842 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Chimpanzee cytomegalovirus. VGAM1842 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[25746] VGAM1842 gene, herein designated VGAM GENE, encodes a VGAM1842 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1842 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly

similar to the nucleotide sequence of VGAM1842 precursor RNA is designated SEQ ID:1828, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1828 is located at position 19726 relative to the genome of Chimpanzee cytomegalovirus.

[25747] VGAM1842 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1842 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25748] An enzyme complex designated DICER COMPLEX, dices the VGAM1842 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1842 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 82%) nucleotide sequence of VGAM1842 RNA is designated SEQ ID:4553, and is provided hereinbelow with reference to the sequence listing part.

[25749] VGAM1842 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1842 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1842 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25750] VGAM1842 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1842 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1842 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3

such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1842 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1842 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25751] The complementary binding of VGAM1842 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1842 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1842 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1842 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[25752] It is appreciated that VGAM1842 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1842 host target genes. The mRNA of each one of this plurality of VGAM1842 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1842 RNA, herein designated VGAM RNA, and which when bound by VGAM1842 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1842 host target proteins.

[25753] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1842 gene, herein designated VGAM GENE, on one or more VGAM1842 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25754] It is yet further appreciated that a function of VGAM1842 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1842 include diagnosis, prevention and treatment of viral infection by Chimpanzee cytomegalovirus. Specific functions, and accordingly utilities, of VGAM1842 correlate with, and may be deduced from, the identity of the host target genes which VGAM1842 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[25755] Nucleotide sequences of the VGAM1842 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1842 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1842 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1842 are further described hereinbelow with reference to Table 1.

[25756] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the

complementarity of each of these host target binding sites to VGAM1842 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[25757] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1843 (VGAM1843) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[25758] VGAM1843 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1843 was detected is described hereinabove with reference to Figs. 2-8.

[25759] VGAM1843 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Chimpanzee cytomegalovirus. VGAM1843 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[25760] VGAM1843 gene, herein designated VGAM GENE, encodes a VGAM1843 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1843 precursor RNA,

herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1843 precursor RNA is designated SEQ ID:1829, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1829 is located at position 14213 relative to the genome of Chimpanzee cytomegalovirus.

[25761] VGAM1843 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1843 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25762] An enzyme complex designated DICER COMPLEX, dices the VGAM1843 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1843 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM1843 RNA is designated SEQ ID:4554, and is provided hereinbelow with reference to the sequence listing part.

[25763] VGAM1843 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1843 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1843 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25764] VGAM1843 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1843 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1843 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed

sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1843 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1843 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25765] The complementary binding of VGAM1843 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1843 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1843 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1843 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target

protein is therefore outlined by a broken line.

[25766] It is appreciated that VGAM1843 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1843 host target genes. The mRNA of each one of this plurality of VGAM1843 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1843 RNA, herein designated VGAM RNA, and which when bound by VGAM1843 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1843 host target proteins.

[25767] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1843 gene, herein designated VGAM GENE, on one or more VGAM1843 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25768] It is yet further appreciated that a function of VGAM1843 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1843 include diagnosis, prevention and treatment of viral infection by Chimpanzee cytomegalovirus. Specific functions, and accordingly utilities, of VGAM1843 correlate with, and may be deduced from, the identity of the host target genes which VGAM1843 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[25769] Nucleotide sequences of the VGAM1843 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1843 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1843 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1843 are further described hereinbelow with reference to Table 1.

[25770] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1843 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[25771] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1844 (VGAM1844) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[25772] VGAM1844 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1844 was detected is described hereinabove with reference to Figs. 2-8.

[25773] VGAM1844 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Chimpanzee cytomegalovirus. VGAM1844 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[25774] VGAM1844 gene, herein designated VGAM GENE, encodes a VGAM1844 precursor RNA, herein designated VGAM

PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1844 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1844 precursor RNA is designated SEQ ID:1830, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1830 is located at position 20461 relative to the genome of Chimpanzee cytomegalovirus.

[25775] VGAM1844 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1844 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25776] An enzyme complex designated DICER COMPLEX, dices the VGAM1844 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1844 RNA,

herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM1844 RNA is designated SEQ ID:4555, and is provided hereinbelow with reference to the sequence listing part.

[25777] VGAM1844 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1844 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1844 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25778] VGAM1844 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1844 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM1844 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1844 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1844 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25779] The complementary binding of VGAM1844 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1844 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1844 host target RNA, herein designated VGAM HOST TARGET

RNA, into VGAM1844 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[25780] It is appreciated that VGAM1844 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1844 host target genes. The mRNA of each one of this plurality of VGAM1844 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1844 RNA, herein designated VGAM RNA, and which when bound by VGAM1844 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1844 host target proteins.

[25781] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1844 gene, herein designated VGAM GENE, on one or more VGAM1844 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25782] It is yet further appreciated that a function of VGAM1844 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1844 include diagnosis, prevention and treatment of viral infection by Chimpanzee cytomegalovirus. Specific functions, and accordingly utilities, of VGAM1844 correlate with, and may be deduced from, the identity of the host target genes which VGAM1844 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[25783] Nucleotide sequences of the VGAM1844 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1844 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1844 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1844 are further

described hereinbelow with reference to Table 1.

[25784] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1844 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[25785] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1845 (VGAM1845) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[25786] VGAM1845 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1845 was detected is described hereinabove with reference to Figs. 2-8.

[25787] VGAM1845 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Chimpanzee cytomegalovirus. VGAM1845 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[25788] VGAM1845 gene, herein designated VGAM GENE, encodes a VGAM1845 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1845 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1845 precursor RNA is designated SEQ ID:1831, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1831 is located at position 23567 relative to the genome of Chimpanzee cytomegalovirus.

[25789] VGAM1845 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1845 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25790] An enzyme complex designated DICER COMPLEX, dices

the VGAM1845 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1845 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM1845 RNA is designated SEQ ID:4556, and is provided hereinbelow with reference to the sequence listing part.

[25791] VGAM1845 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1845 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1845 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25792] VGAM1845 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1845 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1845 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1845 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1845 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25793] The complementary binding of VGAM1845 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1845 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM1845 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1845 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[25794] It is appreciated that VGAM1845 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1845 host target genes. The mRNA of each one of this plurality of VGAM1845 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1845 RNA, herein designated VGAM RNA, and which when bound by VGAM1845 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1845 host target proteins.

[25795] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1845 gene, herein designated VGAM GENE, on one or more VGAM1845 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25796] It is yet further appreciated that a function of VGAM1845 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1845 include diagnosis, prevention and treatment of viral infection by Chimpanzee cytomegalovirus. Specific functions, and accordingly utilities, of VGAM1845 correlate with, and may be deduced from, the identity of the host target genes which VGAM1845 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[25797] Nucleotide sequences of the VGAM1845 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1845 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of

VGAM1845 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1845 are further described hereinbelow with reference to Table 1.

[25798] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1845 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[25799] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1846 (VGAM1846) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[25800] VGAM1846 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1846 was detected is described hereinabove with reference to Figs. 2-8.

[25801] VGAM1846 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Chimpanzee cytomegalovirus. VGAM1846 host target gene, herein desig-

nated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[25802] VGAM1846 gene, herein designated VGAM GENE, encodes a VGAM1846 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1846 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1846 precursor RNA is designated SEQ ID:1832, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1832 is located at position 16140 relative to the genome of Chimpanzee cytomegalovirus.

[25803] VGAM1846 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1846 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[25804] An enzyme complex designated DICER COMPLEX, dices the VGAM1846 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1846 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 71%) nucleotide sequence of VGAM1846 RNA is designated SEQ ID:4557, and is provided hereinbelow with reference to the sequence listing part.

[25805] VGAM1846 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1846 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1846 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25806] VGAM1846 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM1846 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1846 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1846 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1846 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25807] The complementary binding of VGAM1846 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM1846 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1846 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1846 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[25808] It is appreciated that VGAM1846 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1846 host target genes. The mRNA of each one of this plurality of VGAM1846 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1846 RNA, herein designated VGAM RNA, and which when bound by VGAM1846 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1846 host target proteins.

[25809] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1846 gene, herein designated VGAM GENE, on one or more VGAM1846 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25810] It is yet further appreciated that a function of VGAM1846 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1846 include diagnosis, prevention and treatment of viral infection by Chimpanzee cytomegalovirus. Specific functions, and accordingly utilities, of VGAM1846 correlate with, and may be deduced from, the identity of the host target genes which VGAM1846 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[25811] Nucleotide sequences of the VGAM1846 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

diced VGAM1846 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1846 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1846 are further described hereinbelow with reference to Table 1.

[25812] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1846 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[25813] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1847 (VGAM1847) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[25814] VGAM1847 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1847 was detected is described hereinabove with reference to Figs. 2-8.

[25815] VGAM1847 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of Sonchus yellow net virus. VGAM1847 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[25816] VGAM1847 gene, herein designated VGAM GENE, encodes a VGAM1847 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1847 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1847 precursor RNA is designated SEQ ID:1833, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1833 is located at position 6650 relative to the genome of Sonchus yellow net virus.

[25817] VGAM1847 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1847 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25818] An enzyme complex designated DICER COMPLEX, dices the VGAM1847 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1847 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM1847 RNA is designated SEQ ID:4558, and is provided hereinbelow with reference to the sequence listing part.

[25819] VGAM1847 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1847 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1847 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25820] VGAM1847 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1847 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1847 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1847 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1847 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25821] The complementary binding of VGAM1847 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM1847 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1847 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1847 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[25822] It is appreciated that VGAM1847 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1847 host target genes. The mRNA of each one of this plurality of VGAM1847 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1847 RNA, herein designated VGAM RNA, and which when bound by VGAM1847 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1847 host target proteins.

[25823] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1847 gene, herein designated VGAM GENE, on one or more VGAM1847 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25824] It is yet further appreciated that a function of VGAM1847 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1847 include diagnosis, prevention and treatment of viral infection by Sonchus yellow net virus. Specific functions, and accordingly utilities, of VGAM1847 correlate with, and may be deduced from, the identity of the host target genes which VGAM1847 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[25825] Nucleotide sequences of the VGAM1847 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the diced VGAM1847 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1847 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1847 are further described hereinbelow with reference to Table 1.

[25826] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1847 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[25827] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1848 (VGAM1848) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[25828] VGAM1848 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1848 was detected is described hereinabove with reference to Figs. 2-8.

[25829] VGAM1848 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Sonchus yellow net virus. VGAM1848 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[25830] VGAM1848 gene, herein designated VGAM GENE, encodes a VGAM1848 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1848 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1848 precursor RNA is designated SEQ ID:1834, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1834 is located at position 9698 relative to the genome of Sonchus yellow net virus.

[25831] VGAM1848 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1848 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25832] An enzyme complex designated DICER COMPLEX, dices the VGAM1848 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1848 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM1848 RNA is designated SEQ ID:4559, and is provided hereinbelow with reference to the sequence listing part.

[25833] VGAM1848 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1848 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1848 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN COD-

ING and 3UTR respectively.

[25834] VGAM1848 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1848 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1848 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1848 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1848 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25835] The complementary binding of VGAM1848 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1848 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1848 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1848 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[25836] It is appreciated that VGAM1848 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1848 host target genes. The mRNA of each one of this plurality of VGAM1848 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1848 RNA, herein designated VGAM RNA, and which when bound by VGAM1848 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1848 host target proteins.

[25837] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1848 gene, herein designated VGAM GENE, on one

or more VGAM1848 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25838] It is yet further appreciated that a function of VGAM1848 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1848 include diagnosis, prevention and treatment of viral infection by Sonchus yellow net virus. Specific functions, and accordingly utilities, of VGAM1848 correlate with, and may be deduced from, the identity of the host target genes which VGAM1848 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[25839] Nucleotide sequences of the VGAM1848 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1848 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1848 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1848 are further described hereinbelow with reference to Table 1.

[25840] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1848 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[25841] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1849 (VGAM1849) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[25842] VGAM1849 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1849 was detected is de-

scribed hereinabove with reference to Figs. 2-8.

[25843] VGAM1849 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cowpea chlorotic mottle virus. VGAM1849 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[25844] VGAM1849 gene, herein designated VGAM GENE, encodes a VGAM1849 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1849 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1849 precursor RNA is designated SEQ ID:1835, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1835 is located at position 1870 relative to the genome of Cowpea chlorotic mottle virus.

[25845] VGAM1849 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1849 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25846] An enzyme complex designated DICER COMPLEX, dices the VGAM1849 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1849 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 56%) nucleotide sequence of VGAM1849 RNA is designated SEQ ID:4560, and is provided hereinbelow with reference to the sequence listing part.

[25847] VGAM1849 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1849 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1849 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and

a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25848] VGAM1849 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1849 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1849 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1849 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1849 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both

3UTR and 5UTR regions.

[25849] The complementary binding of VGAM1849 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1849 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1849 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1849 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[25850] It is appreciated that VGAM1849 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1849 host target genes. The mRNA of each one of this plurality of VGAM1849 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1849 RNA, herein designated VGAM RNA, and which when bound by VGAM1849 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1849 host target proteins.

[25851] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM1849 gene, herein designated VGAM GENE, on one or more VGAM1849 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25852] It is yet further appreciated that a function of VGAM1849 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1849 include diagnosis, prevention and treatment of viral infection by Cowpea chlorotic mottle virus. Specific functions, and accordingly utilities, of VGAM1849 correlate with, and may be deduced from, the identity of the host target genes which VGAM1849 binds and inhibits, and the function of these host target genes,

as elaborated hereinbelow.

[25853] Nucleotide sequences of the VGAM1849 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1849 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1849 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1849 are further described hereinbelow with reference to Table 1.

[25854] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1849 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[25855] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1850 (VGAM1850) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[25856] VGAM1850 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene.

The method by which VGAM1850 was detected is described hereinabove with reference to Figs. 2-8.

[25857] VGAM1850 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Sonchus yellow net virus. VGAM1850 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[25858] VGAM1850 gene, herein designated VGAM GENE, encodes a VGAM1850 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1850 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1850 precursor RNA is designated SEQ ID:1836, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1836 is located at position 1237 relative to the genome of Sonchus yellow net virus.

[25859] VGAM1850 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1850 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25860] An enzyme complex designated DICER COMPLEX, dices the VGAM1850 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1850 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 59%) nucleotide sequence of VGAM1850 RNA is designated SEQ ID:4561, and is provided hereinbelow with reference to the sequence listing part.

[25861] VGAM1850 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1850 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1850 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding

gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25862] VGAM1850 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1850 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1850 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1850 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1850 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be lo-

cated in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25863] The complementary binding of VGAM1850 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1850 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1850 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1850 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[25864] It is appreciated that VGAM1850 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1850 host target genes. The mRNA of each one of this plurality of VGAM1850 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1850 RNA, herein designated VGAM RNA, and which when bound by VGAM1850 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1850 host target proteins.

[25865] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM1850 gene, herein designated VGAM GENE, on one or more VGAM1850 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25866] It is yet further appreciated that a function of VGAM1850 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1850 include diagnosis, prevention and treatment of viral infection by Sonchus yellow net virus. Specific functions, and accordingly utilities, of VGAM1850 correlate with, and may be deduced from, the identity of the host target genes which VGAM1850 binds and in-

hibits, and the function of these host target genes, as elaborated hereinbelow.

[25867] Nucleotide sequences of the VGAM1850 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1850 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1850 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1850 are further described hereinbelow with reference to Table 1.

[25868] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1850 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[25869] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1851 (VGAM1851) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[25870] VGAM1851 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1851 was detected is described hereinabove with reference to Figs. 2-8.

[25871] VGAM1851 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Sonchus yellow net virus. VGAM1851 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[25872] VGAM1851 gene, herein designated VGAM GENE, encodes a VGAM1851 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1851 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1851 precursor RNA is designated SEQ ID:1837, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1837 is located at position 6021 relative to the genome of Sonchus yellow net virus.

[25873] VGAM1851 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1851 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25874] An enzyme complex designated DICER COMPLEX, dices the VGAM1851 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1851 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM1851 RNA is designated SEQ ID:4562, and is provided hereinbelow with reference to the sequence listing part.

[25875] VGAM1851 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1851 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1851 host target RNA, herein designated VGAM HOST TARGET RNA, comprises

three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25876] VGAM1851 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1851 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1851 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1851 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1851 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an

example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25877] The complementary binding of VGAM1851 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1851 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1851 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1851 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[25878] It is appreciated that VGAM1851 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1851 host target genes. The mRNA of each one of this plurality of VGAM1851 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1851 RNA, herein designated VGAM RNA, and which when bound by VGAM1851 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1851 host target proteins.

[25879] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1851 gene, herein designated VGAM GENE, on one or more VGAM1851 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25880] It is yet further appreciated that a function of VGAM1851 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1851 include diagnosis, prevention and treatment of viral infection by Sonchus yellow net virus. Specific functions, and accordingly utilities, of VGAM1851 correlate with, and may be deduced from, the identity of

the host target genes which VGAM1851 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[25881] Nucleotide sequences of the VGAM1851 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1851 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1851 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1851 are further described hereinbelow with reference to Table 1.

[25882] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1851 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[25883] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1852 (VGAM1852) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[25884] VGAM1852 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1852 was detected is described hereinabove with reference to Figs. 2-8.

[25885] VGAM1852 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Sonchus yellow net virus. VGAM1852 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[25886] VGAM1852 gene, herein designated VGAM GENE, encodes a VGAM1852 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1852 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1852 precursor RNA is designated SEQ ID:1838, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1838 is located at position 1792 relative to the genome of Sonchus yellow net virus.

[25887] VGAM1852 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1852 folded precursor RNA, herein designated VGAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25888] An enzyme complex designated DICER COMPLEX, dices the VGAM1852 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1852 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 71%) nucleotide sequence of VGAM1852 RNA is designated SEQ ID:4563, and is provided hereinbelow with reference to the sequence listing part.

[25889] VGAM1852 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1852 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1852 host target RNA,

herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25890] VGAM1852 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1852 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1852 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1852 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1852 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host tar-

get binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25891] The complementary binding of VGAM1852 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1852 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1852 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1852 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[25892] It is appreciated that VGAM1852 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1852 host target genes. The mRNA of each one of this plurality of VGAM1852 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1852 RNA, herein designated VGAM RNA, and which when bound by VGAM1852 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1852 host target proteins.

[25893] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1852 gene, herein designated VGAM GENE, on one or more VGAM1852 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25894] It is yet further appreciated that a function of VGAM1852 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1852 include diagnosis, prevention and treatment of viral infection by Sonchus yellow net virus. Specific functions, and accordingly utilities, of VGAM1852

correlate with, and may be deduced from, the identity of the host target genes which VGAM1852 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[25895] Nucleotide sequences of the VGAM1852 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1852 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1852 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1852 are further described hereinbelow with reference to Table 1.

[25896] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1852 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[25897] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1853 (VGAM1853) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the

art.

[25898] VGAM1853 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1853 was detected is described hereinabove with reference to Figs. 2-8.

[25899] VGAM1853 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Sonchus yellow net virus. VGAM1853 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[25900] VGAM1853 gene, herein designated VGAM GENE, encodes a VGAM1853 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1853 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1853 precursor RNA is designated SEQ ID:1839, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1839 is located at position 3373 relative to the genome of Sonchus yellow net virus.

[25901] VGAM1853 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1853 folded

precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25902] An enzyme complex designated DICER COMPLEX, dices the VGAM1853 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1853 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM1853 RNA is designated SEQ ID:4564, and is provided hereinbelow with reference to the sequence listing part.

[25903] VGAM1853 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1853 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM1853 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25904] VGAM1853 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1853 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1853 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1853 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1853 host target RNA, herein designated VGAM HOST TARGET RNA.

It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25905] The complementary binding of VGAM1853 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1853 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1853 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1853 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[25906] It is appreciated that VGAM1853 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1853 host target genes. The mRNA of each one of this plurality of VGAM1853 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1853 RNA, herein designated VGAM RNA, and which when bound by VGAM1853 RNA, herein designated VGAM RNA, causes inhibition of translation of

respective one or more VGAM1853 host target proteins.

[25907] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1853 gene, herein designated VGAM GENE, on one or more VGAM1853 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25908] It is yet further appreciated that a function of VGAM1853 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1853 include diagnosis, prevention and treatment of viral infection by Sonchus yellow net virus.

Specific functions, and accordingly utilities, of VGAM1853 correlate with, and may be deduced from, the identity of the host target genes which VGAM1853 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[25909] Nucleotide sequences of the VGAM1853 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1853 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1853 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1853 are further described hereinbelow with reference to Table 1.

[25910] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1853 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[25911] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1854 (VGAM1854) viral gene, which modulates expression of respective host target genes thereof, the func-

tion and utility of which host target genes is known in the art.

[25912] VGAM1854 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1854 was detected is described hereinabove with reference to Figs. 2-8.

[25913] VGAM1854 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cowpea chlorotic mottle virus. VGAM1854 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[25914] VGAM1854 gene, herein designated VGAM GENE, encodes a VGAM1854 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1854 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1854 precursor RNA is designated SEQ ID:1840, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1840 is located at position 1253 relative to the genome of Cowpea chlorotic mottle virus.

[25915] VGAM1854 precursor RNA, herein designated VGAM PRE-

CURSOR RNA, folds onto itself, forming VGAM1854 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25916] An enzyme complex designated DICER COMPLEX, dices the VGAM1854 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1854 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 81%) nucleotide sequence of VGAM1854 RNA is designated SEQ ID:4565, and is provided hereinbelow with reference to the sequence listing part.

[25917] VGAM1854 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM1854 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1854 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25918] VGAM1854 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1854 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1854 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1854 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1854 host

target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25919] The complementary binding of VGAM1854 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1854 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1854 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1854 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[25920] It is appreciated that VGAM1854 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1854 host target genes. The mRNA of each one of this plurality of VGAM1854 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1854 RNA, herein designated VGAM RNA, and which when bound by VGAM1854 RNA, herein

designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1854 host target proteins.

[25921] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1854 gene, herein designated VGAM GENE, on one or more VGAM1854 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25922] It is yet further appreciated that a function of VGAM1854 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1854 include diagnosis, prevention and

treatment of viral infection by Cowpea chlorotic mottle virus. Specific functions, and accordingly utilities, of VGAM1854 correlate with, and may be deduced from, the identity of the host target genes which VGAM1854 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[25923] Nucleotide sequences of the VGAM1854 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1854 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1854 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1854 are further described hereinbelow with reference to Table 1.

[25924] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1854 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[25925] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1855 (VGAM1855) viral gene, which modulates ex-

pression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[25926] VGAM1855 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1855 was detected is described hereinabove with reference to Figs. 2-8.

[25927] VGAM1855 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Sonchus yellow net virus. VGAM1855 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[25928] VGAM1855 gene, herein designated VGAM GENE, encodes a VGAM1855 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1855 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1855 precursor RNA is designated SEQ ID:1841, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1841 is located at position 8120 relative to the genome of Sonchus yellow net virus.

[25929] VGAM1855 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1855 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25930] An enzyme complex designated DICER COMPLEX, dices the VGAM1855 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1855 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM1855 RNA is designated SEQ ID:4566, and is provided hereinbelow with reference to the sequence listing part.

[25931] VGAM1855 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1855 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1855 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25932] VGAM1855 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1855 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1855 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1855 RNA, herein designated VGAM RNA, may have a different number of host target

binding sites in untranslated regions of a VGAM1855 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25933] The complementary binding of VGAM1855 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1855 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1855 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1855 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[25934] It is appreciated that VGAM1855 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1855 host target genes. The mRNA of each one of this plurality of VGAM1855 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1855 RNA, herein designated VGAM

RNA, and which when bound by VGAM1855 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1855 host target proteins.

[25935] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1855 gene, herein designated VGAM GENE, on one or more VGAM1855 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25936] It is yet further appreciated that a function of VGAM1855 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM1855 include diagnosis, prevention and treatment of viral infection by Sonchus yellow net virus. Specific functions, and accordingly utilities, of VGAM1855 correlate with, and may be deduced from, the identity of the host target genes which VGAM1855 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[25937] Nucleotide sequences of the VGAM1855 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1855 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1855 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1855 are further described hereinbelow with reference to Table 1.

[25938] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1855 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[25939] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Mes-

senger 1856 (VGAM1856) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[25940] VGAM1856 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1856 was detected is described hereinabove with reference to Figs. 2-8.

[25941] VGAM1856 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rice yellow stunt virus. VGAM1856 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[25942] VGAM1856 gene, herein designated VGAM GENE, encodes a VGAM1856 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1856 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1856 precursor RNA is designated SEQ ID:1842, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1842 is located at position

13503 relative to the genome of Rice yellow stunt virus.

[25943] VGAM1856 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1856 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25944] An enzyme complex designated DICER COMPLEX, dices the VGAM1856 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1856 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM1856 RNA is designated SEQ ID:4567, and is provided hereinbelow with reference to the sequence listing part.

[25945] VGAM1856 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1856 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1856 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25946] VGAM1856 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1856 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1856 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1856 RNA, herein designated

VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1856 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25947] The complementary binding of VGAM1856 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1856 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1856 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1856 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[25948] It is appreciated that VGAM1856 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1856 host target genes. The mRNA of each one of this plurality of VGAM1856 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM1856 RNA, herein designated VGAM RNA, and which when bound by VGAM1856 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1856 host target proteins.

[25949] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1856 gene, herein designated VGAM GENE, on one or more VGAM1856 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25950] It is yet further appreciated that a function of VGAM1856 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1856 include diagnosis, prevention and treatment of viral infection by Rice yellow stunt virus. Specific functions, and accordingly utilities, of VGAM1856 correlate with, and may be deduced from, the identity of the host target genes which VGAM1856 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[25951] Nucleotide sequences of the VGAM1856 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1856 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1856 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1856 are further described hereinbelow with reference to Table 1.

[25952] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1856 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[25953] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present

invention, referred to here as Viral Genomic Address Messenger 1857 (VGAM1857) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[25954] VGAM1857 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1857 was detected is described hereinabove with reference to Figs. 2-8.

[25955] VGAM1857 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rice yellow stunt virus. VGAM1857 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[25956] VGAM1857 gene, herein designated VGAM GENE, encodes a VGAM1857 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1857 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1857 precursor RNA is designated SEQ ID:1843, and is provided hereinbelow with reference to the sequence listing part. Nu-

cleotide sequence SEQ ID:1843 is located at position 9634 relative to the genome of Rice yellow stunt virus.

[25957] VGAM1857 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1857 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25958] An enzyme complex designated DICER COMPLEX, dices the VGAM1857 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1857 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM1857 RNA is designated SEQ ID:4568, and is provided hereinbelow with reference to the sequence

listing part.

[25959] VGAM1857 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1857 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1857 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25960] VGAM1857 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1857 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1857 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not

meant to be limiting VGAM1857 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1857 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25961] The complementary binding of VGAM1857 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1857 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1857 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1857 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[25962] It is appreciated that VGAM1857 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1857 host target genes. The mRNA of each one of this plurality of VGAM1857 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM1857 RNA, herein designated VGAM RNA, and which when bound by VGAM1857 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1857 host target proteins.

[25963] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1857 gene, herein designated VGAM GENE, on one or more VGAM1857 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25964] It is yet further appreciated that a function of VGAM1857

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1857 include diagnosis, prevention and treatment of viral infection by Rice yellow stunt virus. Specific functions, and accordingly utilities, of VGAM1857 correlate with, and may be deduced from, the identity of the host target genes which VGAM1857 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[25965] Nucleotide sequences of the VGAM1857 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1857 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1857 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1857 are further described hereinbelow with reference to Table 1.

[25966] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1857 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[25967] Fig. 1 further provides a conceptual description of another

novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1858 (VGAM1858) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[25968] VGAM1858 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1858 was detected is described hereinabove with reference to Figs. 2-8.

[25969] VGAM1858 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rice yellow stunt virus. VGAM1858 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[25970] VGAM1858 gene, herein designated VGAM GENE, encodes a VGAM1858 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1858 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1858 precursor RNA is designated SEQ ID:1844, and is provided here-

inbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1844 is located at position 4741 relative to the genome of Rice yellow stunt virus.

[25971] VGAM1858 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1858 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25972] An enzyme complex designated DICER COMPLEX, dices the VGAM1858 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1858 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM1858 RNA is designated SEQ ID:4569, and

is provided hereinbelow with reference to the sequence listing part.

[25973] VGAM1858 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1858 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1858 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25974] VGAM1858 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1858 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1858 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites

shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1858 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1858 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25975] The complementary binding of VGAM1858 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1858 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1858 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1858 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[25976] It is appreciated that VGAM1858 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1858 host target genes. The mRNA of each one of this plurality of VGAM1858 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1858 RNA, herein designated VGAM RNA, and which when bound by VGAM1858 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1858 host target proteins.

[25977] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1858 gene, herein designated VGAM GENE, on one or more VGAM1858 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25978] It is yet further appreciated that a function of VGAM1858 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1858 include diagnosis, prevention and treatment of viral infection by Rice yellow stunt virus. Specific functions, and accordingly utilities, of VGAM1858 correlate with, and may be deduced from, the identity of the host target genes which VGAM1858 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[25979] Nucleotide sequences of the VGAM1858 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1858 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1858 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1858 are further described hereinbelow with reference to Table 1.

[25980] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1858 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[25981] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1859 (VGAM1859) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[25982] VGAM1859 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1859 was detected is described hereinabove with reference to Figs. 2-8.

[25983] VGAM1859 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rice yellow stunt virus. VGAM1859 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[25984] VGAM1859 gene, herein designated VGAM GENE, encodes a VGAM1859 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1859 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1859 precur-

sor RNA is designated SEQ ID:1845, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1845 is located at position 3094 relative to the genome of Rice yellow stunt virus.

[25985] VGAM1859 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1859 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25986] An enzyme complex designated DICER COMPLEX, dices the VGAM1859 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1859 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 59%) nucleotide se-

quence of VGAM1859 RNA is designated SEQ ID:4570, and is provided hereinbelow with reference to the sequence listing part.

[25987] VGAM1859 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1859 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1859 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25988] VGAM1859 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1859 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1859 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is ap-

preciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1859 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1859 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25989] The complementary binding of VGAM1859 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1859 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1859 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1859 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[25990] It is appreciated that VGAM1859 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1859 host target genes. The mRNA of

each one of this plurality of VGAM1859 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1859 RNA, herein designated VGAM RNA, and which when bound by VGAM1859 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1859 host target proteins.

[25991] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1859 gene, herein designated VGAM GENE, on one or more VGAM1859 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science

294,779 (2001)).

[25992] It is yet further appreciated that a function of VGAM1859 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1859 include diagnosis, prevention and treatment of viral infection by Rice yellow stunt virus. Specific functions, and accordingly utilities, of VGAM1859 correlate with, and may be deduced from, the identity of the host target genes which VGAM1859 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[25993] Nucleotide sequences of the VGAM1859 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1859 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1859 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1859 are further described hereinbelow with reference to Table 1.

[25994] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1859 RNA, herein designated VGAM RNA, are de-

scribed hereinbelow with reference to Table 2.

[25995] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1860 (VGAM1860) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[25996] VGAM1860 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1860 was detected is described hereinabove with reference to Figs. 2-8.

[25997] VGAM1860 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rice yellow stunt virus. VGAM1860 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[25998] VGAM1860 gene, herein designated VGAM GENE, encodes a VGAM1860 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1860 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly

similar to the nucleotide sequence of VGAM1860 precursor RNA is designated SEQ ID:1846, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1846 is located at position 9805 relative to the genome of Rice yellow stunt virus.

[25999] VGAM1860 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1860 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26000] An enzyme complex designated DICER COMPLEX, dices the VGAM1860 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1860 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 84%) nucleotide sequence of VGAM1860 RNA is designated SEQ ID:4571, and is provided hereinbelow with reference to the sequence listing part.

[26001] VGAM1860 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1860 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1860 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26002] VGAM1860 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1860 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1860 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I,

BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1860 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1860 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26003] The complementary binding of VGAM1860 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1860 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1860 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1860 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[26004] It is appreciated that VGAM1860 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM1860 host target genes. The mRNA of each one of this plurality of VGAM1860 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1860 RNA, herein designated VGAM RNA, and which when bound by VGAM1860 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1860 host target proteins.

[26005] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1860 gene, herein designated VGAM GENE, on one or more VGAM1860 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26006] It is yet further appreciated that a function of VGAM1860 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1860 include diagnosis, prevention and treatment of viral infection by Rice yellow stunt virus. Specific functions, and accordingly utilities, of VGAM1860 correlate with, and may be deduced from, the identity of the host target genes which VGAM1860 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[26007] Nucleotide sequences of the VGAM1860 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1860 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1860 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1860 are further described hereinbelow with reference to Table 1.

[26008] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites

to VGAM1860 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[26009] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1861 (VGAM1861) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[26010] VGAM1861 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1861 was detected is described hereinabove with reference to Figs. 2-8.

[26011] VGAM1861 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rice yellow stunt virus. VGAM1861 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[26012] VGAM1861 gene, herein designated VGAM GENE, encodes a VGAM1861 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1861 precursor RNA, herein designated VGAM PRECURSOR RNA, does not en-

code a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1861 precursor RNA is designated SEQ ID:1847, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1847 is located at position 11283 relative to the genome of Rice yellow stunt virus.

[26013] VGAM1861 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1861 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26014] An enzyme complex designated DICER COMPLEX, dices the VGAM1861 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1861 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM1861 RNA is designated SEQ ID:4572, and is provided hereinbelow with reference to the sequence listing part.

[26015] VGAM1861 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1861 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1861 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26016] VGAM1861 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1861 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1861 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3

such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1861 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1861 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26017] The complementary binding of VGAM1861 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1861 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1861 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1861 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[26018] It is appreciated that VGAM1861 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1861 host target genes. The mRNA of each one of this plurality of VGAM1861 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1861 RNA, herein designated VGAM RNA, and which when bound by VGAM1861 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1861 host target proteins.

[26019] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1861 gene, herein designated VGAM GENE, on one or more VGAM1861 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26020] It is yet further appreciated that a function of VGAM1861 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1861 include diagnosis, prevention and treatment of viral infection by Rice yellow stunt virus. Specific functions, and accordingly utilities, of VGAM1861 correlate with, and may be deduced from, the identity of the host target genes which VGAM1861 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[26021] Nucleotide sequences of the VGAM1861 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1861 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1861 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1861 are further described hereinbelow with reference to Table 1.

[26022] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the

complementarity of each of these host target binding sites to VGAM1861 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[26023] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1862 (VGAM1862) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[26024] VGAM1862 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1862 was detected is described hereinabove with reference to Figs. 2-8.

[26025] VGAM1862 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Lactate dehydrogenase-elevating virus. VGAM1862 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[26026] VGAM1862 gene, herein designated VGAM GENE, encodes a VGAM1862 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1862 precursor RNA,

herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1862 precursor RNA is designated SEQ ID:1848, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1848 is located at position 5398 relative to the genome of Lactate dehydrogenase-elevating virus.

[26027] VGAM1862 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1862 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26028] An enzyme complex designated DICER COMPLEX, dices the VGAM1862 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1862 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 82%) nucleotide sequence of VGAM1862 RNA is designated SEQ ID:4573, and is provided hereinbelow with reference to the sequence listing part.

[26029] VGAM1862 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1862 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1862 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26030] VGAM1862 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1862 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1862 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed

sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1862 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1862 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26031] The complementary binding of VGAM1862 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1862 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1862 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1862 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target

protein is therefore outlined by a broken line.

[26032] It is appreciated that VGAM1862 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1862 host target genes. The mRNA of each one of this plurality of VGAM1862 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1862 RNA, herein designated VGAM RNA, and which when bound by VGAM1862 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1862 host target proteins.

[26033] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1862 gene, herein designated VGAM GENE, on one or more VGAM1862 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26034] It is yet further appreciated that a function of VGAM1862 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1862 include diagnosis, prevention and treatment of viral infection by Lactate dehydrogenase-elevating virus. Specific functions, and accordingly utilities, of VGAM1862 correlate with, and may be deduced from, the identity of the host target genes which VGAM1862 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[26035] Nucleotide sequences of the VGAM1862 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1862 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1862 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1862 are further described hereinbelow with reference to Table 1.

[26036] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1862 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[26037] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1863 (VGAM1863) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[26038] VGAM1863 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1863 was detected is described hereinabove with reference to Figs. 2-8.

[26039] VGAM1863 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Callitrichine herpesvirus 3. VGAM1863 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[26040] VGAM1863 gene, herein designated VGAM GENE, encodes a VGAM1863 precursor RNA, herein designated VGAM

PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1863 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1863 precursor RNA is designated SEQ ID:1849, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1849 is located at position 121675 relative to the genome of Callitrichine herpesvirus 3.

[26041] VGAM1863 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1863 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26042] An enzyme complex designated DICER COMPLEX, dices the VGAM1863 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1863 RNA,

herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM1863 RNA is designated SEQ ID:4574, and is provided hereinbelow with reference to the sequence listing part.

[26043] VGAM1863 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1863 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1863 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26044] VGAM1863 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1863 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM1863 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1863 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1863 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26045] The complementary binding of VGAM1863 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1863 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1863 host target RNA, herein designated VGAM HOST TARGET

RNA, into VGAM1863 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[26046] It is appreciated that VGAM1863 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1863 host target genes. The mRNA of each one of this plurality of VGAM1863 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1863 RNA, herein designated VGAM RNA, and which when bound by VGAM1863 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1863 host target proteins.

[26047] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1863 gene, herein designated VGAM GENE, on one or more VGAM1863 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26048] It is yet further appreciated that a function of VGAM1863 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1863 include diagnosis, prevention and treatment of viral infection by Callitrichine herpesvirus 3. Specific functions, and accordingly utilities, of VGAM1863 correlate with, and may be deduced from, the identity of the host target genes which VGAM1863 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[26049] Nucleotide sequences of the VGAM1863 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1863 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1863 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1863 are further

described hereinbelow with reference to Table 1.

[26050] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1863 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[26051] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1864 (VGAM1864) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[26052] VGAM1864 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1864 was detected is described hereinabove with reference to Figs. 2-8.

[26053] VGAM1864 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Callitrichine herpesvirus 3. VGAM1864 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[26054] VGAM1864 gene, herein designated VGAM GENE, encodes a VGAM1864 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1864 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1864 precursor RNA is designated SEQ ID:1850, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1850 is located at position 121062 relative to the genome of Callitrichine herpesvirus 3.

[26055] VGAM1864 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1864 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26056] An enzyme complex designated DICER COMPLEX, dices

the VGAM1864 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1864 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 64%) nucleotide sequence of VGAM1864 RNA is designated SEQ ID:4575, and is provided hereinbelow with reference to the sequence listing part.

[26057] VGAM1864 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1864 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1864 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26058] VGAM1864 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1864 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1864 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1864 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1864 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26059] The complementary binding of VGAM1864 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1864 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM1864 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1864 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[26060] It is appreciated that VGAM1864 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1864 host target genes. The mRNA of each one of this plurality of VGAM1864 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1864 RNA, herein designated VGAM RNA, and which when bound by VGAM1864 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1864 host target proteins.

[26061] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1864 gene, herein designated VGAM GENE, on one or more VGAM1864 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26062] It is yet further appreciated that a function of VGAM1864 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1864 include diagnosis, prevention and treatment of viral infection by Callitrichine herpesvirus 3. Specific functions, and accordingly utilities, of VGAM1864 correlate with, and may be deduced from, the identity of the host target genes which VGAM1864 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[26063] Nucleotide sequences of the VGAM1864 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1864 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of

VGAM1864 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1864 are further described hereinbelow with reference to Table 1.

[26064] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1864 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[26065] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1865 (VGAM1865) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[26066] VGAM1865 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1865 was detected is described hereinabove with reference to Figs. 2-8.

[26067] VGAM1865 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Callitrichine herpesvirus 3. VGAM1865 host target gene, herein designated VGAM

HOST TARGET GENE, is a human gene contained in the human genome.

[26068] VGAM1865 gene, herein designated VGAM GENE, encodes a VGAM1865 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1865 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1865 precursor RNA is designated SEQ ID:1851, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1851 is located at position 122877 relative to the genome of Callitrichine herpesvirus 3.

[26069] VGAM1865 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1865 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[26070] An enzyme complex designated DICER COMPLEX, dices the VGAM1865 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1865 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM1865 RNA is designated SEQ ID:4576, and is provided hereinbelow with reference to the sequence listing part.

[26071] VGAM1865 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1865 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1865 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26072] VGAM1865 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM1865 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1865 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1865 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1865 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26073] The complementary binding of VGAM1865 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM1865 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1865 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1865 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[26074] It is appreciated that VGAM1865 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1865 host target genes. The mRNA of each one of this plurality of VGAM1865 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1865 RNA, herein designated VGAM RNA, and which when bound by VGAM1865 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1865 host target proteins.

[26075] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1865 gene, herein designated VGAM GENE, on one or more VGAM1865 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26076] It is yet further appreciated that a function of VGAM1865 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1865 include diagnosis, prevention and treatment of viral infection by Callitrichine herpesvirus 3. Specific functions, and accordingly utilities, of VGAM1865 correlate with, and may be deduced from, the identity of the host target genes which VGAM1865 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[26077] Nucleotide sequences of the VGAM1865 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

diced VGAM1865 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1865 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1865 are further described hereinbelow with reference to Table 1.

[26078] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1865 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[26079] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1866 (VGAM1866) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[26080] VGAM1866 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1866 was detected is described hereinabove with reference to Figs. 2-8.

[26081] VGAM1866 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of Callitrichine herpesvirus 3. VGAM1866 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[26082] VGAM1866 gene, herein designated VGAM GENE, encodes a VGAM1866 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1866 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1866 precursor RNA is designated SEQ ID:1852, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1852 is located at position 121344 relative to the genome of Callitrichine herpesvirus 3.

[26083] VGAM1866 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1866 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26084] An enzyme complex designated DICER COMPLEX, dices the VGAM1866 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1866 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM1866 RNA is designated SEQ ID:4577, and is provided hereinbelow with reference to the sequence listing part.

[26085] VGAM1866 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1866 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1866 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN COD-

ING and 3UTR respectively.

[26086] VGAM1866 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1866 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1866 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1866 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1866 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26087] The complementary binding of VGAM1866 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1866 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1866 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1866 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[26088] It is appreciated that VGAM1866 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1866 host target genes. The mRNA of each one of this plurality of VGAM1866 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1866 RNA, herein designated VGAM RNA, and which when bound by VGAM1866 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1866 host target proteins.

[26089] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1866 gene, herein designated VGAM GENE, on one

or more VGAM1866 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26090] It is yet further appreciated that a function of VGAM1866 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1866 include diagnosis, prevention and treatment of viral infection by Callitrichine herpesvirus 3. Specific functions, and accordingly utilities, of VGAM1866 correlate with, and may be deduced from, the identity of the host target genes which VGAM1866 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[26091] Nucleotide sequences of the VGAM1866 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1866 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1866 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1866 are further described hereinbelow with reference to Table 1.

[26092] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1866 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[26093] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1867 (VGAM1867) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[26094] VGAM1867 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1867 was detected is de-

scribed hereinabove with reference to Figs. 2-8.

[26095] VGAM1867 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Callitrichine herpesvirus 3. VGAM1867 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[26096] VGAM1867 gene, herein designated VGAM GENE, encodes a VGAM1867 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1867 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1867 precursor RNA is designated SEQ ID:1853, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1853 is located at position 121561 relative to the genome of Callitrichine herpesvirus 3.

[26097] VGAM1867 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1867 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26098] An enzyme complex designated DICER COMPLEX, dices the VGAM1867 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1867 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 71%) nucleotide sequence of VGAM1867 RNA is designated SEQ ID:4578, and is provided hereinbelow with reference to the sequence listing part.

[26099] VGAM1867 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1867 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1867 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding

gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26100] VGAM1867 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1867 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1867 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1867 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1867 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be lo-

cated in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26101] The complementary binding of VGAM1867 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1867 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1867 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1867 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[26102] It is appreciated that VGAM1867 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1867 host target genes. The mRNA of each one of this plurality of VGAM1867 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1867 RNA, herein designated VGAM RNA, and which when bound by VGAM1867 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1867 host target proteins.

[26103] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM1867 gene, herein designated VGAM GENE, on one or more VGAM1867 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26104] It is yet further appreciated that a function of VGAM1867 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1867 include diagnosis, prevention and treatment of viral infection by Callitrichine herpesvirus 3. Specific functions, and accordingly utilities, of VGAM1867 correlate with, and may be deduced from, the identity of the host target genes which VGAM1867 binds and in-

hibits, and the function of these host target genes, as elaborated hereinbelow.

[26105] Nucleotide sequences of the VGAM1867 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1867 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1867 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1867 are further described hereinbelow with reference to Table 1.

[26106] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1867 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[26107] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1868 (VGAM1868) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[26108] VGAM1868 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1868 was detected is described hereinabove with reference to Figs. 2-8.

[26109] VGAM1868 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Callitrichine herpesvirus 3. VGAM1868 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[26110] VGAM1868 gene, herein designated VGAM GENE, encodes a VGAM1868 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1868 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1868 precursor RNA is designated SEQ ID:1854, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1854 is located at position 119545 relative to the genome of Callitrichine herpesvirus 3.

[26111] VGAM1868 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1868 folded precursor RNA, herein designated VGAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26112] An enzyme complex designated DICER COMPLEX, dices the VGAM1868 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1868 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 49%) nucleotide sequence of VGAM1868 RNA is designated SEQ ID:4579, and is provided hereinbelow with reference to the sequence listing part.

[26113] VGAM1868 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1868 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1868 host target RNA,

herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26114] VGAM1868 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1868 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1868 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1868 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1868 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host tar-

get binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26115] The complementary binding of VGAM1868 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1868 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1868 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1868 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[26116] It is appreciated that VGAM1868 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1868 host target genes. The mRNA of each one of this plurality of VGAM1868 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1868 RNA, herein designated VGAM RNA, and which when bound by VGAM1868 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1868 host target proteins.

[26117] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1868 gene, herein designated VGAM GENE, on one or more VGAM1868 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26118] It is yet further appreciated that a function of VGAM1868 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1868 include diagnosis, prevention and treatment of viral infection by Callitrichine herpesvirus 3. Specific functions, and accordingly utilities, of VGAM1868

correlate with, and may be deduced from, the identity of the host target genes which VGAM1868 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[26119] Nucleotide sequences of the VGAM1868 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1868 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1868 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1868 are further described hereinbelow with reference to Table 1.

[26120] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1868 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[26121] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1869 (VGAM1869) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the

art.

[26122] VGAM1869 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1869 was detected is described hereinabove with reference to Figs. 2-8.

[26123] VGAM1869 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine herpesvirus 2. VGAM1869 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[26124] VGAM1869 gene, herein designated VGAM GENE, encodes a VGAM1869 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1869 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1869 precursor RNA is designated SEQ ID:1855, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1855 is located at position 125161 relative to the genome of Equine herpesvirus 2.

[26125] VGAM1869 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1869 folded

precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26126] An enzyme complex designated DICER COMPLEX, dices the VGAM1869 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1869 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM1869 RNA is designated SEQ ID:4580, and is provided hereinbelow with reference to the sequence listing part.

[26127] VGAM1869 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1869 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM1869 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26128] VGAM1869 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1869 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1869 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1869 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1869 host target RNA, herein designated VGAM HOST TARGET RNA.

It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26129] The complementary binding of VGAM1869 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1869 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1869 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1869 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[26130] It is appreciated that VGAM1869 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1869 host target genes. The mRNA of each one of this plurality of VGAM1869 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1869 RNA, herein designated VGAM RNA, and which when bound by VGAM1869 RNA, herein designated VGAM RNA, causes inhibition of translation of

respective one or more VGAM1869 host target proteins.

[26131] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1869 gene, herein designated VGAM GENE, on one or more VGAM1869 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26132] It is yet further appreciated that a function of VGAM1869 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1869 include diagnosis, prevention and treatment of viral infection by Equine herpesvirus 2. Spe-

cific functions, and accordingly utilities, of VGAM1869 correlate with, and may be deduced from, the identity of the host target genes which VGAM1869 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[26133] Nucleotide sequences of the VGAM1869 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1869 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1869 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1869 are further described hereinbelow with reference to Table 1.

[26134] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1869 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[26135] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1870 (VGAM1870) viral gene, which modulates expression of respective host target genes thereof, the func-

tion and utility of which host target genes is known in the art.

[26136] VGAM1870 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1870 was detected is described hereinabove with reference to Figs. 2-8.

[26137] VGAM1870 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Fowlpox virus. VGAM1870 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[26138] VGAM1870 gene, herein designated VGAM GENE, encodes a VGAM1870 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1870 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1870 precursor RNA is designated SEQ ID:1856, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1856 is located at position 190565 relative to the genome of Fowlpox virus.

[26139] VGAM1870 precursor RNA, herein designated VGAM PRE-

CURSOR RNA, folds onto itself, forming VGAM1870 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26140] An enzyme complex designated DICER COMPLEX, dices the VGAM1870 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1870 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM1870 RNA is designated SEQ ID:4581, and is provided hereinbelow with reference to the sequence listing part.

[26141] VGAM1870 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM1870 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1870 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26142] VGAM1870 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1870 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1870 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1870 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1870 host

target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26143] The complementary binding of VGAM1870 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1870 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1870 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1870 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[26144] It is appreciated that VGAM1870 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1870 host target genes. The mRNA of each one of this plurality of VGAM1870 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1870 RNA, herein designated VGAM RNA, and which when bound by VGAM1870 RNA, herein

designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1870 host target proteins.

[26145] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1870 gene, herein designated VGAM GENE, on one or more VGAM1870 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26146] It is yet further appreciated that a function of VGAM1870 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1870 include diagnosis, prevention and

treatment of viral infection by Fowlpox virus. Specific functions, and accordingly utilities, of VGAM1870 correlate with, and may be deduced from, the identity of the host target genes which VGAM1870 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[26147] Nucleotide sequences of the VGAM1870 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1870 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1870 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1870 are further described hereinbelow with reference to Table 1.

[26148] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1870 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[26149] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1871 (VGAM1871) viral gene, which modulates ex-

pression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[26150] VGAM1871 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1871 was detected is described hereinabove with reference to Figs. 2-8.

[26151] VGAM1871 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Fowlpox virus. VGAM1871 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[26152] VGAM1871 gene, herein designated VGAM GENE, encodes a VGAM1871 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1871 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1871 precursor RNA is designated SEQ ID:1857, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1857 is located at position 195331 relative to the genome of Fowlpox virus.

[26153] VGAM1871 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1871 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26154] An enzyme complex designated DICER COMPLEX, dices the VGAM1871 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1871 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide sequence of VGAM1871 RNA is designated SEQ ID:4582, and is provided hereinbelow with reference to the sequence listing part.

[26155] VGAM1871 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1871 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1871 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26156] VGAM1871 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1871 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1871 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1871 RNA, herein designated VGAM RNA, may have a different number of host target

binding sites in untranslated regions of a VGAM1871 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26157] The complementary binding of VGAM1871 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1871 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1871 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1871 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[26158] It is appreciated that VGAM1871 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1871 host target genes. The mRNA of each one of this plurality of VGAM1871 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1871 RNA, herein designated VGAM

RNA, and which when bound by VGAM1871 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1871 host target proteins.

[26159] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1871 gene, herein designated VGAM GENE, on one or more VGAM1871 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26160] It is yet further appreciated that a function of VGAM1871 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM1871 include diagnosis, prevention and treatment of viral infection by Fowlpox virus. Specific functions, and accordingly utilities, of VGAM1871 correlate with, and may be deduced from, the identity of the host target genes which VGAM1871 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[26161] Nucleotide sequences of the VGAM1871 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1871 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1871 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1871 are further described hereinbelow with reference to Table 1.

[26162] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1871 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[26163] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Mes-

senger 1872 (VGAM1872) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[26164] VGAM1872 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1872 was detected is described hereinabove with reference to Figs. 2-8.

[26165] VGAM1872 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Fowlpox virus. VGAM1872 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[26166] VGAM1872 gene, herein designated VGAM GENE, encodes a VGAM1872 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1872 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1872 precursor RNA is designated SEQ ID:1858, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1858 is located at position

190660 relative to the genome of Fowlpox virus.

[26167] VGAM1872 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1872 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26168] An enzyme complex designated DICER COMPLEX, dices the VGAM1872 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1872 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM1872 RNA is designated SEQ ID:4583, and is provided hereinbelow with reference to the sequence listing part.

[26169] VGAM1872 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1872 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1872 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26170] VGAM1872 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1872 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1872 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1872 RNA, herein designated

VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1872 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26171] The complementary binding of VGAM1872 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1872 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1872 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1872 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[26172] It is appreciated that VGAM1872 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1872 host target genes. The mRNA of each one of this plurality of VGAM1872 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM1872 RNA, herein designated VGAM RNA, and which when bound by VGAM1872 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1872 host target proteins.

[26173] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1872 gene, herein designated VGAM GENE, on one or more VGAM1872 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26174] It is yet further appreciated that a function of VGAM1872 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1872 include diagnosis, prevention and treatment of viral infection by Fowlpox virus. Specific functions, and accordingly utilities, of VGAM1872 correlate with, and may be deduced from, the identity of the host target genes which VGAM1872 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[26175] Nucleotide sequences of the VGAM1872 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1872 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1872 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1872 are further described hereinbelow with reference to Table 1.

[26176] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1872 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[26177] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present

invention, referred to here as Viral Genomic Address Messenger 1873 (VGAM1873) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[26178] VGAM1873 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1873 was detected is described hereinabove with reference to Figs. 2-8.

[26179] VGAM1873 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Fowlpox virus. VGAM1873 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[26180] VGAM1873 gene, herein designated VGAM GENE, encodes a VGAM1873 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1873 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1873 precursor RNA is designated SEQ ID:1859, and is provided hereinbelow with reference to the sequence listing part. Nu-

cleotide sequence SEQ ID:1859 is located at position 188015 relative to the genome of Fowlpox virus.

[26181] VGAM1873 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1873 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26182] An enzyme complex designated DICER COMPLEX, dices the VGAM1873 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1873 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 64%) nucleotide sequence of VGAM1873 RNA is designated SEQ ID:4584, and is provided hereinbelow with reference to the sequence

listing part.

[26183] VGAM1873 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1873 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1873 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26184] VGAM1873 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1873 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1873 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not

meant to be limiting VGAM1873 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1873 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26185] The complementary binding of VGAM1873 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1873 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1873 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1873 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[26186] It is appreciated that VGAM1873 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1873 host target genes. The mRNA of each one of this plurality of VGAM1873 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM1873 RNA, herein designated VGAM RNA, and which when bound by VGAM1873 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1873 host target proteins.

[26187] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1873 gene, herein designated VGAM GENE, on one or more VGAM1873 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26188] It is yet further appreciated that a function of VGAM1873

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1873 include diagnosis, prevention and treatment of viral infection by Fowlpox virus. Specific functions, and accordingly utilities, of VGAM1873 correlate with, and may be deduced from, the identity of the host target genes which VGAM1873 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[26189] Nucleotide sequences of the VGAM1873 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1873 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1873 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1873 are further described hereinbelow with reference to Table 1.

[26190] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1873 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[26191] Fig. 1 further provides a conceptual description of another

novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1874 (VGAM1874) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[26192] VGAM1874 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1874 was detected is described hereinabove with reference to Figs. 2-8.

[26193] VGAM1874 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Fowlpox virus. VGAM1874 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[26194] VGAM1874 gene, herein designated VGAM GENE, encodes a VGAM1874 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1874 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1874 precursor RNA is designated SEQ ID:1860, and is provided here-

inbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1860 is located at position 196857 relative to the genome of Fowlpox virus.

[26195] VGAM1874 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1874 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26196] An enzyme complex designated DICER COMPLEX, dices the VGAM1874 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1874 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM1874 RNA is designated SEQ ID:4585, and

is provided hereinbelow with reference to the sequence listing part.

[26197] VGAM1874 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1874 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1874 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26198] VGAM1874 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1874 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1874 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites

shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1874 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1874 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26199] The complementary binding of VGAM1874 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1874 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1874 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1874 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[26200] It is appreciated that VGAM1874 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1874 host target genes. The mRNA of each one of this plurality of VGAM1874 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1874 RNA, herein designated VGAM RNA, and which when bound by VGAM1874 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1874 host target proteins.

[26201] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1874 gene, herein designated VGAM GENE, on one or more VGAM1874 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26202] It is yet further appreciated that a function of VGAM1874 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1874 include diagnosis, prevention and treatment of viral infection by Fowlpox virus. Specific functions, and accordingly utilities, of VGAM1874 correlate with, and may be deduced from, the identity of the host target genes which VGAM1874 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[26203] Nucleotide sequences of the VGAM1874 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1874 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1874 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1874 are further described hereinbelow with reference to Table 1.

[26204] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1874 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[26205] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1875 (VGAM1875) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[26206] VGAM1875 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1875 was detected is described hereinabove with reference to Figs. 2-8.

[26207] VGAM1875 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Fowlpox virus.
VGAM1875 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[26208] VGAM1875 gene, herein designated VGAM GENE, encodes a VGAM1875 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1875 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1875 precur-

sor RNA is designated SEQ ID:1861, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1861 is located at position 187831 relative to the genome of Fowlpox virus.

[26209] VGAM1875 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1875 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26210] An enzyme complex designated DICER COMPLEX, dices the VGAM1875 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1875 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 62%) nucleotide se-

quence of VGAM1875 RNA is designated SEQ ID:4586, and is provided hereinbelow with reference to the sequence listing part.

[26211] VGAM1875 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1875 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1875 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26212] VGAM1875 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1875 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1875 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is ap-

preciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1875 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1875 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26213] The complementary binding of VGAM1875 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1875 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1875 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1875 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[26214] It is appreciated that VGAM1875 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1875 host target genes. The mRNA of

each one of this plurality of VGAM1875 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1875 RNA, herein designated VGAM RNA, and which when bound by VGAM1875 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1875 host target proteins.

[26215] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1875 gene, herein designated VGAM GENE, on one or more VGAM1875 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science

294,779 (2001)).

[26216] It is yet further appreciated that a function of VGAM1875 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1875 include diagnosis, prevention and treatment of viral infection by Fowlpox virus. Specific functions, and accordingly utilities, of VGAM1875 correlate with, and may be deduced from, the identity of the host target genes which VGAM1875 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[26217] Nucleotide sequences of the VGAM1875 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1875 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1875 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1875 are further described hereinbelow with reference to Table 1.

[26218] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1875 RNA, herein designated VGAM RNA, are de-

scribed hereinbelow with reference to Table 2.

[26219] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1876 (VGAM1876) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[26220] VGAM1876 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1876 was detected is described hereinabove with reference to Figs. 2-8.

[26221] VGAM1876 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Fowlpox virus. VGAM1876 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[26222] VGAM1876 gene, herein designated VGAM GENE, encodes a VGAM1876 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1876 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly

similar to the nucleotide sequence of VGAM1876 precursor RNA is designated SEQ ID:1862, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1862 is located at position 194761 relative to the genome of Fowlpox virus.

[26223] VGAM1876 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1876 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26224] An enzyme complex designated DICER COMPLEX, dices the VGAM1876 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1876 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 41%) nucleotide sequence of VGAM1876 RNA is designated SEQ ID:4587, and is provided hereinbelow with reference to the sequence listing part.

[26225] VGAM1876 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1876 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1876 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26226] VGAM1876 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1876 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1876 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I,

BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1876 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1876 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26227] The complementary binding of VGAM1876 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1876 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1876 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1876 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[26228] It is appreciated that VGAM1876 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM1876 host target genes. The mRNA of each one of this plurality of VGAM1876 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1876 RNA, herein designated VGAM RNA, and which when bound by VGAM1876 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1876 host target proteins.

[26229] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1876 gene, herein designated VGAM GENE, on one or more VGAM1876 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26230] It is yet further appreciated that a function of VGAM1876 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1876 include diagnosis, prevention and treatment of viral infection by Fowlpox virus. Specific functions, and accordingly utilities, of VGAM1876 correlate with, and may be deduced from, the identity of the host target genes which VGAM1876 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[26231] Nucleotide sequences of the VGAM1876 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1876 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1876 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1876 are further described hereinbelow with reference to Table 1.

[26232] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites

to VGAM1876 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[26233] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1877 (VGAM1877) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[26234] VGAM1877 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1877 was detected is described hereinabove with reference to Figs. 2-8.

[26235] VGAM1877 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Fowlpox virus. VGAM1877 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[26236] VGAM1877 gene, herein designated VGAM GENE, encodes a VGAM1877 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1877 precursor RNA, herein designated VGAM PRECURSOR RNA, does not en-

code a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1877 precursor RNA is designated SEQ ID:1863, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1863 is located at position 184855 relative to the genome of Fowlpox virus.

[26237] VGAM1877 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1877 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26238] An enzyme complex designated DICER COMPLEX, dices the VGAM1877 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1877 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM1877 RNA is designated SEQ ID:4588, and is provided hereinbelow with reference to the sequence listing part.

[26239] VGAM1877 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1877 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1877 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26240] VGAM1877 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1877 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1877 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3

such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1877 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1877 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26241] The complementary binding of VGAM1877 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1877 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1877 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1877 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[26242] It is appreciated that VGAM1877 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1877 host target genes. The mRNA of each one of this plurality of VGAM1877 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1877 RNA, herein designated VGAM RNA, and which when bound by VGAM1877 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1877 host target proteins.

[26243] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1877 gene, herein designated VGAM GENE, on one or more VGAM1877 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26244] It is yet further appreciated that a function of VGAM1877 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1877 include diagnosis, prevention and treatment of viral infection by Fowlpox virus. Specific functions, and accordingly utilities, of VGAM1877 correlate with, and may be deduced from, the identity of the host target genes which VGAM1877 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[26245] Nucleotide sequences of the VGAM1877 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1877 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1877 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1877 are further described hereinbelow with reference to Table 1.

[26246] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the

complementarity of each of these host target binding sites to VGAM1877 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[26247] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1878 (VGAM1878) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[26248] VGAM1878 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1878 was detected is described hereinabove with reference to Figs. 2-8.

[26249] VGAM1878 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Bovine respiratory syncytial virus. VGAM1878 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[26250] VGAM1878 gene, herein designated VGAM GENE, encodes a VGAM1878 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1878 precursor RNA,

herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1878 precursor RNA is designated SEQ ID:1864, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1864 is located at position 7295 relative to the genome of Bovine respiratory syncytial virus.

[26251] VGAM1878 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1878 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26252] An enzyme complex designated DICER COMPLEX, dices the VGAM1878 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1878 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 84%) nucleotide sequence of VGAM1878 RNA is designated SEQ ID:4589, and is provided hereinbelow with reference to the sequence listing part.

[26253] VGAM1878 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1878 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1878 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26254] VGAM1878 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1878 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1878 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed

sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1878 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1878 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26255] The complementary binding of VGAM1878 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1878 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1878 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1878 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target

protein is therefore outlined by a broken line.

[26256] It is appreciated that VGAM1878 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1878 host target genes. The mRNA of each one of this plurality of VGAM1878 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1878 RNA, herein designated VGAM RNA, and which when bound by VGAM1878 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1878 host target proteins.

[26257] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1878 gene, herein designated VGAM GENE, on one or more VGAM1878 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26258] It is yet further appreciated that a function of VGAM1878 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1878 include diagnosis, prevention and treatment of viral infection by Bovine respiratory syncytial virus. Specific functions, and accordingly utilities, of VGAM1878 correlate with, and may be deduced from, the identity of the host target genes which VGAM1878 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[26259] Nucleotide sequences of the VGAM1878 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1878 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1878 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1878 are further described hereinbelow with reference to Table 1.

[26260] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1878 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[26261] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1879 (VGAM1879) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[26262] VGAM1879 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1879 was detected is described hereinabove with reference to Figs. 2-8.

[26263] VGAM1879 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Bovine respiratory syncytial virus. VGAM1879 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[26264] VGAM1879 gene, herein designated VGAM GENE, encodes a VGAM1879 precursor RNA, herein designated VGAM

PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1879 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1879 precursor RNA is designated SEQ ID:1865, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1865 is located at position 5455 relative to the genome of Bovine respiratory syncytial virus.

[26265] VGAM1879 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1879 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26266] An enzyme complex designated DICER COMPLEX, dices the VGAM1879 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1879 RNA,

herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 57%) nucleotide sequence of VGAM1879 RNA is designated SEQ ID:4590, and is provided hereinbelow with reference to the sequence listing part.

[26267] VGAM1879 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1879 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1879 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26268] VGAM1879 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1879 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM1879 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1879 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1879 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26269] The complementary binding of VGAM1879 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1879 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1879 host target RNA, herein designated VGAM HOST TARGET

RNA, into VGAM1879 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[26270] It is appreciated that VGAM1879 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1879 host target genes. The mRNA of each one of this plurality of VGAM1879 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1879 RNA, herein designated VGAM RNA, and which when bound by VGAM1879 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1879 host target proteins.

[26271] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1879 gene, herein designated VGAM GENE, on one or more VGAM1879 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26272] It is yet further appreciated that a function of VGAM1879 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1879 include diagnosis, prevention and treatment of viral infection by Bovine respiratory syncytial virus. Specific functions, and accordingly utilities, of VGAM1879 correlate with, and may be deduced from, the identity of the host target genes which VGAM1879 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[26273] Nucleotide sequences of the VGAM1879 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1879 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1879 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1879 are further

described hereinbelow with reference to Table 1.

[26274] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1879 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[26275] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1880 (VGAM1880) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[26276] VGAM1880 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1880 was detected is described hereinabove with reference to Figs. 2-8.

[26277] VGAM1880 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Bovine respiratory syncytial virus. VGAM1880 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[26278] VGAM1880 gene, herein designated VGAM GENE, encodes a VGAM1880 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1880 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1880 precursor RNA is designated SEQ ID:1866, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1866 is located at position 14933 relative to the genome of Bovine respiratory syncytial virus.

[26279] VGAM1880 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1880 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26280] An enzyme complex designated DICER COMPLEX, dices

the VGAM1880 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1880 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide sequence of VGAM1880 RNA is designated SEQ ID:4591, and is provided hereinbelow with reference to the sequence listing part.

[26281] VGAM1880 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1880 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1880 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26282] VGAM1880 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1880 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1880 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1880 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1880 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26283] The complementary binding of VGAM1880 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1880 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM1880 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1880 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[26284] It is appreciated that VGAM1880 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1880 host target genes. The mRNA of each one of this plurality of VGAM1880 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1880 RNA, herein designated VGAM RNA, and which when bound by VGAM1880 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1880 host target proteins.

[26285] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1880 gene, herein designated VGAM GENE, on one or more VGAM1880 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26286] It is yet further appreciated that a function of VGAM1880 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1880 include diagnosis, prevention and treatment of viral infection by Bovine respiratory syncytial virus. Specific functions, and accordingly utilities, of VGAM1880 correlate with, and may be deduced from, the identity of the host target genes which VGAM1880 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[26287] Nucleotide sequences of the VGAM1880 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1880 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of

VGAM1880 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1880 are further described hereinbelow with reference to Table 1.

[26288] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1880 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[26289] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1881 (VGAM1881) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[26290] VGAM1881 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1881 was detected is described hereinabove with reference to Figs. 2-8.

[26291] VGAM1881 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Bovine respiratory syncytial virus. VGAM1881 host target gene, herein desig-

nated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[26292] VGAM1881 gene, herein designated VGAM GENE, encodes a VGAM1881 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1881 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1881 precursor RNA is designated SEQ ID:1867, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1867 is located at position 7527 relative to the genome of Bovine respiratory syncytial virus.

[26293] VGAM1881 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1881 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[26294] An enzyme complex designated DICER COMPLEX, dices the VGAM1881 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1881 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM1881 RNA is designated SEQ ID:4592, and is provided hereinbelow with reference to the sequence listing part.

[26295] VGAM1881 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1881 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1881 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26296] VGAM1881 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM1881 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1881 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1881 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1881 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26297] The complementary binding of VGAM1881 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM1881 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1881 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1881 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[26298] It is appreciated that VGAM1881 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1881 host target genes. The mRNA of each one of this plurality of VGAM1881 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1881 RNA, herein designated VGAM RNA, and which when bound by VGAM1881 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1881 host target proteins.

[26299] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1881 gene, herein designated VGAM GENE, on one or more VGAM1881 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26300] It is yet further appreciated that a function of VGAM1881 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1881 include diagnosis, prevention and treatment of viral infection by Bovine respiratory syncytial virus. Specific functions, and accordingly utilities, of VGAM1881 correlate with, and may be deduced from, the identity of the host target genes which VGAM1881 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[26301] Nucleotide sequences of the VGAM1881 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

diced VGAM1881 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1881 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1881 are further described hereinbelow with reference to Table 1.

[26302] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1881 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[26303] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1882 (VGAM1882) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[26304] VGAM1882 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1882 was detected is described hereinabove with reference to Figs. 2-8.

[26305] VGAM1882 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of Bovine respiratory syncytial virus. VGAM1882 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[26306] VGAM1882 gene, herein designated VGAM GENE, encodes a VGAM1882 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1882 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1882 precursor RNA is designated SEQ ID:1868, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1868 is located at position 417 relative to the genome of Bovine respiratory syncytial virus.

[26307] VGAM1882 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1882 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26308] An enzyme complex designated DICER COMPLEX, dices the VGAM1882 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1882 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM1882 RNA is designated SEQ ID:4593, and is provided hereinbelow with reference to the sequence listing part.

[26309] VGAM1882 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1882 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1882 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN COD-

ING and 3UTR respectively.

[26310] VGAM1882 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1882 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1882 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1882 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1882 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26311] The complementary binding of VGAM1882 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1882 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1882 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1882 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[26312] It is appreciated that VGAM1882 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1882 host target genes. The mRNA of each one of this plurality of VGAM1882 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1882 RNA, herein designated VGAM RNA, and which when bound by VGAM1882 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1882 host target proteins.

[26313] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1882 gene, herein designated VGAM GENE, on one

or more VGAM1882 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26314] It is yet further appreciated that a function of VGAM1882 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1882 include diagnosis, prevention and treatment of viral infection by Bovine respiratory syncytial virus. Specific functions, and accordingly utilities, of VGAM1882 correlate with, and may be deduced from, the identity of the host target genes which VGAM1882 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[26315] Nucleotide sequences of the VGAM1882 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1882 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1882 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1882 are further described hereinbelow with reference to Table 1.

[26316] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1882 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[26317] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1883 (VGAM1883) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[26318] VGAM1883 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1883 was detected is de-

scribed hereinabove with reference to Figs. 2-8.

[26319] VGAM1883 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Bovine respiratory syncytial virus. VGAM1883 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[26320] VGAM1883 gene, herein designated VGAM GENE, encodes a VGAM1883 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1883 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1883 precursor RNA is designated SEQ ID:1869, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1869 is located at position 10923 relative to the genome of Bovine respiratory syncytial virus.

[26321] VGAM1883 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1883 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26322] An enzyme complex designated DICER COMPLEX, dices the VGAM1883 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1883 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM1883 RNA is designated SEQ ID:4594, and is provided hereinbelow with reference to the sequence listing part.

[26323] VGAM1883 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1883 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1883 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding

gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26324] VGAM1883 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1883 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1883 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1883 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1883 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be lo-

cated in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26325] The complementary binding of VGAM1883 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1883 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1883 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1883 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[26326] It is appreciated that VGAM1883 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1883 host target genes. The mRNA of each one of this plurality of VGAM1883 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1883 RNA, herein designated VGAM RNA, and which when bound by VGAM1883 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1883 host target proteins.

[26327] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM1883 gene, herein designated VGAM GENE, on one or more VGAM1883 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26328] It is yet further appreciated that a function of VGAM1883 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1883 include diagnosis, prevention and treatment of viral infection by Bovine respiratory syncytial virus. Specific functions, and accordingly utilities, of VGAM1883 correlate with, and may be deduced from, the identity of the host target genes which VGAM1883 binds

and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[26329] Nucleotide sequences of the VGAM1883 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1883 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1883 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1883 are further described hereinbelow with reference to Table 1.

[26330] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1883 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[26331] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1884 (VGAM1884) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[26332] VGAM1884 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1884 was detected is described hereinabove with reference to Figs. 2-8.

[26333] VGAM1884 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Bovine respiratory syncytial virus. VGAM1884 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[26334] VGAM1884 gene, herein designated VGAM GENE, encodes a VGAM1884 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1884 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1884 precursor RNA is designated SEQ ID:1870, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1870 is located at position 8134 relative to the genome of Bovine respiratory syncytial virus.

[26335] VGAM1884 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1884 folded precursor RNA, herein designated VGAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26336] An enzyme complex designated DICER COMPLEX, dices the VGAM1884 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1884 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 70%) nucleotide sequence of VGAM1884 RNA is designated SEQ ID:4595, and is provided hereinbelow with reference to the sequence listing part.

[26337] VGAM1884 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1884 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1884 host target RNA,

herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26338] VGAM1884 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1884 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1884 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1884 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1884 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host tar-

get binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26339] The complementary binding of VGAM1884 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1884 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1884 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1884 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[26340] It is appreciated that VGAM1884 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1884 host target genes. The mRNA of each one of this plurality of VGAM1884 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1884 RNA, herein designated VGAM RNA, and which when bound by VGAM1884 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1884 host target proteins.

[26341] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1884 gene, herein designated VGAM GENE, on one or more VGAM1884 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26342] It is yet further appreciated that a function of VGAM1884 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1884 include diagnosis, prevention and treatment of viral infection by Bovine respiratory syncytial virus. Specific functions, and accordingly utilities, of

VGAM1884 correlate with, and may be deduced from, the identity of the host target genes which VGAM1884 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[26343] Nucleotide sequences of the VGAM1884 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1884 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1884 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1884 are further described hereinbelow with reference to Table 1.

[26344] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1884 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[26345] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1885 (VGAM1885) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the

art.

[26346] VGAM1885 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1885 was detected is described hereinabove with reference to Figs. 2-8.

[26347] VGAM1885 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Newcastle disease virus. VGAM1885 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[26348] VGAM1885 gene, herein designated VGAM GENE, encodes a VGAM1885 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1885 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1885 precursor RNA is designated SEQ ID:1871, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1871 is located at position 363 relative to the genome of Newcastle disease virus.

[26349] VGAM1885 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1885 folded

precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26350] An enzyme complex designated DICER COMPLEX, dices the VGAM1885 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1885 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM1885 RNA is designated SEQ ID:4596, and is provided hereinbelow with reference to the sequence listing part.

[26351] VGAM1885 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1885 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM1885 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26352] VGAM1885 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1885 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1885 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1885 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1885 host target RNA, herein designated VGAM HOST TARGET RNA.

It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26353] The complementary binding of VGAM1885 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1885 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1885 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1885 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[26354] It is appreciated that VGAM1885 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1885 host target genes. The mRNA of each one of this plurality of VGAM1885 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1885 RNA, herein designated VGAM RNA, and which when bound by VGAM1885 RNA, herein designated VGAM RNA, causes inhibition of translation of

respective one or more VGAM1885 host target proteins.

[26355] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1885 gene, herein designated VGAM GENE, on one or more VGAM1885 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26356] It is yet further appreciated that a function of VGAM1885 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1885 include diagnosis, prevention and treatment of viral infection by Newcastle disease virus.

Specific functions, and accordingly utilities, of VGAM1885 correlate with, and may be deduced from, the identity of the host target genes which VGAM1885 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[26357] Nucleotide sequences of the VGAM1885 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1885 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1885 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1885 are further described hereinbelow with reference to Table 1.

[26358] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1885 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[26359] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1886 (VGAM1886) viral gene, which modulates expression of respective host target genes thereof, the func-

tion and utility of which host target genes is known in the art.

[26360] VGAM1886 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1886 was detected is described hereinabove with reference to Figs. 2-8.

[26361] VGAM1886 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Newcastle disease virus. VGAM1886 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[26362] VGAM1886 gene, herein designated VGAM GENE, encodes a VGAM1886 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1886 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1886 precursor RNA is designated SEQ ID:1872, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1872 is located at position 7875 relative to the genome of Newcastle disease virus.

[26363] VGAM1886 precursor RNA, herein designated VGAM PRE-

CURSOR RNA, folds onto itself, forming VGAM1886 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26364] An enzyme complex designated DICER COMPLEX, dices the VGAM1886 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1886 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM1886 RNA is designated SEQ ID:4597, and is provided hereinbelow with reference to the sequence listing part.

[26365] VGAM1886 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM1886 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1886 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26366] VGAM1886 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1886 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1886 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1886 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1886 host

target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26367] The complementary binding of VGAM1886 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1886 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1886 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1886 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[26368] It is appreciated that VGAM1886 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1886 host target genes. The mRNA of each one of this plurality of VGAM1886 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1886 RNA, herein designated VGAM RNA, and which when bound by VGAM1886 RNA, herein

designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1886 host target proteins.

[26369] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1886 gene, herein designated VGAM GENE, on one or more VGAM1886 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26370] It is yet further appreciated that a function of VGAM1886 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1886 include diagnosis, prevention and

treatment of viral infection by Newcastle disease virus. Specific functions, and accordingly utilities, of VGAM1886 correlate with, and may be deduced from, the identity of the host target genes which VGAM1886 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[26371] Nucleotide sequences of the VGAM1886 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1886 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1886 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1886 are further described hereinbelow with reference to Table 1.

[26372] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1886 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[26373] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1887 (VGAM1887) viral gene, which modulates ex-

pression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[26374] VGAM1887 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1887 was detected is described hereinabove with reference to Figs. 2-8.

[26375] VGAM1887 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Newcastle disease virus. VGAM1887 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[26376] VGAM1887 gene, herein designated VGAM GENE, encodes a VGAM1887 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1887 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1887 precursor RNA is designated SEQ ID:1873, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1873 is located at position 4276 relative to the genome of Newcastle disease virus.

[26377] VGAM1887 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1887 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26378] An enzyme complex designated DICER COMPLEX, dices the VGAM1887 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1887 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 85%) nucleotide sequence of VGAM1887 RNA is designated SEQ ID:4598, and is provided hereinbelow with reference to the sequence listing part.

[26379] VGAM1887 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1887 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1887 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26380] VGAM1887 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1887 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1887 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1887 RNA, herein designated VGAM RNA, may have a different number of host target

binding sites in untranslated regions of a VGAM1887 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26381] The complementary binding of VGAM1887 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1887 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1887 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1887 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[26382] It is appreciated that VGAM1887 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1887 host target genes. The mRNA of each one of this plurality of VGAM1887 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1887 RNA, herein designated VGAM

RNA, and which when bound by VGAM1887 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1887 host target proteins.

[26383] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1887 gene, herein designated VGAM GENE, on one or more VGAM1887 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26384] It is yet further appreciated that a function of VGAM1887 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM1887 include diagnosis, prevention and treatment of viral infection by Newcastle disease virus. Specific functions, and accordingly utilities, of VGAM1887 correlate with, and may be deduced from, the identity of the host target genes which VGAM1887 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[26385] Nucleotide sequences of the VGAM1887 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1887 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1887 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1887 are further described hereinbelow with reference to Table 1.

[26386] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1887 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[26387] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Mes-

senger 1888 (VGAM1888) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[26388] VGAM1888 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1888 was detected is described hereinabove with reference to Figs. 2-8.

[26389] VGAM1888 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Newcastle disease virus. VGAM1888 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[26390] VGAM1888 gene, herein designated VGAM GENE, encodes a VGAM1888 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1888 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1888 precursor RNA is designated SEQ ID:1874, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1874 is located at position

12826 relative to the genome of Newcastle disease virus.

[26391] VGAM1888 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1888 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26392] An enzyme complex designated DICER COMPLEX, dices the VGAM1888 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1888 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 76%) nucleotide sequence of VGAM1888 RNA is designated SEQ ID:4599, and is provided hereinbelow with reference to the sequence listing part.

[26393] VGAM1888 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1888 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1888 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26394] VGAM1888 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1888 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1888 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1888 RNA, herein designated

VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1888 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26395] The complementary binding of VGAM1888 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1888 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1888 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1888 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[26396] It is appreciated that VGAM1888 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1888 host target genes. The mRNA of each one of this plurality of VGAM1888 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM1888 RNA, herein designated VGAM RNA, and which when bound by VGAM1888 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1888 host target proteins.

[26397] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1888 gene, herein designated VGAM GENE, on one or more VGAM1888 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26398] It is yet further appreciated that a function of VGAM1888 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1888 include diagnosis, prevention and treatment of viral infection by Newcastle disease virus. Specific functions, and accordingly utilities, of VGAM1888 correlate with, and may be deduced from, the identity of the host target genes which VGAM1888 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[26399] Nucleotide sequences of the VGAM1888 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1888 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1888 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1888 are further described hereinbelow with reference to Table 1.

[26400] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1888 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[26401] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present

invention, referred to here as Viral Genomic Address Messenger 1889 (VGAM1889) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[26402] VGAM1889 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1889 was detected is described hereinabove with reference to Figs. 2-8.

[26403] VGAM1889 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Newcastle disease virus. VGAM1889 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[26404] VGAM1889 gene, herein designated VGAM GENE, encodes a VGAM1889 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1889 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1889 precursor RNA is designated SEQ ID:1875, and is provided hereinbelow with reference to the sequence listing part. Nu-

cleotide sequence SEQ ID:1875 is located at position 48 relative to the genome of Newcastle disease virus.

[26405] VGAM1889 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1889 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26406] An enzyme complex designated DICER COMPLEX, dices the VGAM1889 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1889 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM1889 RNA is designated SEQ ID:4600, and is provided hereinbelow with reference to the sequence

listing part.

[26407] VGAM1889 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1889 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1889 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26408] VGAM1889 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1889 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1889 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not

meant to be limiting VGAM1889 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1889 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26409] The complementary binding of VGAM1889 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1889 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1889 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1889 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[26410] It is appreciated that VGAM1889 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1889 host target genes. The mRNA of each one of this plurality of VGAM1889 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM1889 RNA, herein designated VGAM RNA, and which when bound by VGAM1889 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1889 host target proteins.

[26411] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1889 gene, herein designated VGAM GENE, on one or more VGAM1889 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26412] It is yet further appreciated that a function of VGAM1889

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1889 include diagnosis, prevention and treatment of viral infection by Newcastle disease virus. Specific functions, and accordingly utilities, of VGAM1889 correlate with, and may be deduced from, the identity of the host target genes which VGAM1889 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[26413] Nucleotide sequences of the VGAM1889 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1889 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1889 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1889 are further described hereinbelow with reference to Table 1.

[26414] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1889 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[26415] Fig. 1 further provides a conceptual description of another

novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1890 (VGAM1890) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[26416] VGAM1890 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1890 was detected is described hereinabove with reference to Figs. 2-8.

[26417] VGAM1890 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Newcastle disease virus. VGAM1890 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[26418] VGAM1890 gene, herein designated VGAM GENE, encodes a VGAM1890 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1890 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1890 precursor RNA is designated SEQ ID:1876, and is provided here-

inbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1876 is located at position 14381 relative to the genome of Newcastle disease virus.

[26419] VGAM1890 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1890 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26420] An enzyme complex designated DICER COMPLEX, dices the VGAM1890 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1890 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM1890 RNA is designated SEQ ID:4601, and

is provided hereinbelow with reference to the sequence listing part.

[26421] VGAM1890 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1890 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1890 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26422] VGAM1890 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1890 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1890 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites

shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1890 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1890 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26423] The complementary binding of VGAM1890 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1890 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1890 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1890 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[26424] It is appreciated that VGAM1890 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1890 host target genes. The mRNA of each one of this plurality of VGAM1890 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1890 RNA, herein designated VGAM RNA, and which when bound by VGAM1890 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1890 host target proteins.

[26425] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1890 gene, herein designated VGAM GENE, on one or more VGAM1890 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26426] It is yet further appreciated that a function of VGAM1890 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1890 include diagnosis, prevention and treatment of viral infection by Newcastle disease virus. Specific functions, and accordingly utilities, of VGAM1890 correlate with, and may be deduced from, the identity of the host target genes which VGAM1890 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[26427] Nucleotide sequences of the VGAM1890 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1890 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1890 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1890 are further described hereinbelow with reference to Table 1.

[26428] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1890 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[26429] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1891 (VGAM1891) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[26430] VGAM1891 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1891 was detected is described hereinabove with reference to Figs. 2-8.

[26431] VGAM1891 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Newcastle disease virus. VGAM1891 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[26432] VGAM1891 gene, herein designated VGAM GENE, encodes a VGAM1891 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1891 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1891 precur-

sor RNA is designated SEQ ID:1877, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1877 is located at position 8373 relative to the genome of Newcastle disease virus.

[26433] VGAM1891 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1891 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26434] An enzyme complex designated DICER COMPLEX, dices the VGAM1891 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1891 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 66%) nucleotide se-

quence of VGAM1891 RNA is designated SEQ ID:4602, and is provided hereinbelow with reference to the sequence listing part.

[26435] VGAM1891 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1891 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1891 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26436] VGAM1891 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1891 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1891 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is ap-

preciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1891 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1891 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26437] The complementary binding of VGAM1891 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1891 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1891 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1891 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[26438] It is appreciated that VGAM1891 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1891 host target genes. The mRNA of

each one of this plurality of VGAM1891 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1891 RNA, herein designated VGAM RNA, and which when bound by VGAM1891 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1891 host target proteins.

[26439] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1891 gene, herein designated VGAM GENE, on one or more VGAM1891 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science

294,779 (2001)).

[26440] It is yet further appreciated that a function of VGAM1891 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1891 include diagnosis, prevention and treatment of viral infection by Newcastle disease virus. Specific functions, and accordingly utilities, of VGAM1891 correlate with, and may be deduced from, the identity of the host target genes which VGAM1891 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[26441] Nucleotide sequences of the VGAM1891 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1891 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1891 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1891 are further described hereinbelow with reference to Table 1.

[26442] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1891 RNA, herein designated VGAM RNA, are de-

scribed hereinbelow with reference to Table 2.

[26443] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1892 (VGAM1892) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[26444] VGAM1892 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1892 was detected is described hereinabove with reference to Figs. 2-8.

[26445] VGAM1892 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Newcastle disease virus. VGAM1892 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[26446] VGAM1892 gene, herein designated VGAM GENE, encodes a VGAM1892 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1892 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly

similar to the nucleotide sequence of VGAM1892 precursor RNA is designated SEQ ID:1878, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1878 is located at position 13642 relative to the genome of Newcastle disease virus.

[26447] VGAM1892 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1892 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26448] An enzyme complex designated DICER COMPLEX, dices the VGAM1892 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1892 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 49%) nucleotide sequence of VGAM1892 RNA is designated SEQ ID:4603, and is provided hereinbelow with reference to the sequence listing part.

[26449] VGAM1892 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1892 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1892 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26450] VGAM1892 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1892 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1892 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I,

BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1892 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1892 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26451] The complementary binding of VGAM1892 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1892 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1892 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1892 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[26452] It is appreciated that VGAM1892 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM1892 host target genes. The mRNA of each one of this plurality of VGAM1892 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1892 RNA, herein designated VGAM RNA, and which when bound by VGAM1892 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1892 host target proteins.

[26453] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1892 gene, herein designated VGAM GENE, on one or more VGAM1892 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26454] It is yet further appreciated that a function of VGAM1892 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1892 include diagnosis, prevention and treatment of viral infection by Newcastle disease virus. Specific functions, and accordingly utilities, of VGAM1892 correlate with, and may be deduced from, the identity of the host target genes which VGAM1892 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[26455] Nucleotide sequences of the VGAM1892 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1892 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1892 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1892 are further described hereinbelow with reference to Table 1.

[26456] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites

to VGAM1892 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[26457] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1893 (VGAM1893) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[26458] VGAM1893 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1893 was detected is described hereinabove with reference to Figs. 2-8.

[26459] VGAM1893 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Newcastle disease virus. VGAM1893 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[26460] VGAM1893 gene, herein designated VGAM GENE, encodes a VGAM1893 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1893 precursor RNA, herein designated VGAM PRECURSOR RNA, does not en-

code a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1893 precursor RNA is designated SEQ ID:1879, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1879 is located at position 2483 relative to the genome of Newcastle disease virus.

[26461] VGAM1893 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1893 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26462] An enzyme complex designated DICER COMPLEX, dices the VGAM1893 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1893 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM1893 RNA is designated SEQ ID:4604, and is provided hereinbelow with reference to the sequence listing part.

[26463] VGAM1893 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1893 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1893 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26464] VGAM1893 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1893 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1893 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3

such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1893 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1893 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26465] The complementary binding of VGAM1893 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1893 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1893 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1893 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[26466] It is appreciated that VGAM1893 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1893 host target genes. The mRNA of each one of this plurality of VGAM1893 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1893 RNA, herein designated VGAM RNA, and which when bound by VGAM1893 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1893 host target proteins.

[26467] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1893 gene, herein designated VGAM GENE, on one or more VGAM1893 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26468] It is yet further appreciated that a function of VGAM1893 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1893 include diagnosis, prevention and treatment of viral infection by Newcastle disease virus. Specific functions, and accordingly utilities, of VGAM1893 correlate with, and may be deduced from, the identity of the host target genes which VGAM1893 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[26469] Nucleotide sequences of the VGAM1893 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1893 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1893 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1893 are further described hereinbelow with reference to Table 1.

[26470] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the

complementarity of each of these host target binding sites to VGAM1893 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[26471] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1894 (VGAM1894) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[26472] VGAM1894 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1894 was detected is described hereinabove with reference to Figs. 2-8.

[26473] VGAM1894 gene, herein designated VGAM GENE, is a viral gene contained in the genome of respiratory syncytial virus. VGAM1894 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[26474] VGAM1894 gene, herein designated VGAM GENE, encodes a VGAM1894 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1894 precursor RNA,

herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1894 precursor RNA is designated SEQ ID:1880, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1880 is located at position 6434 relative to the genome of respiratory syncytial virus.

[26475] VGAM1894 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1894 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26476] An enzyme complex designated DICER COMPLEX, dices the VGAM1894 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1894 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM1894 RNA is designated SEQ ID:4605, and is provided hereinbelow with reference to the sequence listing part.

[26477] VGAM1894 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1894 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1894 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26478] VGAM1894 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1894 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1894 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host

target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1894 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1894 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26479] The complementary binding of VGAM1894 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1894 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1894 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1894 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[26480] It is appreciated that VGAM1894 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1894 host target genes. The mRNA of each one of this plurality of VGAM1894 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1894 RNA, herein designated VGAM RNA, and which when bound by VGAM1894 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1894 host target proteins.

[26481] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1894 gene, herein designated VGAM GENE, on one or more VGAM1894 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26482] It is yet further appreciated that a function of VGAM1894 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1894 include diagnosis, prevention and treatment of viral infection by respiratory syncytial virus. Specific functions, and accordingly utilities, of VGAM1894 correlate with, and may be deduced from, the identity of the host target genes which VGAM1894 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[26483] Nucleotide sequences of the VGAM1894 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1894 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1894 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1894 are further described hereinbelow with reference to Table 1.

[26484] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1894 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[26485] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1895 (VGAM1895) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[26486] VGAM1895 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1895 was detected is described hereinabove with reference to Figs. 2-8.

[26487] VGAM1895 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Garlic latent virus. VGAM1895 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[26488] VGAM1895 gene, herein designated VGAM GENE, encodes a VGAM1895 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and un-

like most ordinary genes, VGAM1895 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1895 precursor RNA is designated SEQ ID:1881, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1881 is located at position 2156 relative to the genome of Garlic latent virus.

[26489] VGAM1895 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1895 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26490] An enzyme complex designated DICER COMPLEX, dices the VGAM1895 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1895 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of VGAM1895 RNA is designated SEQ ID:4606, and is provided hereinbelow with reference to the sequence listing part.

[26491] VGAM1895 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1895 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1895 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26492] VGAM1895 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1895 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1895 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed

sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1895 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1895 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26493] The complementary binding of VGAM1895 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1895 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1895 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1895 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target

protein is therefore outlined by a broken line.

[26494] It is appreciated that VGAM1895 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1895 host target genes. The mRNA of each one of this plurality of VGAM1895 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1895 RNA, herein designated VGAM RNA, and which when bound by VGAM1895 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1895 host target proteins.

[26495] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1895 gene, herein designated VGAM GENE, on one or more VGAM1895 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26496] It is yet further appreciated that a function of VGAM1895 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1895 include diagnosis, prevention and treatment of viral infection by Garlic latent virus. Specific functions, and accordingly utilities, of VGAM1895 correlate with, and may be deduced from, the identity of the host target genes which VGAM1895 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[26497] Nucleotide sequences of the VGAM1895 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1895 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1895 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1895 are further described hereinbelow with reference to Table 1.

[26498] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1895 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[26499] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1896 (VGAM1896) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[26500] VGAM1896 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1896 was detected is described hereinabove with reference to Figs. 2-8.

[26501] VGAM1896 gene, herein designated VGAM GENE, is a viral gene contained in the genome of respiratory syncytial virus. VGAM1896 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[26502] VGAM1896 gene, herein designated VGAM GENE, encodes a VGAM1896 precursor RNA, herein designated VGAM

PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1896 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1896 precursor RNA is designated SEQ ID:1882, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1882 is located at position 4399 relative to the genome of respiratory syncytial virus.

[26503] VGAM1896 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1896 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26504] An enzyme complex designated DICER COMPLEX, dices the VGAM1896 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1896 RNA, herein designated VGAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM1896 RNA is designated SEQ ID:4607, and is provided hereinbelow with reference to the sequence listing part.

[26505] VGAM1896 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1896 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1896 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26506] VGAM1896 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1896 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1896 RNA, herein designated

VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1896 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1896 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26507] The complementary binding of VGAM1896 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1896 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1896 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1896 host target protein, herein desig-

nated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[26508] It is appreciated that VGAM1896 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1896 host target genes. The mRNA of each one of this plurality of VGAM1896 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1896 RNA, herein designated VGAM RNA, and which when bound by VGAM1896 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1896 host target proteins.

[26509] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1896 gene, herein designated VGAM GENE, on one or more VGAM1896 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26510] It is yet further appreciated that a function of VGAM1896 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1896 include diagnosis, prevention and treatment of viral infection by respiratory syncytial virus. Specific functions, and accordingly utilities, of VGAM1896 correlate with, and may be deduced from, the identity of the host target genes which VGAM1896 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[26511] Nucleotide sequences of the VGAM1896 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1896 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1896 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1896 are further described hereinbelow with reference to Table 1.

[26512] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1896 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[26513] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1897 (VGAM1897) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[26514] VGAM1897 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1897 was detected is described hereinabove with reference to Figs. 2-8.

[26515] VGAM1897 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Garlic latent virus. VGAM1897 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[26516] VGAM1897 gene, herein designated VGAM GENE, encodes a VGAM1897 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1897 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1897 precur-

sor RNA is designated SEQ ID:1883, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1883 is located at position 5382 relative to the genome of Garlic latent virus.

[26517] VGAM1897 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1897 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26518] An enzyme complex designated DICER COMPLEX, dices the VGAM1897 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1897 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide se-

quence of VGAM1897 RNA is designated SEQ ID:4608, and is provided hereinbelow with reference to the sequence listing part.

[26519] VGAM1897 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1897 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1897 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26520] VGAM1897 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1897 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1897 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is ap-

preciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1897 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1897 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26521] The complementary binding of VGAM1897 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1897 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1897 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1897 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[26522] It is appreciated that VGAM1897 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1897 host target genes. The mRNA of

each one of this plurality of VGAM1897 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1897 RNA, herein designated VGAM RNA, and which when bound by VGAM1897 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1897 host target proteins.

[26523] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1897 gene, herein designated VGAM GENE, on one or more VGAM1897 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science

294,779 (2001)).

[26524] It is yet further appreciated that a function of VGAM1897 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1897 include diagnosis, prevention and treatment of viral infection by Garlic latent virus. Specific functions, and accordingly utilities, of VGAM1897 correlate with, and may be deduced from, the identity of the host target genes which VGAM1897 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[26525] Nucleotide sequences of the VGAM1897 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1897 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1897 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1897 are further described hereinbelow with reference to Table 1.

[26526] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1897 RNA, herein designated VGAM RNA, are de-

scribed hereinbelow with reference to Table 2.

[26527] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1898 (VGAM1898) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[26528] VGAM1898 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1898 was detected is described hereinabove with reference to Figs. 2-8.

[26529] VGAM1898 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Garlic latent virus. VGAM1898 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[26530] VGAM1898 gene, herein designated VGAM GENE, encodes a VGAM1898 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1898 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly

similar to the nucleotide sequence of VGAM1898 precursor RNA is designated SEQ ID:1884, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1884 is located at position 4971 relative to the genome of Garlic latent virus.

[26531] VGAM1898 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1898 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26532] An enzyme complex designated DICER COMPLEX, dices the VGAM1898 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1898 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 50%) nucleotide sequence of VGAM1898 RNA is designated SEQ ID:4609, and is provided hereinbelow with reference to the sequence listing part.

[26533] VGAM1898 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1898 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1898 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26534] VGAM1898 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1898 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1898 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I,

BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1898 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1898 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26535] The complementary binding of VGAM1898 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1898 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1898 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1898 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[26536] It is appreciated that VGAM1898 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM1898 host target genes. The mRNA of each one of this plurality of VGAM1898 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1898 RNA, herein designated VGAM RNA, and which when bound by VGAM1898 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1898 host target proteins.

[26537] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1898 gene, herein designated VGAM GENE, on one or more VGAM1898 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26538] It is yet further appreciated that a function of VGAM1898 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1898 include diagnosis, prevention and treatment of viral infection by Garlic latent virus. Specific functions, and accordingly utilities, of VGAM1898 correlate with, and may be deduced from, the identity of the host target genes which VGAM1898 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[26539] Nucleotide sequences of the VGAM1898 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1898 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1898 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1898 are further described hereinbelow with reference to Table 1.

[26540] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites

to VGAM1898 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[26541] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1899 (VGAM1899) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[26542] VGAM1899 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1899 was detected is described hereinabove with reference to Figs. 2-8.

[26543] VGAM1899 gene, herein designated VGAM GENE, is a viral gene contained in the genome of respiratory syncytial virus. VGAM1899 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[26544] VGAM1899 gene, herein designated VGAM GENE, encodes a VGAM1899 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1899 precursor RNA, herein designated VGAM PRECURSOR RNA, does not en-

code a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1899 precursor RNA is designated SEQ ID:1885, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1885 is located at position 7191 relative to the genome of respiratory syncytial virus.

[26545] VGAM1899 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1899 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26546] An enzyme complex designated DICER COMPLEX, dices the VGAM1899 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1899 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 47%) nucleotide sequence of VGAM1899 RNA is designated SEQ ID:4610, and is provided hereinbelow with reference to the sequence listing part.

[26547] VGAM1899 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1899 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1899 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26548] VGAM1899 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1899 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1899 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3

such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1899 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1899 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26549] The complementary binding of VGAM1899 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1899 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1899 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1899 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[26550] It is appreciated that VGAM1899 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1899 host target genes. The mRNA of each one of this plurality of VGAM1899 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1899 RNA, herein designated VGAM RNA, and which when bound by VGAM1899 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1899 host target proteins.

[26551] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1899 gene, herein designated VGAM GENE, on one or more VGAM1899 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26552] It is yet further appreciated that a function of VGAM1899 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1899 include diagnosis, prevention and treatment of viral infection by respiratory syncytial virus. Specific functions, and accordingly utilities, of VGAM1899 correlate with, and may be deduced from, the identity of the host target genes which VGAM1899 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[26553] Nucleotide sequences of the VGAM1899 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1899 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1899 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1899 are further described hereinbelow with reference to Table 1.

[26554] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the

complementarity of each of these host target binding sites to VGAM1899 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[26555] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1900 (VGAM1900) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[26556] VGAM1900 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1900 was detected is described hereinabove with reference to Figs. 2-8.

[26557] VGAM1900 gene, herein designated VGAM GENE, is a viral gene contained in the genome of respiratory syncytial virus. VGAM1900 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[26558] VGAM1900 gene, herein designated VGAM GENE, encodes a VGAM1900 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1900 precursor RNA,

herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1900 precursor RNA is designated SEQ ID:1886, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1886 is located at position 438 relative to the genome of respiratory syncytial virus.

[26559] VGAM1900 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1900 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26560] An enzyme complex designated DICER COMPLEX, dices the VGAM1900 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1900 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 57%) nucleotide sequence of VGAM1900 RNA is designated SEQ ID:4611, and is provided hereinbelow with reference to the sequence listing part.

[26561] VGAM1900 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1900 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1900 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26562] VGAM1900 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1900 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1900 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host

target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1900 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1900 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26563] The complementary binding of VGAM1900 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1900 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1900 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1900 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[26564] It is appreciated that VGAM1900 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1900 host target genes. The mRNA of each one of this plurality of VGAM1900 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1900 RNA, herein designated VGAM RNA, and which when bound by VGAM1900 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1900 host target proteins.

[26565] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1900 gene, herein designated VGAM GENE, on one or more VGAM1900 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26566] It is yet further appreciated that a function of VGAM1900 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1900 include diagnosis, prevention and treatment of viral infection by respiratory syncytial virus. Specific functions, and accordingly utilities, of VGAM1900 correlate with, and may be deduced from, the identity of the host target genes which VGAM1900 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[26567] Nucleotide sequences of the VGAM1900 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1900 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1900 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1900 are further described hereinbelow with reference to Table 1.

[26568] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1900 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[26569] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1901 (VGAM1901) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[26570] VGAM1901 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1901 was detected is described hereinabove with reference to Figs. 2-8.

[26571] VGAM1901 gene, herein designated VGAM GENE, is a viral gene contained in the genome of respiratory syncytial virus. VGAM1901 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[26572] VGAM1901 gene, herein designated VGAM GENE, encodes a VGAM1901 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and un-

like most ordinary genes, VGAM1901 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1901 precursor RNA is designated SEQ ID:1887, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1887 is located at position 2370 relative to the genome of respiratory syncytial virus.

[26573] VGAM1901 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1901 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26574] An enzyme complex designated DICER COMPLEX, dices the VGAM1901 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1901 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 53%) nucleotide sequence of VGAM1901 RNA is designated SEQ ID:4612, and is provided hereinbelow with reference to the sequence listing part.

[26575] VGAM1901 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1901 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1901 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26576] VGAM1901 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1901 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1901 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed

sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1901 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1901 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26577] The complementary binding of VGAM1901 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1901 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1901 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1901 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target

protein is therefore outlined by a broken line.

[26578] It is appreciated that VGAM1901 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1901 host target genes. The mRNA of each one of this plurality of VGAM1901 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1901 RNA, herein designated VGAM RNA, and which when bound by VGAM1901 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1901 host target proteins.

[26579] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1901 gene, herein designated VGAM GENE, on one or more VGAM1901 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26580] It is yet further appreciated that a function of VGAM1901 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1901 include diagnosis, prevention and treatment of viral infection by respiratory syncytial virus. Specific functions, and accordingly utilities, of VGAM1901 correlate with, and may be deduced from, the identity of the host target genes which VGAM1901 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[26581] Nucleotide sequences of the VGAM1901 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1901 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1901 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1901 are further described hereinbelow with reference to Table 1.

[26582] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1901 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[26583] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1902 (VGAM1902) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[26584] VGAM1902 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1902 was detected is described hereinabove with reference to Figs. 2-8.

[26585] VGAM1902 gene, herein designated VGAM GENE, is a viral gene contained in the genome of respiratory syncytial virus. VGAM1902 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[26586] VGAM1902 gene, herein designated VGAM GENE, encodes a VGAM1902 precursor RNA, herein designated VGAM

PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1902 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1902 precursor RNA is designated SEQ ID:1888, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1888 is located at position 8673 relative to the genome of respiratory syncytial virus.

[26587] VGAM1902 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1902 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26588] An enzyme complex designated DICER COMPLEX, dices the VGAM1902 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1902 RNA, herein designated VGAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM1902 RNA is designated SEQ ID:4613, and is provided hereinbelow with reference to the sequence listing part.

[26589] VGAM1902 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1902 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1902 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26590] VGAM1902 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1902 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1902 RNA, herein designated

VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1902 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1902 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26591] The complementary binding of VGAM1902 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1902 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1902 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1902 host target protein, herein desig-

nated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[26592] It is appreciated that VGAM1902 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1902 host target genes. The mRNA of each one of this plurality of VGAM1902 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1902 RNA, herein designated VGAM RNA, and which when bound by VGAM1902 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1902 host target proteins.

[26593] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1902 gene, herein designated VGAM GENE, on one or more VGAM1902 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26594] It is yet further appreciated that a function of VGAM1902 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1902 include diagnosis, prevention and treatment of viral infection by respiratory syncytial virus. Specific functions, and accordingly utilities, of VGAM1902 correlate with, and may be deduced from, the identity of the host target genes which VGAM1902 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[26595] Nucleotide sequences of the VGAM1902 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1902 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1902 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1902 are further described hereinbelow with reference to Table 1.

[26596] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1902 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[26597] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1903 (VGAM1903) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[26598] VGAM1903 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1903 was detected is described hereinabove with reference to Figs. 2-8.

[26599] VGAM1903 gene, herein designated VGAM GENE, is a viral gene contained in the genome of respiratory syncytial virus. VGAM1903 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[26600] VGAM1903 gene, herein designated VGAM GENE, encodes

a VGAM1903 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1903 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1903 precursor RNA is designated SEQ ID:1889, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1889 is located at position 14231 relative to the genome of respiratory syncytial virus.

[26601] VGAM1903 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1903 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26602] An enzyme complex designated DICER COMPLEX, dices the VGAM1903 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, into VGAM1903 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM1903 RNA is designated SEQ ID:4614, and is provided hereinbelow with reference to the sequence listing part.

[26603] VGAM1903 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1903 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1903 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26604] VGAM1903 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1903 host target RNA, herein designated VGAM HOST TARGET RNA. This

complementary binding is due to the fact that the nucleotide sequence of VGAM1903 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1903 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1903 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26605] The complementary binding of VGAM1903 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1903 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1903

host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1903 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[26606] It is appreciated that VGAM1903 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1903 host target genes. The mRNA of each one of this plurality of VGAM1903 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1903 RNA, herein designated VGAM RNA, and which when bound by VGAM1903 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1903 host target proteins.

[26607] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1903 gene, herein designated VGAM GENE, on one or more VGAM1903 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26608] It is yet further appreciated that a function of VGAM1903 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1903 include diagnosis, prevention and treatment of viral infection by respiratory syncytial virus. Specific functions, and accordingly utilities, of VGAM1903 correlate with, and may be deduced from, the identity of the host target genes which VGAM1903 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[26609] Nucleotide sequences of the VGAM1903 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1903 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1903 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM1903 are further described hereinbelow with reference to Table 1.

[26610] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1903 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[26611] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1904 (VGAM1904) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[26612] VGAM1904 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1904 was detected is described hereinabove with reference to Figs. 2-8.

[26613] VGAM1904 gene, herein designated VGAM GENE, is a viral gene contained in the genome of respiratory syncytial virus. VGAM1904 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in

the human genome.

[26614] VGAM1904 gene, herein designated VGAM GENE, encodes a VGAM1904 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1904 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1904 precursor RNA is designated SEQ ID:1890, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1890 is located at position 8364 relative to the genome of respiratory syncytial virus.

[26615] VGAM1904 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1904 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26616] An enzyme complex designated DICER COMPLEX, dices

the VGAM1904 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1904 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of VGAM1904 RNA is designated SEQ ID:4615, and is provided hereinbelow with reference to the sequence listing part.

[26617] VGAM1904 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1904 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1904 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26618] VGAM1904 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1904 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1904 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1904 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1904 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26619] The complementary binding of VGAM1904 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1904 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM1904 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1904 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[26620] It is appreciated that VGAM1904 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1904 host target genes. The mRNA of each one of this plurality of VGAM1904 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1904 RNA, herein designated VGAM RNA, and which when bound by VGAM1904 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1904 host target proteins.

[26621] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1904 gene, herein designated VGAM GENE, on one or more VGAM1904 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26622] It is yet further appreciated that a function of VGAM1904 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1904 include diagnosis, prevention and treatment of viral infection by respiratory syncytial virus. Specific functions, and accordingly utilities, of VGAM1904 correlate with, and may be deduced from, the identity of the host target genes which VGAM1904 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[26623] Nucleotide sequences of the VGAM1904 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1904 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of

VGAM1904 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1904 are further described hereinbelow with reference to Table 1.

[26624] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1904 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[26625] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1905 (VGAM1905) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[26626] VGAM1905 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1905 was detected is described hereinabove with reference to Figs. 2-8.

[26627] VGAM1905 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Sendai virus. VGAM1905 host target gene, herein designated VGAM HOST TARGET

GENE, is a human gene contained in the human genome.

[26628] VGAM1905 gene, herein designated VGAM GENE, encodes a VGAM1905 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1905 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1905 precursor RNA is designated SEQ ID:1891, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1891 is located at position 5191 relative to the genome of Sendai virus.

[26629] VGAM1905 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1905 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26630] An enzyme complex designated DICER COMPLEX, dices

the VGAM1905 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1905 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 64%) nucleotide sequence of VGAM1905 RNA is designated SEQ ID:4616, and is provided hereinbelow with reference to the sequence listing part.

[26631] VGAM1905 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1905 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1905 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26632] VGAM1905 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1905 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1905 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1905 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1905 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26633] The complementary binding of VGAM1905 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1905 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM1905 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1905 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[26634] It is appreciated that VGAM1905 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1905 host target genes. The mRNA of each one of this plurality of VGAM1905 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1905 RNA, herein designated VGAM RNA, and which when bound by VGAM1905 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1905 host target proteins.

[26635] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1905 gene, herein designated VGAM GENE, on one or more VGAM1905 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26636] It is yet further appreciated that a function of VGAM1905 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1905 include diagnosis, prevention and treatment of viral infection by Sendai virus. Specific functions, and accordingly utilities, of VGAM1905 correlate with, and may be deduced from, the identity of the host target genes which VGAM1905 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[26637] Nucleotide sequences of the VGAM1905 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1905 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of

VGAM1905 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1905 are further described hereinbelow with reference to Table 1.

[26638] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1905 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[26639] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1906 (VGAM1906) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[26640] VGAM1906 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1906 was detected is described hereinabove with reference to Figs. 2-8.

[26641] VGAM1906 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Sendai virus. VGAM1906 host target gene, herein designated VGAM HOST TARGET

GENE, is a human gene contained in the human genome.

[26642] VGAM1906 gene, herein designated VGAM GENE, encodes a VGAM1906 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1906 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1906 precursor RNA is designated SEQ ID:1892, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1892 is located at position 15052 relative to the genome of Sendai virus.

[26643] VGAM1906 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1906 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26644] An enzyme complex designated DICER COMPLEX, dices

the VGAM1906 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1906 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM1906 RNA is designated SEQ ID:4617, and is provided hereinbelow with reference to the sequence listing part.

[26645] VGAM1906 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1906 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1906 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26646] VGAM1906 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1906 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1906 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1906 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1906 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26647] The complementary binding of VGAM1906 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1906 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM1906 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1906 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[26648] It is appreciated that VGAM1906 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1906 host target genes. The mRNA of each one of this plurality of VGAM1906 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1906 RNA, herein designated VGAM RNA, and which when bound by VGAM1906 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1906 host target proteins.

[26649] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1906 gene, herein designated VGAM GENE, on one or more VGAM1906 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26650] It is yet further appreciated that a function of VGAM1906 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1906 include diagnosis, prevention and treatment of viral infection by Sendai virus. Specific functions, and accordingly utilities, of VGAM1906 correlate with, and may be deduced from, the identity of the host target genes which VGAM1906 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[26651] Nucleotide sequences of the VGAM1906 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1906 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of

VGAM1906 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1906 are further described hereinbelow with reference to Table 1.

[26652] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1906 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[26653] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1907 (VGAM1907) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[26654] VGAM1907 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1907 was detected is described hereinabove with reference to Figs. 2-8.

[26655] VGAM1907 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human parainfluenza virus 3. VGAM1907 host target gene, herein designated

VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[26656] VGAM1907 gene, herein designated VGAM GENE, encodes a VGAM1907 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1907 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1907 precursor RNA is designated SEQ ID:1893, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1893 is located at position 7040 relative to the genome of Human parainfluenza virus 3.

[26657] VGAM1907 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1907 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26658] An enzyme complex designated DICER COMPLEX, dices the VGAM1907 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1907 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 83%) nucleotide sequence of VGAM1907 RNA is designated SEQ ID:4618, and is provided hereinbelow with reference to the sequence listing part.

[26659] VGAM1907 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1907 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1907 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26660] VGAM1907 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites

located in untranslated regions of VGAM1907 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1907 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1907 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1907 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26661] The complementary binding of VGAM1907 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1907 host target RNA, herein designated VGAM

HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1907 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1907 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[26662] It is appreciated that VGAM1907 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1907 host target genes. The mRNA of each one of this plurality of VGAM1907 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1907 RNA, herein designated VGAM RNA, and which when bound by VGAM1907 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1907 host target proteins.

[26663] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1907 gene, herein designated VGAM GENE, on one or more VGAM1907 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove

with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26664] It is yet further appreciated that a function of VGAM1907 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1907 include diagnosis, prevention and treatment of viral infection by Human parainfluenza virus 3. Specific functions, and accordingly utilities, of VGAM1907 correlate with, and may be deduced from, the identity of the host target genes which VGAM1907 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[26665] Nucleotide sequences of the VGAM1907 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1907 RNA, herein designated VGAM RNA, and

a schematic representation of the secondary folding of VGAM1907 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1907 are further described hereinbelow with reference to Table 1.

[26666] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1907 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[26667] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1908 (VGAM1908) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[26668] VGAM1908 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1908 was detected is described hereinabove with reference to Figs. 2-8.

[26669] VGAM1908 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human parainfluenza

virus 3. VGAM1908 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[26670] VGAM1908 gene, herein designated VGAM GENE, encodes a VGAM1908 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1908 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1908 precursor RNA is designated SEQ ID:1894, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1894 is located at position 8620 relative to the genome of Human parainfluenza virus 3.

[26671] VGAM1908 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1908 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[26672] An enzyme complex designated DICER COMPLEX, dices the VGAM1908 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1908 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM1908 RNA is designated SEQ ID:4619, and is provided hereinbelow with reference to the sequence listing part.

[26673] VGAM1908 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1908 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1908 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26674] VGAM1908 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM1908 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1908 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1908 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1908 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26675] The complementary binding of VGAM1908 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM1908 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1908 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1908 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[26676] It is appreciated that VGAM1908 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1908 host target genes. The mRNA of each one of this plurality of VGAM1908 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1908 RNA, herein designated VGAM RNA, and which when bound by VGAM1908 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1908 host target proteins.

[26677] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1908 gene, herein designated VGAM GENE, on one or more VGAM1908 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26678] It is yet further appreciated that a function of VGAM1908 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1908 include diagnosis, prevention and treatment of viral infection by Human parainfluenza virus 3. Specific functions, and accordingly utilities, of VGAM1908 correlate with, and may be deduced from, the identity of the host target genes which VGAM1908 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[26679] Nucleotide sequences of the VGAM1908 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

diced VGAM1908 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1908 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1908 are further described hereinbelow with reference to Table 1.

[26680] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1908 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[26681] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1909 (VGAM1909) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[26682] VGAM1909 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1909 was detected is described hereinabove with reference to Figs. 2-8.

[26683] VGAM1909 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of Human parainfluenza virus 3. VGAM1909 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[26684] VGAM1909 gene, herein designated VGAM GENE, encodes a VGAM1909 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1909 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1909 precursor RNA is designated SEQ ID:1895, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1895 is located at position 5850 relative to the genome of Human parainfluenza virus 3.

[26685] VGAM1909 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1909 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26686] An enzyme complex designated DICER COMPLEX, dices the VGAM1909 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1909 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM1909 RNA is designated SEQ ID:4620, and is provided hereinbelow with reference to the sequence listing part.

[26687] VGAM1909 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1909 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1909 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26688] VGAM1909 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1909 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1909 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1909 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1909 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26689] The complementary binding of VGAM1909 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM1909 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1909 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1909 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[26690] It is appreciated that VGAM1909 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1909 host target genes. The mRNA of each one of this plurality of VGAM1909 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1909 RNA, herein designated VGAM RNA, and which when bound by VGAM1909 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1909 host target proteins.

[26691] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1909 gene, herein designated VGAM GENE, on one or more VGAM1909 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26692] It is yet further appreciated that a function of VGAM1909 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1909 include diagnosis, prevention and treatment of viral infection by Human parainfluenza virus 3. Specific functions, and accordingly utilities, of VGAM1909 correlate with, and may be deduced from, the identity of the host target genes which VGAM1909 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[26693] Nucleotide sequences of the VGAM1909 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the diced VGAM1909 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1909 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1909 are further described hereinbelow with reference to Table 1.

[26694] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1909 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[26695] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1910 (VGAM1910) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[26696] VGAM1910 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1910 was detected is described hereinabove with reference to Figs. 2-8.

[26697] VGAM1910 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human parainfluenza virus 3. VGAM1910 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[26698] VGAM1910 gene, herein designated VGAM GENE, encodes a VGAM1910 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1910 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1910 precursor RNA is designated SEQ ID:1896, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1896 is located at position 8937 relative to the genome of Human parainfluenza virus 3.

[26699] VGAM1910 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1910 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26700] An enzyme complex designated DICER COMPLEX, dices the VGAM1910 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1910 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM1910 RNA is designated SEQ ID:4621, and is provided hereinbelow with reference to the sequence listing part.

[26701] VGAM1910 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1910 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1910 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN COD-

ING and 3UTR respectively.

[26702] VGAM1910 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1910 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1910 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1910 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1910 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26703] The complementary binding of VGAM1910 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1910 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1910 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1910 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[26704] It is appreciated that VGAM1910 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1910 host target genes. The mRNA of each one of this plurality of VGAM1910 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1910 RNA, herein designated VGAM RNA, and which when bound by VGAM1910 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1910 host target proteins.

[26705] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1910 gene, herein designated VGAM GENE, on one

or more VGAM1910 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26706] It is yet further appreciated that a function of VGAM1910 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1910 include diagnosis, prevention and treatment of viral infection by Human parainfluenza virus 3. Specific functions, and accordingly utilities, of VGAM1910 correlate with, and may be deduced from, the identity of the host target genes which VGAM1910 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[26707] Nucleotide sequences of the VGAM1910 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1910 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1910 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1910 are further described hereinbelow with reference to Table 1.

[26708] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1910 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[26709] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1911 (VGAM1911) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[26710] VGAM1911 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1911 was detected is de-

scribed hereinabove with reference to Figs. 2-8.

[26711] VGAM1911 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human parainfluenza virus 3. VGAM1911 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[26712] VGAM1911 gene, herein designated VGAM GENE, encodes a VGAM1911 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1911 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1911 precursor RNA is designated SEQ ID:1897, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1897 is located at position 1061 relative to the genome of Human parainfluenza virus 3.

[26713] VGAM1911 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1911 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26714] An enzyme complex designated DICER COMPLEX, dices the VGAM1911 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1911 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM1911 RNA is designated SEQ ID:4622, and is provided hereinbelow with reference to the sequence listing part.

[26715] VGAM1911 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1911 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1911 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and

a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26716] VGAM1911 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1911 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1911 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1911 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1911 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both

3UTR and 5UTR regions.

[26717] The complementary binding of VGAM1911 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1911 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1911 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1911 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[26718] It is appreciated that VGAM1911 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1911 host target genes. The mRNA of each one of this plurality of VGAM1911 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1911 RNA, herein designated VGAM RNA, and which when bound by VGAM1911 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1911 host target proteins.

[26719] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM1911 gene, herein designated VGAM GENE, on one or more VGAM1911 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26720] It is yet further appreciated that a function of VGAM1911 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1911 include diagnosis, prevention and treatment of viral infection by Human parainfluenza virus 3. Specific functions, and accordingly utilities, of VGAM1911 correlate with, and may be deduced from, the identity of the host target genes which VGAM1911 binds and inhibits, and the function of these host target genes,

as elaborated hereinbelow.

[26721] Nucleotide sequences of the VGAM1911 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1911 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1911 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1911 are further described hereinbelow with reference to Table 1.

[26722] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1911 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[26723] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1912 (VGAM1912) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[26724] VGAM1912 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene.

The method by which VGAM1912 was detected is described hereinabove with reference to Figs. 2-8.

[26725] VGAM1912 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human parainfluenza virus 3. VGAM1912 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[26726] VGAM1912 gene, herein designated VGAM GENE, encodes a VGAM1912 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1912 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1912 precursor RNA is designated SEQ ID:1898, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1898 is located at position 12367 relative to the genome of Human parainfluenza virus 3.

[26727] VGAM1912 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1912 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26728] An enzyme complex designated DICER COMPLEX, dices the VGAM1912 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1912 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 65%) nucleotide sequence of VGAM1912 RNA is designated SEQ ID:4623, and is provided hereinbelow with reference to the sequence listing part.

[26729] VGAM1912 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1912 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1912 host target RNA, herein designated VGAM HOST TARGET RNA, comprises

three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26730] VGAM1912 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1912 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1912 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1912 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1912 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an

example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26731] The complementary binding of VGAM1912 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1912 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1912 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1912 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[26732] It is appreciated that VGAM1912 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1912 host target genes. The mRNA of each one of this plurality of VGAM1912 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1912 RNA, herein designated VGAM RNA, and which when bound by VGAM1912 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1912 host target proteins.

[26733] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1912 gene, herein designated VGAM GENE, on one or more VGAM1912 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26734] It is yet further appreciated that a function of VGAM1912 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1912 include diagnosis, prevention and treatment of viral infection by Human parainfluenza virus 3. Specific functions, and accordingly utilities, of VGAM1912 correlate with, and may be deduced from, the

identity of the host target genes which VGAM1912 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[26735] Nucleotide sequences of the VGAM1912 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1912 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1912 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1912 are further described hereinbelow with reference to Table 1.

[26736] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1912 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[26737] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1913 (VGAM1913) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[26738] VGAM1913 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1913 was detected is described hereinabove with reference to Figs. 2-8.

[26739] VGAM1913 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human parainfluenza virus 3. VGAM1913 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[26740] VGAM1913 gene, herein designated VGAM GENE, encodes a VGAM1913 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1913 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1913 precursor RNA is designated SEQ ID:1899, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1899 is located at position 8166 relative to the genome of Human parainfluenza virus 3.

[26741] VGAM1913 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1913 folded precursor RNA, herein designated VGAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26742] An enzyme complex designated DICER COMPLEX, dices the VGAM1913 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1913 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 54%) nucleotide sequence of VGAM1913 RNA is designated SEQ ID:4624, and is provided hereinbelow with reference to the sequence listing part.

[26743] VGAM1913 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1913 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1913 host target RNA,

herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26744] VGAM1913 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1913 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1913 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1913 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1913 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host tar-

get binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26745] The complementary binding of VGAM1913 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1913 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1913 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1913 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[26746] It is appreciated that VGAM1913 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1913 host target genes. The mRNA of each one of this plurality of VGAM1913 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1913 RNA, herein designated VGAM RNA, and which when bound by VGAM1913 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1913 host target proteins.

[26747] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1913 gene, herein designated VGAM GENE, on one or more VGAM1913 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26748] It is yet further appreciated that a function of VGAM1913 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1913 include diagnosis, prevention and treatment of viral infection by Human parainfluenza virus 3. Specific functions, and accordingly utilities, of

VGAM1913 correlate with, and may be deduced from, the identity of the host target genes which VGAM1913 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[26749] Nucleotide sequences of the VGAM1913 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1913 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1913 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1913 are further described hereinbelow with reference to Table 1.

[26750] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1913 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[26751] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1914 (VGAM1914) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the

art.

[26752] VGAM1914 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1914 was detected is described hereinabove with reference to Figs. 2-8.

[26753] VGAM1914 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human parainfluenza virus 3. VGAM1914 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[26754] VGAM1914 gene, herein designated VGAM GENE, encodes a VGAM1914 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1914 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1914 precursor RNA is designated SEQ ID:1900, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1900 is located at position 14210 relative to the genome of Human parainfluenza virus 3.

[26755] VGAM1914 precursor RNA, herein designated VGAM PRE-

CURSOR RNA, folds onto itself, forming VGAM1914 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26756] An enzyme complex designated DICER COMPLEX, dices the VGAM1914 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1914 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM1914 RNA is designated SEQ ID:4625, and is provided hereinbelow with reference to the sequence listing part.

[26757] VGAM1914 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM1914 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1914 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26758] VGAM1914 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1914 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1914 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1914 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1914 host

target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26759] The complementary binding of VGAM1914 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1914 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1914 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1914 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[26760] It is appreciated that VGAM1914 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1914 host target genes. The mRNA of each one of this plurality of VGAM1914 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1914 RNA, herein designated VGAM RNA, and which when bound by VGAM1914 RNA, herein

designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1914 host target proteins.

[26761] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1914 gene, herein designated VGAM GENE, on one or more VGAM1914 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26762] It is yet further appreciated that a function of VGAM1914 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1914 include diagnosis, prevention and

treatment of viral infection by Human parainfluenza virus 3. Specific functions, and accordingly utilities, of VGAM1914 correlate with, and may be deduced from, the identity of the host target genes which VGAM1914 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[26763] Nucleotide sequences of the VGAM1914 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1914 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1914 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1914 are further described hereinbelow with reference to Table 1.

[26764] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1914 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[26765] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1915 (VGAM1915) viral gene, which modulates ex-

pression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[26766] VGAM1915 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1915 was detected is described hereinabove with reference to Figs. 2-8.

[26767] VGAM1915 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human parainfluenza virus 3. VGAM1915 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[26768] VGAM1915 gene, herein designated VGAM GENE, encodes a VGAM1915 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1915 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1915 precursor RNA is designated SEQ ID:1901, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1901 is located at position 225 relative to the genome of Human parainfluenza virus 3.

[26769] VGAM1915 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1915 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26770] An enzyme complex designated DICER COMPLEX, dices the VGAM1915 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1915 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM1915 RNA is designated SEQ ID:4626, and is provided hereinbelow with reference to the sequence listing part.

[26771] VGAM1915 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1915 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1915 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26772] VGAM1915 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1915 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1915 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1915 RNA, herein designated VGAM RNA, may have a different number of host target

binding sites in untranslated regions of a VGAM1915 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26773] The complementary binding of VGAM1915 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1915 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1915 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1915 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[26774] It is appreciated that VGAM1915 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1915 host target genes. The mRNA of each one of this plurality of VGAM1915 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1915 RNA, herein designated VGAM

RNA, and which when bound by VGAM1915 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1915 host target proteins.

[26775] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1915 gene, herein designated VGAM GENE, on one or more VGAM1915 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26776] It is yet further appreciated that a function of VGAM1915 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM1915 include diagnosis, prevention and treatment of viral infection by Human parainfluenza virus 3. Specific functions, and accordingly utilities, of VGAM1915 correlate with, and may be deduced from, the identity of the host target genes which VGAM1915 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[26777] Nucleotide sequences of the VGAM1915 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1915 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1915 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1915 are further described hereinbelow with reference to Table 1.

[26778] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1915 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[26779] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Mes-

senger 1916 (VGAM1916) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[26780] VGAM1916 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1916 was detected is described hereinabove with reference to Figs. 2-8.

[26781] VGAM1916 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human parainfluenza virus 1 strain Washington/1964. VGAM1916 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[26782] VGAM1916 gene, herein designated VGAM GENE, encodes a VGAM1916 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1916 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1916 precursor RNA is designated SEQ ID:1902, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1902 is located at position 4687

relative to the genome of Human parainfluenza virus 1 strain Washington/1964.

[26783] VGAM1916 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1916 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26784] An enzyme complex designated DICER COMPLEX, dices the VGAM1916 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1916 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM1916 RNA is designated SEQ ID:4627, and is provided hereinbelow with reference to the sequence

listing part.

[26785] VGAM1916 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1916 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1916 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26786] VGAM1916 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1916 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1916 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not

meant to be limiting VGAM1916 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1916 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26787] The complementary binding of VGAM1916 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1916 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1916 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1916 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[26788] It is appreciated that VGAM1916 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1916 host target genes. The mRNA of each one of this plurality of VGAM1916 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM1916 RNA, herein designated VGAM RNA, and which when bound by VGAM1916 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1916 host target proteins.

[26789] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1916 gene, herein designated VGAM GENE, on one or more VGAM1916 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26790] It is yet further appreciated that a function of VGAM1916

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1916 include diagnosis, prevention and treatment of viral infection by Human parainfluenza virus 1 strain Washington/1964. Specific functions, and accordingly utilities, of VGAM1916 correlate with, and may be deduced from, the identity of the host target genes which VGAM1916 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[26791] Nucleotide sequences of the VGAM1916 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1916 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1916 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1916 are further described hereinbelow with reference to Table 1.

[26792] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1916 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[26793] Fig. 1 further provides a conceptual description of another

novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1917 (VGAM1917) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[26794] VGAM1917 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1917 was detected is described hereinabove with reference to Figs. 2-8.

[26795] VGAM1917 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human parainfluenza virus 1 strain Washington/1964. VGAM1917 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[26796] VGAM1917 gene, herein designated VGAM GENE, encodes a VGAM1917 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1917 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1917 precursor RNA is designated SEQ ID:1903, and is provided here-

inbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1903 is located at position 14949 relative to the genome of Human parainfluenza virus 1 strain Washington/1964.

[26797] VGAM1917 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1917 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26798] An enzyme complex designated DICER COMPLEX, dices the VGAM1917 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1917 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 63%) nucleotide se-

quence of VGAM1917 RNA is designated SEQ ID:4628, and is provided hereinbelow with reference to the sequence listing part.

[26799] VGAM1917 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1917 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1917 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26800] VGAM1917 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1917 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1917 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is ap-

preciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1917 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1917 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26801] The complementary binding of VGAM1917 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1917 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1917 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1917 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[26802] It is appreciated that VGAM1917 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1917 host target genes. The mRNA of

each one of this plurality of VGAM1917 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1917 RNA, herein designated VGAM RNA, and which when bound by VGAM1917 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1917 host target proteins.

[26803] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1917 gene, herein designated VGAM GENE, on one or more VGAM1917 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science

294,779 (2001)).

[26804] It is yet further appreciated that a function of VGAM1917 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1917 include diagnosis, prevention and treatment of viral infection by Human parainfluenza virus 1 strain Washington/1964. Specific functions, and accordingly utilities, of VGAM1917 correlate with, and may be deduced from, the identity of the host target genes which VGAM1917 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[26805] Nucleotide sequences of the VGAM1917 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1917 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1917 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1917 are further described hereinbelow with reference to Table 1.

[26806] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1917 RNA, herein designated VGAM RNA, are de-

scribed hereinbelow with reference to Table 2.

[26807] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1918 (VGAM1918) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[26808] VGAM1918 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1918 was detected is described hereinabove with reference to Figs. 2-8.

[26809] VGAM1918 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human parainfluenza virus 1 strain Washington/1964. VGAM1918 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[26810] VGAM1918 gene, herein designated VGAM GENE, encodes a VGAM1918 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1918 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly

similar to the nucleotide sequence of VGAM1918 precursor RNA is designated SEQ ID:1904, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1904 is located at position 7051 relative to the genome of Human parainfluenza virus 1 strain Washington/1964.

[26811] VGAM1918 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1918 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26812] An enzyme complex designated DICER COMPLEX, dices the VGAM1918 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1918 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 82%) nucleotide sequence of VGAM1918 RNA is designated SEQ ID:4629, and is provided hereinbelow with reference to the sequence listing part.

[26813] VGAM1918 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1918 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1918 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26814] VGAM1918 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1918 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1918 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3

such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1918 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1918 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26815] The complementary binding of VGAM1918 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1918 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1918 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1918 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[26816] It is appreciated that VGAM1918 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1918 host target genes. The mRNA of each one of this plurality of VGAM1918 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1918 RNA, herein designated VGAM RNA, and which when bound by VGAM1918 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1918 host target proteins.

[26817] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1918 gene, herein designated VGAM GENE, on one or more VGAM1918 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26818] It is yet further appreciated that a function of VGAM1918 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1918 include diagnosis, prevention and treatment of viral infection by Human parainfluenza virus 1 strain Washington/1964. Specific functions, and accordingly utilities, of VGAM1918 correlate with, and may be deduced from, the identity of the host target genes which VGAM1918 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[26819] Nucleotide sequences of the VGAM1918 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1918 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1918 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1918 are further described hereinbelow with reference to Table 1.

[26820] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the

complementarity of each of these host target binding sites to VGAM1918 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[26821] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1919 (VGAM1919) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[26822] VGAM1919 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1919 was detected is described hereinabove with reference to Figs. 2-8.

[26823] VGAM1919 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine herpesvirus 1. VGAM1919 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[26824] VGAM1919 gene, herein designated VGAM GENE, encodes a VGAM1919 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1919 precursor RNA,

herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1919 precursor RNA is designated SEQ ID:1905, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1905 is located at position 109925 relative to the genome of Equine herpesvirus 1.

[26825] VGAM1919 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1919 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26826] An enzyme complex designated DICER COMPLEX, dices the VGAM1919 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1919 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM1919 RNA is designated SEQ ID:4630, and is provided hereinbelow with reference to the sequence listing part.

[26827] VGAM1919 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1919 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1919 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26828] VGAM1919 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1919 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1919 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host

target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1919 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1919 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26829] The complementary binding of VGAM1919 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1919 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1919 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1919 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[26830] It is appreciated that VGAM1919 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1919 host target genes. The mRNA of each one of this plurality of VGAM1919 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1919 RNA, herein designated VGAM RNA, and which when bound by VGAM1919 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1919 host target proteins.

[26831] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1919 gene, herein designated VGAM GENE, on one or more VGAM1919 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26832] It is yet further appreciated that a function of VGAM1919 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1919 include diagnosis, prevention and treatment of viral infection by Equine herpesvirus 1. Specific functions, and accordingly utilities, of VGAM1919 correlate with, and may be deduced from, the identity of the host target genes which VGAM1919 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[26833] Nucleotide sequences of the VGAM1919 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1919 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1919 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1919 are further described hereinbelow with reference to Table 1.

[26834] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1919 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[26835] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1920 (VGAM1920) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[26836] VGAM1920 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1920 was detected is described hereinabove with reference to Figs. 2-8.

[26837] VGAM1920 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Canine distemper virus. VGAM1920 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[26838] VGAM1920 gene, herein designated VGAM GENE, encodes a VGAM1920 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and un-

like most ordinary genes, VGAM1920 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1920 precursor RNA is designated SEQ ID:1906, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1906 is located at position 12749 relative to the genome of Canine distemper virus.

[26839] VGAM1920 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1920 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26840] An enzyme complex designated DICER COMPLEX, dices the VGAM1920 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1920 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM1920 RNA is designated SEQ ID:4631, and is provided hereinbelow with reference to the sequence listing part.

[26841] VGAM1920 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1920 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1920 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26842] VGAM1920 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1920 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1920 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed

sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1920 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1920 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26843] The complementary binding of VGAM1920 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1920 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1920 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1920 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target

protein is therefore outlined by a broken line.

[26844] It is appreciated that VGAM1920 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1920 host target genes. The mRNA of each one of this plurality of VGAM1920 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1920 RNA, herein designated VGAM RNA, and which when bound by VGAM1920 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1920 host target proteins.

[26845] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1920 gene, herein designated VGAM GENE, on one or more VGAM1920 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26846] It is yet further appreciated that a function of VGAM1920 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1920 include diagnosis, prevention and treatment of viral infection by Canine distemper virus. Specific functions, and accordingly utilities, of VGAM1920 correlate with, and may be deduced from, the identity of the host target genes which VGAM1920 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[26847] Nucleotide sequences of the VGAM1920 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1920 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1920 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1920 are further described hereinbelow with reference to Table 1.

[26848] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1920 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[26849] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1921 (VGAM1921) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[26850] VGAM1921 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1921 was detected is described hereinabove with reference to Figs. 2-8.

[26851] VGAM1921 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Canine distemper virus. VGAM1921 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[26852] VGAM1921 gene, herein designated VGAM GENE, encodes a VGAM1921 precursor RNA, herein designated VGAM

PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1921 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1921 precursor RNA is designated SEQ ID:1907, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1907 is located at position 9746 relative to the genome of Canine distemper virus.

[26853] VGAM1921 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1921 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26854] An enzyme complex designated DICER COMPLEX, dices the VGAM1921 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1921 RNA, herein designated VGAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM1921 RNA is designated SEQ ID:4632, and is provided hereinbelow with reference to the sequence listing part.

[26855] VGAM1921 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1921 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1921 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26856] VGAM1921 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1921 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1921 RNA, herein designated

VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1921 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1921 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26857] The complementary binding of VGAM1921 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1921 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1921 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1921 host target protein, herein desig-

nated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[26858] It is appreciated that VGAM1921 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1921 host target genes. The mRNA of each one of this plurality of VGAM1921 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1921 RNA, herein designated VGAM RNA, and which when bound by VGAM1921 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1921 host target proteins.

[26859] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1921 gene, herein designated VGAM GENE, on one or more VGAM1921 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26860] It is yet further appreciated that a function of VGAM1921 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1921 include diagnosis, prevention and treatment of viral infection by Canine distemper virus. Specific functions, and accordingly utilities, of VGAM1921 correlate with, and may be deduced from, the identity of the host target genes which VGAM1921 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[26861] Nucleotide sequences of the VGAM1921 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1921 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1921 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1921 are further described hereinbelow with reference to Table 1.

[26862] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1921 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[26863] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1922 (VGAM1922) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[26864] VGAM1922 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1922 was detected is described hereinabove with reference to Figs. 2-8.

[26865] VGAM1922 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Canine distemper virus. VGAM1922 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[26866] VGAM1922 gene, herein designated VGAM GENE, encodes

a VGAM1922 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1922 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1922 precursor RNA is designated SEQ ID:1908, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1908 is located at position 11765 relative to the genome of Canine distemper virus.

[26867] VGAM1922 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1922 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26868] An enzyme complex designated DICER COMPLEX, dices the VGAM1922 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1922 RNA,

herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM1922 RNA is designated SEQ ID:4633, and is provided hereinbelow with reference to the sequence listing part.

[26869] VGAM1922 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1922 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1922 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26870] VGAM1922 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1922 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM1922 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1922 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1922 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26871] The complementary binding of VGAM1922 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1922 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1922 host target RNA, herein designated VGAM HOST TARGET

RNA, into VGAM1922 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[26872] It is appreciated that VGAM1922 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1922 host target genes. The mRNA of each one of this plurality of VGAM1922 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1922 RNA, herein designated VGAM RNA, and which when bound by VGAM1922 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1922 host target proteins.

[26873] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1922 gene, herein designated VGAM GENE, on one or more VGAM1922 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26874] It is yet further appreciated that a function of VGAM1922 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1922 include diagnosis, prevention and treatment of viral infection by Canine distemper virus. Specific functions, and accordingly utilities, of VGAM1922 correlate with, and may be deduced from, the identity of the host target genes which VGAM1922 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[26875] Nucleotide sequences of the VGAM1922 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1922 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1922 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1922 are further

described hereinbelow with reference to Table 1.

[26876] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1922 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[26877] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1923 (VGAM1923) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[26878] VGAM1923 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1923 was detected is described hereinabove with reference to Figs. 2-8.

[26879] VGAM1923 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Canine distemper virus. VGAM1923 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[26880] VGAM1923 gene, herein designated VGAM GENE, encodes a VGAM1923 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1923 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1923 precursor RNA is designated SEQ ID:1909, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1909 is located at position 3849 relative to the genome of Canine distemper virus.

[26881] VGAM1923 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1923 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26882] An enzyme complex designated DICER COMPLEX, dices the VGAM1923 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, into VGAM1923 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM1923 RNA is designated SEQ ID:4634, and is provided hereinbelow with reference to the sequence listing part.

[26883] VGAM1923 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1923 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1923 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26884] VGAM1923 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1923 host target RNA, herein designated VGAM HOST TARGET RNA. This

complementary binding is due to the fact that the nucleotide sequence of VGAM1923 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1923 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1923 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26885] The complementary binding of VGAM1923 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1923 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1923

host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1923 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[26886] It is appreciated that VGAM1923 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1923 host target genes. The mRNA of each one of this plurality of VGAM1923 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1923 RNA, herein designated VGAM RNA, and which when bound by VGAM1923 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1923 host target proteins.

[26887] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1923 gene, herein designated VGAM GENE, on one or more VGAM1923 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26888] It is yet further appreciated that a function of VGAM1923 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1923 include diagnosis, prevention and treatment of viral infection by Canine distemper virus. Specific functions, and accordingly utilities, of VGAM1923 correlate with, and may be deduced from, the identity of the host target genes which VGAM1923 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[26889] Nucleotide sequences of the VGAM1923 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1923 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1923 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM1923 are further described hereinbelow with reference to Table 1.

[26890] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1923 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[26891] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1924 (VGAM1924) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[26892] VGAM1924 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1924 was detected is described hereinabove with reference to Figs. 2-8.

[26893] VGAM1924 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Canine distemper virus. VGAM1924 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the

human genome.

[26894] VGAM1924 gene, herein designated VGAM GENE, encodes a VGAM1924 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1924 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1924 precursor RNA is designated SEQ ID:1910, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1910 is located at position 1287 relative to the genome of Canine distemper virus.

[26895] VGAM1924 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1924 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26896] An enzyme complex designated DICER COMPLEX, dices

the VGAM1924 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1924 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM1924 RNA is designated SEQ ID:4635, and is provided hereinbelow with reference to the sequence listing part.

[26897] VGAM1924 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1924 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1924 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26898] VGAM1924 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1924 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1924 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1924 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1924 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26899] The complementary binding of VGAM1924 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1924 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM1924 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1924 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[26900] It is appreciated that VGAM1924 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1924 host target genes. The mRNA of each one of this plurality of VGAM1924 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1924 RNA, herein designated VGAM RNA, and which when bound by VGAM1924 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1924 host target proteins.

[26901] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1924 gene, herein designated VGAM GENE, on one or more VGAM1924 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26902] It is yet further appreciated that a function of VGAM1924 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1924 include diagnosis, prevention and treatment of viral infection by Canine distemper virus. Specific functions, and accordingly utilities, of VGAM1924 correlate with, and may be deduced from, the identity of the host target genes which VGAM1924 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[26903] Nucleotide sequences of the VGAM1924 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1924 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of

VGAM1924 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1924 are further described hereinbelow with reference to Table 1.

[26904] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1924 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[26905] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1925 (VGAM1925) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[26906] VGAM1925 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1925 was detected is described hereinabove with reference to Figs. 2-8.

[26907] VGAM1925 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Canine distemper virus. VGAM1925 host target gene, herein designated VGAM

HOST TARGET GENE, is a human gene contained in the human genome.

[26908] VGAM1925 gene, herein designated VGAM GENE, encodes a VGAM1925 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1925 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1925 precursor RNA is designated SEQ ID:1911, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1911 is located at position 5609 relative to the genome of Canine distemper virus.

[26909] VGAM1925 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1925 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26910] An enzyme complex designated DICER COMPLEX, dices the VGAM1925 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1925 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM1925 RNA is designated SEQ ID:4636, and is provided hereinbelow with reference to the sequence listing part.

[26911] VGAM1925 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1925 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1925 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26912] VGAM1925 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites

located in untranslated regions of VGAM1925 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1925 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1925 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1925 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26913] The complementary binding of VGAM1925 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1925 host target RNA, herein designated VGAM

HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1925 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1925 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[26914] It is appreciated that VGAM1925 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1925 host target genes. The mRNA of each one of this plurality of VGAM1925 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1925 RNA, herein designated VGAM RNA, and which when bound by VGAM1925 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1925 host target proteins.

[26915] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1925 gene, herein designated VGAM GENE, on one or more VGAM1925 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove

with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26916] It is yet further appreciated that a function of VGAM1925 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1925 include diagnosis, prevention and treatment of viral infection by Canine distemper virus. Specific functions, and accordingly utilities, of VGAM1925 correlate with, and may be deduced from, the identity of the host target genes which VGAM1925 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[26917] Nucleotide sequences of the VGAM1925 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1925 RNA, herein designated VGAM RNA, and

a schematic representation of the secondary folding of VGAM1925 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1925 are further described hereinbelow with reference to Table 1.

[26918] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1925 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[26919] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1926 (VGAM1926) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[26920] VGAM1926 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1926 was detected is described hereinabove with reference to Figs. 2-8.

[26921] VGAM1926 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Canine distemper virus.

VGAM1926 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[26922] VGAM1926 gene, herein designated VGAM GENE, encodes a VGAM1926 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1926 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1926 precursor RNA is designated SEQ ID:1912, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1912 is located at position 8304 relative to the genome of Canine distemper virus.

[26923] VGAM1926 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1926 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[26924] An enzyme complex designated DICER COMPLEX, dices the VGAM1926 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1926 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM1926 RNA is designated SEQ ID:4637, and is provided hereinbelow with reference to the sequence listing part.

[26925] VGAM1926 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1926 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1926 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26926] VGAM1926 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM1926 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1926 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1926 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1926 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26927] The complementary binding of VGAM1926 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM1926 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1926 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1926 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[26928] It is appreciated that VGAM1926 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1926 host target genes. The mRNA of each one of this plurality of VGAM1926 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1926 RNA, herein designated VGAM RNA, and which when bound by VGAM1926 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1926 host target proteins.

[26929] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1926 gene, herein designated VGAM GENE, on one or more VGAM1926 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26930] It is yet further appreciated that a function of VGAM1926 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1926 include diagnosis, prevention and treatment of viral infection by Canine distemper virus. Specific functions, and accordingly utilities, of VGAM1926 correlate with, and may be deduced from, the identity of the host target genes which VGAM1926 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[26931] Nucleotide sequences of the VGAM1926 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

diced VGAM1926 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1926 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1926 are further described hereinbelow with reference to Table 1.

[26932] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1926 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[26933] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1927 (VGAM1927) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[26934] VGAM1927 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1927 was detected is described hereinabove with reference to Figs. 2-8.

[26935] VGAM1927 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of Canine distemper virus. VGAM1927 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[26936] VGAM1927 gene, herein designated VGAM GENE, encodes a VGAM1927 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1927 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1927 precursor RNA is designated SEQ ID:1913, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1913 is located at position 9614 relative to the genome of Canine distemper virus.

[26937] VGAM1927 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1927 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26938] An enzyme complex designated DICER COMPLEX, dices the VGAM1927 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1927 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 83%) nucleotide sequence of VGAM1927 RNA is designated SEQ ID:4638, and is provided hereinbelow with reference to the sequence listing part.

[26939] VGAM1927 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1927 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1927 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26940] VGAM1927 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1927 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1927 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1927 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1927 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26941] The complementary binding of VGAM1927 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM1927 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1927 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1927 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[26942] It is appreciated that VGAM1927 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1927 host target genes. The mRNA of each one of this plurality of VGAM1927 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1927 RNA, herein designated VGAM RNA, and which when bound by VGAM1927 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1927 host target proteins.

[26943] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1927 gene, herein designated VGAM GENE, on one or more VGAM1927 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26944] It is yet further appreciated that a function of VGAM1927 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1927 include diagnosis, prevention and treatment of viral infection by Canine distemper virus. Specific functions, and accordingly utilities, of VGAM1927 correlate with, and may be deduced from, the identity of the host target genes which VGAM1927 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[26945] Nucleotide sequences of the VGAM1927 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the diced VGAM1927 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1927 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1927 are further described hereinbelow with reference to Table 1.

[26946] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1927 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[26947] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1928 (VGAM1928) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[26948] VGAM1928 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1928 was detected is described hereinabove with reference to Figs. 2-8.

[26949] VGAM1928 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Canine distemper virus. VGAM1928 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[26950] VGAM1928 gene, herein designated VGAM GENE, encodes a VGAM1928 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1928 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1928 precursor RNA is designated SEQ ID:1914, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1914 is located at position 5392 relative to the genome of Canine distemper virus.

[26951] VGAM1928 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1928 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26952] An enzyme complex designated DICER COMPLEX, dices the VGAM1928 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1928 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM1928 RNA is designated SEQ ID:4639, and is provided hereinbelow with reference to the sequence listing part.

[26953] VGAM1928 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1928 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1928 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN COD-

ING and 3UTR respectively.

[26954] VGAM1928 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1928 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1928 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1928 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1928 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26955] The complementary binding of VGAM1928 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1928 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1928 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1928 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[26956] It is appreciated that VGAM1928 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1928 host target genes. The mRNA of each one of this plurality of VGAM1928 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1928 RNA, herein designated VGAM RNA, and which when bound by VGAM1928 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1928 host target proteins.

[26957] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1928 gene, herein designated VGAM GENE, on one

or more VGAM1928 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26958] It is yet further appreciated that a function of VGAM1928 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1928 include diagnosis, prevention and treatment of viral infection by Canine distemper virus. Specific functions, and accordingly utilities, of VGAM1928 correlate with, and may be deduced from, the identity of the host target genes which VGAM1928 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[26959] Nucleotide sequences of the VGAM1928 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1928 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1928 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1928 are further described hereinbelow with reference to Table 1.

[26960] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1928 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[26961] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1929 (VGAM1929) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[26962] VGAM1929 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1929 was detected is de-

scribed hereinabove with reference to Figs. 2-8.

[26963] VGAM1929 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Simian hemorrhagic fever virus. VGAM1929 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[26964] VGAM1929 gene, herein designated VGAM GENE, encodes a VGAM1929 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1929 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1929 precursor RNA is designated SEQ ID:1915, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1915 is located at position 11778 relative to the genome of Simian hemorrhagic fever virus.

[26965] VGAM1929 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1929 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26966] An enzyme complex designated DICER COMPLEX, dices the VGAM1929 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1929 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 87%) nucleotide sequence of VGAM1929 RNA is designated SEQ ID:4640, and is provided hereinbelow with reference to the sequence listing part.

[26967] VGAM1929 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1929 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1929 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding

gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26968] VGAM1929 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1929 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1929 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1929 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1929 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be lo-

cated in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26969] The complementary binding of VGAM1929 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1929 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1929 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1929 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[26970] It is appreciated that VGAM1929 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1929 host target genes. The mRNA of each one of this plurality of VGAM1929 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1929 RNA, herein designated VGAM RNA, and which when bound by VGAM1929 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1929 host target proteins.

[26971] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM1929 gene, herein designated VGAM GENE, on one or more VGAM1929 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26972] It is yet further appreciated that a function of VGAM1929 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1929 include diagnosis, prevention and treatment of viral infection by Simian hemorrhagic fever virus. Specific functions, and accordingly utilities, of VGAM1929 correlate with, and may be deduced from, the identity of the host target genes which VGAM1929 binds

and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[26973] Nucleotide sequences of the VGAM1929 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1929 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1929 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1929 are further described hereinbelow with reference to Table 1.

[26974] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1929 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[26975] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1930 (VGAM1930) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[26976] VGAM1930 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1930 was detected is described hereinabove with reference to Figs. 2-8.

[26977] VGAM1930 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human herpesvirus 4. VGAM1930 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[26978] VGAM1930 gene, herein designated VGAM GENE, encodes a VGAM1930 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1930 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1930 precursor RNA is designated SEQ ID:1916, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1916 is located at position 150946 relative to the genome of Human herpesvirus 4.

[26979] VGAM1930 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1930 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26980] An enzyme complex designated DICER COMPLEX, dices the VGAM1930 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1930 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM1930 RNA is designated SEQ ID:4641, and is provided hereinbelow with reference to the sequence listing part.

[26981] VGAM1930 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1930 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1930 host target RNA, herein designated VGAM HOST TARGET RNA, comprises

three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26982] VGAM1930 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1930 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1930 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1930 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1930 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an

example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26983] The complementary binding of VGAM1930 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1930 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1930 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1930 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[26984] It is appreciated that VGAM1930 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1930 host target genes. The mRNA of each one of this plurality of VGAM1930 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1930 RNA, herein designated VGAM RNA, and which when bound by VGAM1930 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1930 host target proteins.

[26985] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1930 gene, herein designated VGAM GENE, on one or more VGAM1930 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26986] It is yet further appreciated that a function of VGAM1930 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1930 include diagnosis, prevention and treatment of viral infection by Human herpesvirus 4. Specific functions, and accordingly utilities, of VGAM1930 correlate with, and may be deduced from, the identity of

the host target genes which VGAM1930 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[26987] Nucleotide sequences of the VGAM1930 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1930 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1930 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1930 are further described hereinbelow with reference to Table 1.

[26988] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1930 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[26989] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1931 (VGAM1931) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[26990] VGAM1931 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1931 was detected is described hereinabove with reference to Figs. 2-8.

[26991] VGAM1931 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human herpesvirus 4. VGAM1931 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[26992] VGAM1931 gene, herein designated VGAM GENE, encodes a VGAM1931 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1931 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1931 precursor RNA is designated SEQ ID:1917, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1917 is located at position 151629 relative to the genome of Human herpesvirus 4.

[26993] VGAM1931 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1931 folded precursor RNA, herein designated VGAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26994] An enzyme complex designated DICER COMPLEX, dices the VGAM1931 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1931 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 74%) nucleotide sequence of VGAM1931 RNA is designated SEQ ID:4642, and is provided hereinbelow with reference to the sequence listing part.

[26995] VGAM1931 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1931 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1931 host target RNA,

herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26996] VGAM1931 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1931 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1931 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1931 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1931 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host tar-

get binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26997] The complementary binding of VGAM1931 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1931 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1931 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1931 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[26998] It is appreciated that VGAM1931 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1931 host target genes. The mRNA of each one of this plurality of VGAM1931 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1931 RNA, herein designated VGAM RNA, and which when bound by VGAM1931 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1931 host target proteins.

[26999] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1931 gene, herein designated VGAM GENE, on one or more VGAM1931 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27000] It is yet further appreciated that a function of VGAM1931 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1931 include diagnosis, prevention and treatment of viral infection by Human herpesvirus 4. Specific functions, and accordingly utilities, of VGAM1931

correlate with, and may be deduced from, the identity of the host target genes which VGAM1931 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[27001] Nucleotide sequences of the VGAM1931 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1931 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1931 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1931 are further described hereinbelow with reference to Table 1.

[27002] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1931 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[27003] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1932 (VGAM1932) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the

art.

[27004] VGAM1932 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1932 was detected is described hereinabove with reference to Figs. 2-8.

[27005] VGAM1932 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human herpesvirus 4. VGAM1932 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[27006] VGAM1932 gene, herein designated VGAM GENE, encodes a VGAM1932 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1932 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1932 precursor RNA is designated SEQ ID:1918, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1918 is located at position 159902 relative to the genome of Human herpesvirus 4.

[27007] VGAM1932 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1932 folded

precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27008] An enzyme complex designated DICER COMPLEX, dices the VGAM1932 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1932 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM1932 RNA is designated SEQ ID:4643, and is provided hereinbelow with reference to the sequence listing part.

[27009] VGAM1932 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1932 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM1932 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[27010] VGAM1932 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1932 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1932 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1932 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1932 host target RNA, herein designated VGAM HOST TARGET RNA.

It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[27011] The complementary binding of VGAM1932 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1932 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1932 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1932 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[27012] It is appreciated that VGAM1932 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1932 host target genes. The mRNA of each one of this plurality of VGAM1932 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1932 RNA, herein designated VGAM RNA, and which when bound by VGAM1932 RNA, herein designated VGAM RNA, causes inhibition of translation of

respective one or more VGAM1932 host target proteins.

[27013] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1932 gene, herein designated VGAM GENE, on one or more VGAM1932 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27014] It is yet further appreciated that a function of VGAM1932 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1932 include diagnosis, prevention and treatment of viral infection by Human herpesvirus 4. Spe-

cific functions, and accordingly utilities, of VGAM1932 correlate with, and may be deduced from, the identity of the host target genes which VGAM1932 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[27015] Nucleotide sequences of the VGAM1932 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1932 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1932 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1932 are further described hereinbelow with reference to Table 1.

[27016] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1932 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[27017] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1933 (VGAM1933) viral gene, which modulates expression of respective host target genes thereof, the func-

tion and utility of which host target genes is known in the art.

[27018] VGAM1933 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1933 was detected is described hereinabove with reference to Figs. 2-8.

[27019] VGAM1933 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human herpesvirus 4. VGAM1933 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[27020] VGAM1933 gene, herein designated VGAM GENE, encodes a VGAM1933 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1933 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1933 precursor RNA is designated SEQ ID:1919, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1919 is located at position 156037 relative to the genome of Human herpesvirus 4.

[27021] VGAM1933 precursor RNA, herein designated VGAM PRE-

CURSOR RNA, folds onto itself, forming VGAM1933 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27022] An enzyme complex designated DICER COMPLEX, dices the VGAM1933 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1933 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM1933 RNA is designated SEQ ID:4644, and is provided hereinbelow with reference to the sequence listing part.

[27023] VGAM1933 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM1933 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1933 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[27024] VGAM1933 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1933 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1933 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1933 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1933 host

target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[27025] The complementary binding of VGAM1933 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1933 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1933 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1933 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[27026] It is appreciated that VGAM1933 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1933 host target genes. The mRNA of each one of this plurality of VGAM1933 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1933 RNA, herein designated VGAM RNA, and which when bound by VGAM1933 RNA, herein

designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1933 host target proteins.

[27027] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1933 gene, herein designated VGAM GENE, on one or more VGAM1933 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27028] It is yet further appreciated that a function of VGAM1933 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1933 include diagnosis, prevention and

treatment of viral infection by Human herpesvirus 4. Specific functions, and accordingly utilities, of VGAM1933 correlate with, and may be deduced from, the identity of the host target genes which VGAM1933 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[27029] Nucleotide sequences of the VGAM1933 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1933 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1933 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1933 are further described hereinbelow with reference to Table 1.

[27030] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1933 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[27031] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1934 (VGAM1934) viral gene, which modulates ex-

pression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[27032] VGAM1934 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1934 was detected is described hereinabove with reference to Figs. 2-8.

[27033] VGAM1934 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human herpesvirus 4. VGAM1934 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[27034] VGAM1934 gene, herein designated VGAM GENE, encodes a VGAM1934 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1934 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1934 precursor RNA is designated SEQ ID:1920, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1920 is located at position 157308 relative to the genome of Human herpesvirus 4.

[27035] VGAM1934 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1934 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27036] An enzyme complex designated DICER COMPLEX, dices the VGAM1934 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1934 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 59%) nucleotide sequence of VGAM1934 RNA is designated SEQ ID:4645, and is provided hereinbelow with reference to the sequence listing part.

[27037] VGAM1934 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1934 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1934 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[27038] VGAM1934 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1934 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1934 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1934 RNA, herein designated VGAM RNA, may have a different number of host target

binding sites in untranslated regions of a VGAM1934 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[27039] The complementary binding of VGAM1934 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1934 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1934 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1934 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[27040] It is appreciated that VGAM1934 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1934 host target genes. The mRNA of each one of this plurality of VGAM1934 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1934 RNA, herein designated VGAM

RNA, and which when bound by VGAM1934 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1934 host target proteins.

[27041] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1934 gene, herein designated VGAM GENE, on one or more VGAM1934 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27042] It is yet further appreciated that a function of VGAM1934 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM1934 include diagnosis, prevention and treatment of viral infection by Human herpesvirus 4. Specific functions, and accordingly utilities, of VGAM1934 correlate with, and may be deduced from, the identity of the host target genes which VGAM1934 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[27043] Nucleotide sequences of the VGAM1934 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1934 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1934 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1934 are further described hereinbelow with reference to Table 1.

[27044] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1934 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[27045] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Mes-

senger 1935 (VGAM1935) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[27046] VGAM1935 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1935 was detected is described hereinabove with reference to Figs. 2-8.

[27047] VGAM1935 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human herpesvirus 4. VGAM1935 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[27048] VGAM1935 gene, herein designated VGAM GENE, encodes a VGAM1935 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1935 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1935 precursor RNA is designated SEQ ID:1921, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1921 is located at position

155556 relative to the genome of Human herpesvirus 4.

[27049] VGAM1935 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1935 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27050] An enzyme complex designated DICER COMPLEX, dices the VGAM1935 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1935 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM1935 RNA is designated SEQ ID:4646, and is provided hereinbelow with reference to the sequence listing part.

[27051] VGAM1935 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1935 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1935 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[27052] VGAM1935 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1935 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1935 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1935 RNA, herein designated

VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1935 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[27053] The complementary binding of VGAM1935 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1935 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1935 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1935 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[27054] It is appreciated that VGAM1935 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1935 host target genes. The mRNA of each one of this plurality of VGAM1935 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM1935 RNA, herein designated VGAM RNA, and which when bound by VGAM1935 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1935 host target proteins.

[27055] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1935 gene, herein designated VGAM GENE, on one or more VGAM1935 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27056] It is yet further appreciated that a function of VGAM1935 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1935 include diagnosis, prevention and treatment of viral infection by Human herpesvirus 4. Specific functions, and accordingly utilities, of VGAM1935 correlate with, and may be deduced from, the identity of the host target genes which VGAM1935 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[27057] Nucleotide sequences of the VGAM1935 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1935 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1935 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1935 are further described hereinbelow with reference to Table 1.

[27058] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1935 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[27059] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present

invention, referred to here as Viral Genomic Address Messenger 1936 (VGAM1936) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[27060] VGAM1936 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1936 was detected is described hereinabove with reference to Figs. 2-8.

[27061] VGAM1936 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human herpesvirus 4. VGAM1936 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[27062] VGAM1936 gene, herein designated VGAM GENE, encodes a VGAM1936 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1936 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1936 precursor RNA is designated SEQ ID:1922, and is provided hereinbelow with reference to the sequence listing part. Nu-

cleotide sequence SEQ ID:1922 is located at position 152064 relative to the genome of Human herpesvirus 4.

[27063] VGAM1936 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1936 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27064] An enzyme complex designated DICER COMPLEX, dices the VGAM1936 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1936 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM1936 RNA is designated SEQ ID:4647, and is provided hereinbelow with reference to the sequence

listing part.

[27065] VGAM1936 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1936 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1936 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[27066] VGAM1936 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1936 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1936 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not

meant to be limiting VGAM1936 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1936 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[27067] The complementary binding of VGAM1936 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1936 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1936 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1936 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[27068] It is appreciated that VGAM1936 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1936 host target genes. The mRNA of each one of this plurality of VGAM1936 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM1936 RNA, herein designated VGAM RNA, and which when bound by VGAM1936 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1936 host target proteins.

[27069] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1936 gene, herein designated VGAM GENE, on one or more VGAM1936 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27070] It is yet further appreciated that a function of VGAM1936

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1936 include diagnosis, prevention and treatment of viral infection by Human herpesvirus 4. Specific functions, and accordingly utilities, of VGAM1936 correlate with, and may be deduced from, the identity of the host target genes which VGAM1936 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[27071] Nucleotide sequences of the VGAM1936 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1936 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1936 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1936 are further described hereinbelow with reference to Table 1.

[27072] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1936 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[27073] Fig. 1 further provides a conceptual description of another

novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1937 (VGAM1937) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[27074] VGAM1937 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1937 was detected is described hereinabove with reference to Figs. 2-8.

[27075] VGAM1937 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human herpesvirus 4. VGAM1937 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[27076] VGAM1937 gene, herein designated VGAM GENE, encodes a VGAM1937 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1937 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1937 precursor RNA is designated SEQ ID:1923, and is provided here-

inbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1923 is located at position 161986 relative to the genome of Human herpesvirus 4.

[27077] VGAM1937 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1937 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27078] An enzyme complex designated DICER COMPLEX, dices the VGAM1937 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1937 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM1937 RNA is designated SEQ ID:4648, and

is provided hereinbelow with reference to the sequence listing part.

[27079] VGAM1937 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1937 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1937 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[27080] VGAM1937 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1937 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1937 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites

shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1937 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1937 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[27081] The complementary binding of VGAM1937 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1937 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1937 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1937 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[27082] It is appreciated that VGAM1937 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1937 host target genes. The mRNA of each one of this plurality of VGAM1937 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1937 RNA, herein designated VGAM RNA, and which when bound by VGAM1937 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1937 host target proteins.

[27083] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1937 gene, herein designated VGAM GENE, on one or more VGAM1937 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27084] It is yet further appreciated that a function of VGAM1937 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1937 include diagnosis, prevention and treatment of viral infection by Human herpesvirus 4. Specific functions, and accordingly utilities, of VGAM1937 correlate with, and may be deduced from, the identity of the host target genes which VGAM1937 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[27085] Nucleotide sequences of the VGAM1937 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1937 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1937 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1937 are further described hereinbelow with reference to Table 1.

[27086] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1937 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[27087] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1938 (VGAM1938) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[27088] VGAM1938 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1938 was detected is described hereinabove with reference to Figs. 2-8.

[27089] VGAM1938 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human herpesvirus 4. VGAM1938 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[27090] VGAM1938 gene, herein designated VGAM GENE, encodes a VGAM1938 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1938 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1938 precur-

sor RNA is designated SEQ ID:1924, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1924 is located at position 151796 relative to the genome of Human herpesvirus 4.

[27091] VGAM1938 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1938 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27092] An enzyme complex designated DICER COMPLEX, dices the VGAM1938 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1938 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 52%) nucleotide se-

quence of VGAM1938 RNA is designated SEQ ID:4649, and is provided hereinbelow with reference to the sequence listing part.

[27093] VGAM1938 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1938 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1938 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[27094] VGAM1938 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1938 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1938 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is ap-

preciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1938 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1938 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[27095] The complementary binding of VGAM1938 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1938 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1938 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1938 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[27096] It is appreciated that VGAM1938 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1938 host target genes. The mRNA of

each one of this plurality of VGAM1938 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1938 RNA, herein designated VGAM RNA, and which when bound by VGAM1938 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1938 host target proteins.

[27097] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1938 gene, herein designated VGAM GENE, on one or more VGAM1938 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science

294,779 (2001)).

[27098] It is yet further appreciated that a function of VGAM1938 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1938 include diagnosis, prevention and treatment of viral infection by Human herpesvirus 4. Specific functions, and accordingly utilities, of VGAM1938 correlate with, and may be deduced from, the identity of the host target genes which VGAM1938 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[27099] Nucleotide sequences of the VGAM1938 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1938 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1938 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1938 are further described hereinbelow with reference to Table 1.

[27100] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1938 RNA, herein designated VGAM RNA, are de-

scribed hereinbelow with reference to Table 2.

[27101] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1939 (VGAM1939) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[27102] VGAM1939 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1939 was detected is described hereinabove with reference to Figs. 2-8.

[27103] VGAM1939 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Measles virus.
VGAM1939 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[27104] VGAM1939 gene, herein designated VGAM GENE, encodes a VGAM1939 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1939 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly

similar to the nucleotide sequence of VGAM1939 precursor RNA is designated SEQ ID:1925, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1925 is located at position 15073 relative to the genome of Measles virus.

[27105] VGAM1939 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1939 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27106] An enzyme complex designated DICER COMPLEX, dices the VGAM1939 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1939 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 79%) nucleotide sequence of VGAM1939 RNA is designated SEQ ID:4650, and is provided hereinbelow with reference to the sequence listing part.

[27107] VGAM1939 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1939 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1939 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[27108] VGAM1939 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1939 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1939 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I,

BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1939 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1939 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[27109] The complementary binding of VGAM1939 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1939 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1939 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1939 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[27110] It is appreciated that VGAM1939 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM1939 host target genes. The mRNA of each one of this plurality of VGAM1939 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1939 RNA, herein designated VGAM RNA, and which when bound by VGAM1939 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1939 host target proteins.

[27111] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1939 gene, herein designated VGAM GENE, on one or more VGAM1939 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27112] It is yet further appreciated that a function of VGAM1939 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1939 include diagnosis, prevention and treatment of viral infection by Measles virus. Specific functions, and accordingly utilities, of VGAM1939 correlate with, and may be deduced from, the identity of the host target genes which VGAM1939 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[27113] Nucleotide sequences of the VGAM1939 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1939 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1939 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1939 are further described hereinbelow with reference to Table 1.

[27114] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites

to VGAM1939 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[27115] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1940 (VGAM1940) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[27116] VGAM1940 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1940 was detected is described hereinabove with reference to Figs. 2-8.

[27117] VGAM1940 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Variola virus. VGAM1940 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[27118] VGAM1940 gene, herein designated VGAM GENE, encodes a VGAM1940 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1940 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly

similar to the nucleotide sequence of VGAM1940 precursor RNA is designated SEQ ID:1926, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1926 is located at position 17783 relative to the genome of Variola virus.

[27119] VGAM1940 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1940 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27120] An enzyme complex designated DICER COMPLEX, dices the VGAM1940 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1940 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 53%) nucleotide sequence of VGAM1940 RNA is designated SEQ ID:4651, and is provided hereinbelow with reference to the sequence listing part.

[27121] VGAM1940 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1940 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1940 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[27122] VGAM1940 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1940 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1940 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I,

BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1940 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1940 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[27123] The complementary binding of VGAM1940 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1940 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1940 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1940 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[27124] It is appreciated that VGAM1940 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM1940 host target genes. The mRNA of each one of this plurality of VGAM1940 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1940 RNA, herein designated VGAM RNA, and which when bound by VGAM1940 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1940 host target proteins.

[27125] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1940 gene, herein designated VGAM GENE, on one or more VGAM1940 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27126] It is yet further appreciated that a function of VGAM1940 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1940 include diagnosis, prevention and treatment of viral infection by Variola virus. Specific functions, and accordingly utilities, of VGAM1940 correlate with, and may be deduced from, the identity of the host target genes which VGAM1940 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[27127] Nucleotide sequences of the VGAM1940 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1940 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1940 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1940 are further described hereinbelow with reference to Table 1.

[27128] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites

to VGAM1940 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[27129] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1941 (VGAM1941) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[27130] VGAM1941 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1941 was detected is described hereinabove with reference to Figs. 2-8.

[27131] VGAM1941 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Variola virus. VGAM1941 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[27132] VGAM1941 gene, herein designated VGAM GENE, encodes a VGAM1941 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1941 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly

similar to the nucleotide sequence of VGAM1941 precursor RNA is designated SEQ ID:1927, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1927 is located at position 17196 relative to the genome of Variola virus.

[27133] VGAM1941 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1941 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27134] An enzyme complex designated DICER COMPLEX, dices the VGAM1941 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1941 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 42%) nucleotide sequence of VGAM1941 RNA is designated SEQ ID:4652, and is provided hereinbelow with reference to the sequence listing part.

[27135] VGAM1941 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1941 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1941 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[27136] VGAM1941 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1941 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1941 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I,

BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1941 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1941 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[27137] The complementary binding of VGAM1941 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1941 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1941 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1941 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[27138] It is appreciated that VGAM1941 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM1941 host target genes. The mRNA of each one of this plurality of VGAM1941 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1941 RNA, herein designated VGAM RNA, and which when bound by VGAM1941 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1941 host target proteins.

[27139] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1941 gene, herein designated VGAM GENE, on one or more VGAM1941 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27140] It is yet further appreciated that a function of VGAM1941 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1941 include diagnosis, prevention and treatment of viral infection by Variola virus. Specific functions, and accordingly utilities, of VGAM1941 correlate with, and may be deduced from, the identity of the host target genes which VGAM1941 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[27141] Nucleotide sequences of the VGAM1941 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1941 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1941 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1941 are further described hereinbelow with reference to Table 1.

[27142] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites

to VGAM1941 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[27143] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1942 (VGAM1942) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[27144] VGAM1942 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1942 was detected is described hereinabove with reference to Figs. 2-8.

[27145] VGAM1942 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Variola virus. VGAM1942 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[27146] VGAM1942 gene, herein designated VGAM GENE, encodes a VGAM1942 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1942 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly

similar to the nucleotide sequence of VGAM1942 precursor RNA is designated SEQ ID:1928, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1928 is located at position 17313 relative to the genome of Variola virus.

[27147] VGAM1942 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1942 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27148] An enzyme complex designated DICER COMPLEX, dices the VGAM1942 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1942 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 81%) nucleotide sequence of VGAM1942 RNA is designated SEQ ID:4653, and is provided hereinbelow with reference to the sequence listing part.

[27149] VGAM1942 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1942 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1942 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[27150] VGAM1942 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1942 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1942 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I,

BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1942 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1942 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[27151] The complementary binding of VGAM1942 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1942 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1942 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1942 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[27152] It is appreciated that VGAM1942 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM1942 host target genes. The mRNA of each one of this plurality of VGAM1942 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1942 RNA, herein designated VGAM RNA, and which when bound by VGAM1942 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1942 host target proteins.

[27153] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1942 gene, herein designated VGAM GENE, on one or more VGAM1942 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27154] It is yet further appreciated that a function of VGAM1942 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1942 include diagnosis, prevention and treatment of viral infection by Variola virus. Specific functions, and accordingly utilities, of VGAM1942 correlate with, and may be deduced from, the identity of the host target genes which VGAM1942 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[27155] Nucleotide sequences of the VGAM1942 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1942 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1942 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1942 are further described hereinbelow with reference to Table 1.

[27156] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites

to VGAM1942 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[27157] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1943 (VGAM1943) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[27158] VGAM1943 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1943 was detected is described hereinabove with reference to Figs. 2-8.

[27159] VGAM1943 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Variola virus. VGAM1943 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[27160] VGAM1943 gene, herein designated VGAM GENE, encodes a VGAM1943 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1943 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly

similar to the nucleotide sequence of VGAM1943 precursor RNA is designated SEQ ID:1929, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1929 is located at position 6220 relative to the genome of Variola virus.

[27161] VGAM1943 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1943 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27162] An enzyme complex designated DICER COMPLEX, dices the VGAM1943 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1943 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 43%) nucleotide sequence of VGAM1943 RNA is designated SEQ ID:4654, and is provided hereinbelow with reference to the sequence listing part.

[27163] VGAM1943 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1943 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1943 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[27164] VGAM1943 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1943 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1943 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I,

BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1943 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1943 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[27165] The complementary binding of VGAM1943 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1943 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1943 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1943 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[27166] It is appreciated that VGAM1943 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM1943 host target genes. The mRNA of each one of this plurality of VGAM1943 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1943 RNA, herein designated VGAM RNA, and which when bound by VGAM1943 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1943 host target proteins.

[27167] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1943 gene, herein designated VGAM GENE, on one or more VGAM1943 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27168] It is yet further appreciated that a function of VGAM1943 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1943 include diagnosis, prevention and treatment of viral infection by Variola virus. Specific functions, and accordingly utilities, of VGAM1943 correlate with, and may be deduced from, the identity of the host target genes which VGAM1943 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[27169] Nucleotide sequences of the VGAM1943 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1943 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1943 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1943 are further described hereinbelow with reference to Table 1.

[27170] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites

to VGAM1943 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[27171] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1944 (VGAM1944) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[27172] VGAM1944 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1944 was detected is described hereinabove with reference to Figs. 2-8.

[27173] VGAM1944 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Variola virus. VGAM1944 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[27174] VGAM1944 gene, herein designated VGAM GENE, encodes a VGAM1944 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1944 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly

similar to the nucleotide sequence of VGAM1944 precursor RNA is designated SEQ ID:1930, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1930 is located at position 4789 relative to the genome of Variola virus.

[27175] VGAM1944 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1944 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27176] An enzyme complex designated DICER COMPLEX, dices the VGAM1944 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1944 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 45%) nucleotide sequence of VGAM1944 RNA is designated SEQ ID:4655, and is provided hereinbelow with reference to the sequence listing part.

[27177] VGAM1944 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1944 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1944 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[27178] VGAM1944 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1944 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1944 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I,

BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1944 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1944 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[27179] The complementary binding of VGAM1944 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1944 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1944 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1944 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[27180] It is appreciated that VGAM1944 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM1944 host target genes. The mRNA of each one of this plurality of VGAM1944 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1944 RNA, herein designated VGAM RNA, and which when bound by VGAM1944 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1944 host target proteins.

[27181] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1944 gene, herein designated VGAM GENE, on one or more VGAM1944 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27182] It is yet further appreciated that a function of VGAM1944 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1944 include diagnosis, prevention and treatment of viral infection by Variola virus. Specific functions, and accordingly utilities, of VGAM1944 correlate with, and may be deduced from, the identity of the host target genes which VGAM1944 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[27183] Nucleotide sequences of the VGAM1944 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1944 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1944 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1944 are further described hereinbelow with reference to Table 1.

[27184] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites

to VGAM1944 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[27185] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1945 (VGAM1945) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[27186] VGAM1945 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1945 was detected is described hereinabove with reference to Figs. 2-8.

[27187] VGAM1945 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Variola virus. VGAM1945 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[27188] VGAM1945 gene, herein designated VGAM GENE, encodes a VGAM1945 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1945 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly

similar to the nucleotide sequence of VGAM1945 precursor RNA is designated SEQ ID:1931, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1931 is located at position 7746 relative to the genome of Variola virus.

[27189] VGAM1945 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1945 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27190] An enzyme complex designated DICER COMPLEX, dices the VGAM1945 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1945 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 41%) nucleotide sequence of VGAM1945 RNA is designated SEQ ID:4656, and is provided hereinbelow with reference to the sequence listing part.

[27191] VGAM1945 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1945 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1945 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[27192] VGAM1945 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1945 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1945 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I,

BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1945 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1945 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[27193] The complementary binding of VGAM1945 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1945 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1945 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1945 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[27194] It is appreciated that VGAM1945 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM1945 host target genes. The mRNA of each one of this plurality of VGAM1945 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1945 RNA, herein designated VGAM RNA, and which when bound by VGAM1945 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1945 host target proteins.

[27195] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1945 gene, herein designated VGAM GENE, on one or more VGAM1945 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27196] It is yet further appreciated that a function of VGAM1945 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1945 include diagnosis, prevention and treatment of viral infection by Variola virus. Specific functions, and accordingly utilities, of VGAM1945 correlate with, and may be deduced from, the identity of the host target genes which VGAM1945 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[27197] Nucleotide sequences of the VGAM1945 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1945 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1945 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1945 are further described hereinbelow with reference to Table 1.

[27198] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites

to VGAM1945 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[27199] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1946 (VGAM1946) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[27200] VGAM1946 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1946 was detected is described hereinabove with reference to Figs. 2-8.

[27201] VGAM1946 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Variola virus. VGAM1946 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[27202] VGAM1946 gene, herein designated VGAM GENE, encodes a VGAM1946 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1946 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly

similar to the nucleotide sequence of VGAM1946 precursor RNA is designated SEQ ID:1932, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1932 is located at position 11538 relative to the genome of Variola virus.

[27203] VGAM1946 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1946 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27204] An enzyme complex designated DICER COMPLEX, dices the VGAM1946 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1946 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 42%) nucleotide sequence of VGAM1946 RNA is designated SEQ ID:4657, and is provided hereinbelow with reference to the sequence listing part.

[27205] VGAM1946 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1946 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1946 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[27206] VGAM1946 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1946 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1946 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I,

BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1946 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1946 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[27207] The complementary binding of VGAM1946 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1946 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1946 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1946 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[27208] It is appreciated that VGAM1946 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM1946 host target genes. The mRNA of each one of this plurality of VGAM1946 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1946 RNA, herein designated VGAM RNA, and which when bound by VGAM1946 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1946 host target proteins.

[27209] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1946 gene, herein designated VGAM GENE, on one or more VGAM1946 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27210] It is yet further appreciated that a function of VGAM1946 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1946 include diagnosis, prevention and treatment of viral infection by Variola virus. Specific functions, and accordingly utilities, of VGAM1946 correlate with, and may be deduced from, the identity of the host target genes which VGAM1946 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[27211] Nucleotide sequences of the VGAM1946 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1946 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1946 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1946 are further described hereinbelow with reference to Table 1.

[27212] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites

to VGAM1946 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[27213] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1947 (VGAM1947) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[27214] VGAM1947 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1947 was detected is described hereinabove with reference to Figs. 2-8.

[27215] VGAM1947 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Variola virus. VGAM1947 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[27216] VGAM1947 gene, herein designated VGAM GENE, encodes a VGAM1947 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1947 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly

similar to the nucleotide sequence of VGAM1947 precursor RNA is designated SEQ ID:1933, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1933 is located at position 16704 relative to the genome of Variola virus.

[27217] VGAM1947 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1947 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27218] An enzyme complex designated DICER COMPLEX, dices the VGAM1947 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1947 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 68%) nucleotide sequence of VGAM1947 RNA is designated SEQ ID:4658, and is provided hereinbelow with reference to the sequence listing part.

[27219] VGAM1947 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1947 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1947 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[27220] VGAM1947 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1947 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1947 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I,

BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1947 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1947 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[27221] The complementary binding of VGAM1947 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1947 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1947 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1947 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[27222] It is appreciated that VGAM1947 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM1947 host target genes. The mRNA of each one of this plurality of VGAM1947 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1947 RNA, herein designated VGAM RNA, and which when bound by VGAM1947 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1947 host target proteins.

[27223] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1947 gene, herein designated VGAM GENE, on one or more VGAM1947 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27224] It is yet further appreciated that a function of VGAM1947 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1947 include diagnosis, prevention and treatment of viral infection by Variola virus. Specific functions, and accordingly utilities, of VGAM1947 correlate with, and may be deduced from, the identity of the host target genes which VGAM1947 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[27225] Nucleotide sequences of the VGAM1947 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1947 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1947 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1947 are further described hereinbelow with reference to Table 1.

[27226] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites

to VGAM1947 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[27227] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1948 (VGAM1948) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[27228] VGAM1948 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1948 was detected is described hereinabove with reference to Figs. 2-8.

[27229] VGAM1948 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Avian paramyxovirus 6. VGAM1948 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[27230] VGAM1948 gene, herein designated VGAM GENE, encodes a VGAM1948 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1948 precursor RNA, herein designated VGAM PRECURSOR RNA, does not en-

code a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1948 precursor RNA is designated SEQ ID:1934, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1934 is located at position 4256 relative to the genome of Avian paramyxovirus 6.

[27231] VGAM1948 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1948 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27232] An enzyme complex designated DICER COMPLEX, dices the VGAM1948 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1948 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM1948 RNA is designated SEQ ID:4659, and is provided hereinbelow with reference to the sequence listing part.

[27233] VGAM1948 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1948 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1948 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[27234] VGAM1948 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1948 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1948 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3

such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1948 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1948 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[27235] The complementary binding of VGAM1948 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1948 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1948 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1948 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[27236] It is appreciated that VGAM1948 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1948 host target genes. The mRNA of each one of this plurality of VGAM1948 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1948 RNA, herein designated VGAM RNA, and which when bound by VGAM1948 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1948 host target proteins.

[27237] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1948 gene, herein designated VGAM GENE, on one or more VGAM1948 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27238] It is yet further appreciated that a function of VGAM1948 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1948 include diagnosis, prevention and treatment of viral infection by Avian paramyxovirus 6. Specific functions, and accordingly utilities, of VGAM1948 correlate with, and may be deduced from, the identity of the host target genes which VGAM1948 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[27239] Nucleotide sequences of the VGAM1948 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1948 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1948 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1948 are further described hereinbelow with reference to Table 1.

[27240] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the

complementarity of each of these host target binding sites to VGAM1948 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[27241] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1949 (VGAM1949) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[27242] VGAM1949 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1949 was detected is described hereinabove with reference to Figs. 2-8.

[27243] VGAM1949 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Avian paramyxovirus 6. VGAM1949 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[27244] VGAM1949 gene, herein designated VGAM GENE, encodes a VGAM1949 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1949 precursor RNA,

herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1949 precursor RNA is designated SEQ ID:1935, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1935 is located at position 14249 relative to the genome of Avian paramyxovirus 6.

[27245] VGAM1949 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1949 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27246] An enzyme complex designated DICER COMPLEX, dices the VGAM1949 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1949 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM1949 RNA is designated SEQ ID:4660, and is provided hereinbelow with reference to the sequence listing part.

[27247] VGAM1949 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1949 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1949 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[27248] VGAM1949 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1949 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1949 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host

target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1949 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1949 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[27249] The complementary binding of VGAM1949 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1949 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1949 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1949 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[27250] It is appreciated that VGAM1949 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1949 host target genes. The mRNA of each one of this plurality of VGAM1949 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1949 RNA, herein designated VGAM RNA, and which when bound by VGAM1949 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1949 host target proteins.

[27251] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1949 gene, herein designated VGAM GENE, on one or more VGAM1949 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27252] It is yet further appreciated that a function of VGAM1949 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1949 include diagnosis, prevention and treatment of viral infection by Avian paramyxovirus 6. Specific functions, and accordingly utilities, of VGAM1949 correlate with, and may be deduced from, the identity of the host target genes which VGAM1949 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[27253] Nucleotide sequences of the VGAM1949 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1949 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1949 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1949 are further described hereinbelow with reference to Table 1.

[27254] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1949 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[27255] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1950 (VGAM1950) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[27256] VGAM1950 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1950 was detected is described hereinabove with reference to Figs. 2-8.

[27257] VGAM1950 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Avian paramyxovirus 6. VGAM1950 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[27258] VGAM1950 gene, herein designated VGAM GENE, encodes a VGAM1950 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and un-

like most ordinary genes, VGAM1950 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1950 precursor RNA is designated SEQ ID:1936, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1936 is located at position 14024 relative to the genome of Avian paramyxovirus 6.

[27259] VGAM1950 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1950 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27260] An enzyme complex designated DICER COMPLEX, dices the VGAM1950 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1950 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM1950 RNA is designated SEQ ID:4661, and is provided hereinbelow with reference to the sequence listing part.

[27261] VGAM1950 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1950 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1950 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[27262] VGAM1950 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1950 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1950 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed

sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1950 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1950 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[27263] The complementary binding of VGAM1950 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1950 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1950 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1950 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target

protein is therefore outlined by a broken line.

[27264] It is appreciated that VGAM1950 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1950 host target genes. The mRNA of each one of this plurality of VGAM1950 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1950 RNA, herein designated VGAM RNA, and which when bound by VGAM1950 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1950 host target proteins.

[27265] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1950 gene, herein designated VGAM GENE, on one or more VGAM1950 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27266] It is yet further appreciated that a function of VGAM1950 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1950 include diagnosis, prevention and treatment of viral infection by Avian paramyxovirus 6. Specific functions, and accordingly utilities, of VGAM1950 correlate with, and may be deduced from, the identity of the host target genes which VGAM1950 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[27267] Nucleotide sequences of the VGAM1950 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1950 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1950 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1950 are further described hereinbelow with reference to Table 1.

[27268] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1950 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[27269] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1951 (VGAM1951) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[27270] VGAM1951 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1951 was detected is described hereinabove with reference to Figs. 2-8.

[27271] VGAM1951 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Avian paramyxovirus 6. VGAM1951 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[27272] VGAM1951 gene, herein designated VGAM GENE, encodes a VGAM1951 precursor RNA, herein designated VGAM

PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1951 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1951 precursor RNA is designated SEQ ID:1937, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1937 is located at position 5552 relative to the genome of Avian paramyxovirus 6.

[27273] VGAM1951 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1951 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27274] An enzyme complex designated DICER COMPLEX, dices the VGAM1951 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1951 RNA, herein designated VGAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM1951 RNA is designated SEQ ID:4662, and is provided hereinbelow with reference to the sequence listing part.

[27275] VGAM1951 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1951 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1951 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[27276] VGAM1951 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1951 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1951 RNA, herein designated

VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1951 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1951 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[27277] The complementary binding of VGAM1951 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1951 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1951 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1951 host target protein, herein desig-

nated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[27278] It is appreciated that VGAM1951 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1951 host target genes. The mRNA of each one of this plurality of VGAM1951 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1951 RNA, herein designated VGAM RNA, and which when bound by VGAM1951 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1951 host target proteins.

[27279] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1951 gene, herein designated VGAM GENE, on one or more VGAM1951 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27280] It is yet further appreciated that a function of VGAM1951 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1951 include diagnosis, prevention and treatment of viral infection by Avian paramyxovirus 6. Specific functions, and accordingly utilities, of VGAM1951 correlate with, and may be deduced from, the identity of the host target genes which VGAM1951 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[27281] Nucleotide sequences of the VGAM1951 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1951 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1951 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1951 are further described hereinbelow with reference to Table 1.

[27282] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1951 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[27283] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1952 (VGAM1952) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[27284] VGAM1952 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1952 was detected is described hereinabove with reference to Figs. 2-8.

[27285] VGAM1952 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Avian paramyxovirus 6. VGAM1952 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[27286] VGAM1952 gene, herein designated VGAM GENE, encodes

a VGAM1952 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1952 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1952 precursor RNA is designated SEQ ID:1938, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1938 is located at position 12992 relative to the genome of Avian paramyxovirus 6.

[27287] VGAM1952 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1952 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27288] An enzyme complex designated DICER COMPLEX, dices the VGAM1952 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1952 RNA,

herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM1952 RNA is designated SEQ ID:4663, and is provided hereinbelow with reference to the sequence listing part.

[27289] VGAM1952 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1952 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1952 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[27290] VGAM1952 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1952 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM1952 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1952 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1952 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[27291] The complementary binding of VGAM1952 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1952 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1952 host target RNA, herein designated VGAM HOST TARGET

RNA, into VGAM1952 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[27292] It is appreciated that VGAM1952 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1952 host target genes. The mRNA of each one of this plurality of VGAM1952 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1952 RNA, herein designated VGAM RNA, and which when bound by VGAM1952 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1952 host target proteins.

[27293] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1952 gene, herein designated VGAM GENE, on one or more VGAM1952 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27294] It is yet further appreciated that a function of VGAM1952 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1952 include diagnosis, prevention and treatment of viral infection by Avian paramyxovirus 6. Specific functions, and accordingly utilities, of VGAM1952 correlate with, and may be deduced from, the identity of the host target genes which VGAM1952 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[27295] Nucleotide sequences of the VGAM1952 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1952 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1952 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1952 are further

described hereinbelow with reference to Table 1.

[27296] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1952 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[27297] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1953 (VGAM1953) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[27298] VGAM1953 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1953 was detected is described hereinabove with reference to Figs. 2-8.

[27299] VGAM1953 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Avian paramyxovirus 6. VGAM1953 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[27300] VGAM1953 gene, herein designated VGAM GENE, encodes a VGAM1953 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1953 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1953 precursor RNA is designated SEQ ID:1939, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1939 is located at position 3760 relative to the genome of Avian paramyxovirus 6.

[27301] VGAM1953 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1953 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27302] An enzyme complex designated DICER COMPLEX, dices the VGAM1953 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, into VGAM1953 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM1953 RNA is designated SEQ ID:4664, and is provided hereinbelow with reference to the sequence listing part.

[27303] VGAM1953 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1953 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1953 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[27304] VGAM1953 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1953 host target RNA, herein designated VGAM HOST TARGET RNA. This

complementary binding is due to the fact that the nucleotide sequence of VGAM1953 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1953 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1953 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[27305] The complementary binding of VGAM1953 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1953 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1953

host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1953 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[27306] It is appreciated that VGAM1953 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1953 host target genes. The mRNA of each one of this plurality of VGAM1953 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1953 RNA, herein designated VGAM RNA, and which when bound by VGAM1953 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1953 host target proteins.

[27307] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1953 gene, herein designated VGAM GENE, on one or more VGAM1953 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27308] It is yet further appreciated that a function of VGAM1953 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1953 include diagnosis, prevention and treatment of viral infection by Avian paramyxovirus 6. Specific functions, and accordingly utilities, of VGAM1953 correlate with, and may be deduced from, the identity of the host target genes which VGAM1953 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[27309] Nucleotide sequences of the VGAM1953 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1953 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1953 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM1953 are further described hereinbelow with reference to Table 1.

[27310] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1953 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[27311] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1954 (VGAM1954) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[27312] VGAM1954 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1954 was detected is described hereinabove with reference to Figs. 2-8.

[27313] VGAM1954 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Avian paramyxovirus 6. VGAM1954 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the

human genome.

[27314] VGAM1954 gene, herein designated VGAM GENE, encodes a VGAM1954 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1954 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1954 precursor RNA is designated SEQ ID:1940, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1940 is located at position 6741 relative to the genome of Avian paramyxovirus 6.

[27315] VGAM1954 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1954 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27316] An enzyme complex designated DICER COMPLEX, dices

the VGAM1954 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1954 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 70%) nucleotide sequence of VGAM1954 RNA is designated SEQ ID:4665, and is provided hereinbelow with reference to the sequence listing part.

[27317] VGAM1954 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1954 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1954 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[27318] VGAM1954 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1954 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1954 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1954 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1954 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[27319] The complementary binding of VGAM1954 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1954 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM1954 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1954 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[27320] It is appreciated that VGAM1954 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1954 host target genes. The mRNA of each one of this plurality of VGAM1954 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1954 RNA, herein designated VGAM RNA, and which when bound by VGAM1954 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1954 host target proteins.

[27321] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1954 gene, herein designated VGAM GENE, on one or more VGAM1954 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27322] It is yet further appreciated that a function of VGAM1954 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1954 include diagnosis, prevention and treatment of viral infection by Avian paramyxovirus 6. Specific functions, and accordingly utilities, of VGAM1954 correlate with, and may be deduced from, the identity of the host target genes which VGAM1954 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[27323] Nucleotide sequences of the VGAM1954 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1954 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of

VGAM1954 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1954 are further described hereinbelow with reference to Table 1.

[27324] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1954 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[27325] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1955 (VGAM1955) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[27326] VGAM1955 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1955 was detected is described hereinabove with reference to Figs. 2-8.

[27327] VGAM1955 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Macaca mulatta rhadinovirus. VGAM1955 host target gene, herein designated

VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[27328] VGAM1955 gene, herein designated VGAM GENE, encodes a VGAM1955 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1955 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1955 precursor RNA is designated SEQ ID:1941, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1941 is located at position 6373 relative to the genome of Macaca mulatta rhadinovirus.

[27329] VGAM1955 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1955 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27330] An enzyme complex designated DICER COMPLEX, dices the VGAM1955 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1955 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 49%) nucleotide sequence of VGAM1955 RNA is designated SEQ ID:4666, and is provided hereinbelow with reference to the sequence listing part.

[27331] VGAM1955 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1955 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1955 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[27332] VGAM1955 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites

located in untranslated regions of VGAM1955 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1955 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1955 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1955 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[27333] The complementary binding of VGAM1955 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1955 host target RNA, herein designated VGAM

HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1955 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1955 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[27334] It is appreciated that VGAM1955 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1955 host target genes. The mRNA of each one of this plurality of VGAM1955 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1955 RNA, herein designated VGAM RNA, and which when bound by VGAM1955 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1955 host target proteins.

[27335] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1955 gene, herein designated VGAM GENE, on one or more VGAM1955 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove

with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27336] It is yet further appreciated that a function of VGAM1955 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1955 include diagnosis, prevention and treatment of viral infection by Macaca mulatta rhadinovirus. Specific functions, and accordingly utilities, of VGAM1955 correlate with, and may be deduced from, the identity of the host target genes which VGAM1955 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[27337] Nucleotide sequences of the VGAM1955 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1955 RNA, herein designated VGAM RNA, and

a schematic representation of the secondary folding of VGAM1955 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1955 are further described hereinbelow with reference to Table 1.

[27338] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1955 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[27339] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1956 (VGAM1956) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[27340] VGAM1956 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1956 was detected is described hereinabove with reference to Figs. 2-8.

[27341] VGAM1956 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Macaca mulatta rhadi-

novirus. VGAM1956 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[27342] VGAM1956 gene, herein designated VGAM GENE, encodes a VGAM1956 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1956 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1956 precursor RNA is designated SEQ ID:1942, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1942 is located at position 11662 relative to the genome of Macaca mulatta rhadinovirus.

[27343] VGAM1956 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1956 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27344] An enzyme complex designated DICER COMPLEX, dices the VGAM1956 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1956 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM1956 RNA is designated SEQ ID:4667, and is provided hereinbelow with reference to the sequence listing part.

[27345] VGAM1956 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1956 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1956 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[27346] VGAM1956 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1956 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1956 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1956 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1956 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[27347] The complementary binding of VGAM1956 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM1956 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1956 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1956 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[27348] It is appreciated that VGAM1956 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1956 host target genes. The mRNA of each one of this plurality of VGAM1956 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1956 RNA, herein designated VGAM RNA, and which when bound by VGAM1956 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1956 host target proteins.

[27349] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1956 gene, herein designated VGAM GENE, on one or more VGAM1956 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27350] It is yet further appreciated that a function of VGAM1956 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1956 include diagnosis, prevention and treatment of viral infection by Macaca mulatta rhadinovirus. Specific functions, and accordingly utilities, of VGAM1956 correlate with, and may be deduced from, the identity of the host target genes which VGAM1956 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[27351] Nucleotide sequences of the VGAM1956 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the diced VGAM1956 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1956 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1956 are further described hereinbelow with reference to Table 1.

[27352] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1956 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[27353] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1957 (VGAM1957) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[27354] VGAM1957 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1957 was detected is described hereinabove with reference to Figs. 2-8.

[27355] VGAM1957 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Macaca mulatta rhadinovirus. VGAM1957 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[27356] VGAM1957 gene, herein designated VGAM GENE, encodes a VGAM1957 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1957 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1957 precursor RNA is designated SEQ ID:1943, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1943 is located at position 5479 relative to the genome of Macaca mulatta rhadinovirus.

[27357] VGAM1957 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1957 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27358] An enzyme complex designated DICER COMPLEX, dices the VGAM1957 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1957 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM1957 RNA is designated SEQ ID:4668, and is provided hereinbelow with reference to the sequence listing part.

[27359] VGAM1957 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1957 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1957 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN COD-

ING and 3UTR respectively.

[27360] VGAM1957 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1957 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1957 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1957 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1957 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[27361] The complementary binding of VGAM1957 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1957 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1957 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1957 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[27362] It is appreciated that VGAM1957 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1957 host target genes. The mRNA of each one of this plurality of VGAM1957 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1957 RNA, herein designated VGAM RNA, and which when bound by VGAM1957 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1957 host target proteins.

[27363] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1957 gene, herein designated VGAM GENE, on one

or more VGAM1957 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27364] It is yet further appreciated that a function of VGAM1957 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1957 include diagnosis, prevention and treatment of viral infection by Macaca mulatta rhadinovirus. Specific functions, and accordingly utilities, of VGAM1957 correlate with, and may be deduced from, the identity of the host target genes which VGAM1957 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[27365] Nucleotide sequences of the VGAM1957 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1957 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1957 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1957 are further described hereinbelow with reference to Table 1.

[27366] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1957 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[27367] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1958 (VGAM1958) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[27368] VGAM1958 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1958 was detected is de-

scribed hereinabove with reference to Figs. 2-8.

[27369] VGAM1958 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Macaca mulatta rhadinovirus. VGAM1958 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[27370] VGAM1958 gene, herein designated VGAM GENE, encodes a VGAM1958 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1958 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1958 precursor RNA is designated SEQ ID:1944, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1944 is located at position 13516 relative to the genome of Macaca mulatta rhadinovirus.

[27371] VGAM1958 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1958 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27372] An enzyme complex designated DICER COMPLEX, dices the VGAM1958 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1958 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM1958 RNA is designated SEQ ID:4669, and is provided hereinbelow with reference to the sequence listing part.

[27373] VGAM1958 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1958 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1958 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding

gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[27374] VGAM1958 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1958 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1958 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1958 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1958 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be lo-

cated in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[27375] The complementary binding of VGAM1958 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1958 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1958 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1958 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[27376] It is appreciated that VGAM1958 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1958 host target genes. The mRNA of each one of this plurality of VGAM1958 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1958 RNA, herein designated VGAM RNA, and which when bound by VGAM1958 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1958 host target proteins.

[27377] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM1958 gene, herein designated VGAM GENE, on one or more VGAM1958 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27378] It is yet further appreciated that a function of VGAM1958 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1958 include diagnosis, prevention and treatment of viral infection by Macaca mulatta rhadinovirus. Specific functions, and accordingly utilities, of VGAM1958 correlate with, and may be deduced from, the identity of the host target genes which VGAM1958 binds

and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[27379] Nucleotide sequences of the VGAM1958 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1958 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1958 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1958 are further described hereinbelow with reference to Table 1.

[27380] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1958 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[27381] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1959 (VGAM1959) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[27382] VGAM1959 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1959 was detected is described hereinabove with reference to Figs. 2-8.

[27383] VGAM1959 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Macaca mulatta rhadinovirus. VGAM1959 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[27384] VGAM1959 gene, herein designated VGAM GENE, encodes a VGAM1959 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1959 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1959 precursor RNA is designated SEQ ID:1945, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1945 is located at position 16300 relative to the genome of Macaca mulatta rhadinovirus.

[27385] VGAM1959 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1959 folded precursor RNA, herein designated VGAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27386] An enzyme complex designated DICER COMPLEX, dices the VGAM1959 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1959 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM1959 RNA is designated SEQ ID:4670, and is provided hereinbelow with reference to the sequence listing part.

[27387] VGAM1959 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1959 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1959 host target RNA,

herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[27388] VGAM1959 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1959 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1959 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1959 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1959 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host tar-

get binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[27389] The complementary binding of VGAM1959 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1959 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1959 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1959 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[27390] It is appreciated that VGAM1959 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1959 host target genes. The mRNA of each one of this plurality of VGAM1959 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1959 RNA, herein designated VGAM RNA, and which when bound by VGAM1959 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1959 host target proteins.

[27391] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1959 gene, herein designated VGAM GENE, on one or more VGAM1959 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27392] It is yet further appreciated that a function of VGAM1959 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1959 include diagnosis, prevention and treatment of viral infection by Macaca mulatta rhadinovirus. Specific functions, and accordingly utilities, of

VGAM1959 correlate with, and may be deduced from, the identity of the host target genes which VGAM1959 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[27393] Nucleotide sequences of the VGAM1959 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1959 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1959 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1959 are further described hereinbelow with reference to Table 1.

[27394] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1959 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[27395] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1960 (VGAM1960) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the

art.

[27396] VGAM1960 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1960 was detected is described hereinabove with reference to Figs. 2-8.

[27397] VGAM1960 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Macaca mulatta rhadinovirus. VGAM1960 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[27398] VGAM1960 gene, herein designated VGAM GENE, encodes a VGAM1960 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1960 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1960 precursor RNA is designated SEQ ID:1946, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1946 is located at position 10523 relative to the genome of Macaca mulatta rhadinovirus.

[27399] VGAM1960 precursor RNA, herein designated VGAM PRE-

CURSOR RNA, folds onto itself, forming VGAM1960 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27400] An enzyme complex designated DICER COMPLEX, dices the VGAM1960 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1960 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM1960 RNA is designated SEQ ID:4671, and is provided hereinbelow with reference to the sequence listing part.

[27401] VGAM1960 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM1960 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1960 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[27402] VGAM1960 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1960 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1960 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1960 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1960 host

target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[27403] The complementary binding of VGAM1960 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1960 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1960 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1960 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[27404] It is appreciated that VGAM1960 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1960 host target genes. The mRNA of each one of this plurality of VGAM1960 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1960 RNA, herein designated VGAM RNA, and which when bound by VGAM1960 RNA, herein

designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1960 host target proteins.

[27405] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1960 gene, herein designated VGAM GENE, on one or more VGAM1960 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27406] It is yet further appreciated that a function of VGAM1960 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1960 include diagnosis, prevention and

treatment of viral infection by Macaca mulatta rhadinovirus. Specific functions, and accordingly utilities, of VGAM1960 correlate with, and may be deduced from, the identity of the host target genes which VGAM1960 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[27407] Nucleotide sequences of the VGAM1960 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1960 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1960 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1960 are further described hereinbelow with reference to Table 1.

[27408] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1960 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[27409] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1961 (VGAM1961) viral gene, which modulates ex-

pression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[27410] VGAM1961 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1961 was detected is described hereinabove with reference to Figs. 2-8.

[27411] VGAM1961 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Camelpox virus. VGAM1961 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[27412] VGAM1961 gene, herein designated VGAM GENE, encodes a VGAM1961 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1961 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1961 precursor RNA is designated SEQ ID:1947, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1947 is located at position 16323 relative to the genome of Camelpox virus.

[27413] VGAM1961 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1961 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27414] An enzyme complex designated DICER COMPLEX, dices the VGAM1961 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1961 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM1961 RNA is designated SEQ ID:4672, and is provided hereinbelow with reference to the sequence listing part.

[27415] VGAM1961 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1961 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1961 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[27416] VGAM1961 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1961 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1961 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1961 RNA, herein designated VGAM RNA, may have a different number of host target

binding sites in untranslated regions of a VGAM1961 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[27417] The complementary binding of VGAM1961 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1961 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1961 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1961 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[27418] It is appreciated that VGAM1961 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1961 host target genes. The mRNA of each one of this plurality of VGAM1961 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1961 RNA, herein designated VGAM

RNA, and which when bound by VGAM1961 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1961 host target proteins.

[27419] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1961 gene, herein designated VGAM GENE, on one or more VGAM1961 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27420] It is yet further appreciated that a function of VGAM1961 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM1961 include diagnosis, prevention and treatment of viral infection by Camelpox virus. Specific functions, and accordingly utilities, of VGAM1961 correlate with, and may be deduced from, the identity of the host target genes which VGAM1961 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[27421] Nucleotide sequences of the VGAM1961 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1961 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1961 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1961 are further described hereinbelow with reference to Table 1.

[27422] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1961 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[27423] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Mes-

senger 1962 (VGAM1962) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[27424] VGAM1962 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1962 was detected is described hereinabove with reference to Figs. 2-8.

[27425] VGAM1962 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Camelpox virus. VGAM1962 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[27426] VGAM1962 gene, herein designated VGAM GENE, encodes a VGAM1962 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1962 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1962 precursor RNA is designated SEQ ID:1948, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1948 is located at position

16962 relative to the genome of Camelpox virus.

[27427] VGAM1962 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1962 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27428] An enzyme complex designated DICER COMPLEX, dices the VGAM1962 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1962 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM1962 RNA is designated SEQ ID:4673, and is provided hereinbelow with reference to the sequence listing part.

[27429] VGAM1962 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1962 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1962 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[27430] VGAM1962 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1962 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1962 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1962 RNA, herein designated

VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1962 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[27431] The complementary binding of VGAM1962 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1962 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1962 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1962 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[27432] It is appreciated that VGAM1962 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1962 host target genes. The mRNA of each one of this plurality of VGAM1962 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM1962 RNA, herein designated VGAM RNA, and which when bound by VGAM1962 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1962 host target proteins.

[27433] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1962 gene, herein designated VGAM GENE, on one or more VGAM1962 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27434] It is yet further appreciated that a function of VGAM1962 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1962 include diagnosis, prevention and treatment of viral infection by Camelpox virus. Specific functions, and accordingly utilities, of VGAM1962 correlate with, and may be deduced from, the identity of the host target genes which VGAM1962 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[27435] Nucleotide sequences of the VGAM1962 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1962 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1962 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1962 are further described hereinbelow with reference to Table 1.

[27436] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1962 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[27437] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present

invention, referred to here as Viral Genomic Address Messenger 1963 (VGAM1963) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[27438] VGAM1963 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1963 was detected is described hereinabove with reference to Figs. 2-8.

[27439] VGAM1963 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Camelpox virus. VGAM1963 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[27440] VGAM1963 gene, herein designated VGAM GENE, encodes a VGAM1963 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1963 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1963 precursor RNA is designated SEQ ID:1949, and is provided hereinbelow with reference to the sequence listing part. Nu-

cleotide sequence SEQ ID:1949 is located at position 17595 relative to the genome of Camelpox virus.

[27441] VGAM1963 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1963 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27442] An enzyme complex designated DICER COMPLEX, dices the VGAM1963 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1963 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM1963 RNA is designated SEQ ID:4674, and is provided hereinbelow with reference to the sequence

listing part.

[27443] VGAM1963 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1963 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1963 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[27444] VGAM1963 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1963 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1963 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not

meant to be limiting VGAM1963 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1963 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[27445] The complementary binding of VGAM1963 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1963 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1963 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1963 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[27446] It is appreciated that VGAM1963 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1963 host target genes. The mRNA of each one of this plurality of VGAM1963 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM1963 RNA, herein designated VGAM RNA, and which when bound by VGAM1963 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1963 host target proteins.

[27447] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1963 gene, herein designated VGAM GENE, on one or more VGAM1963 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27448] It is yet further appreciated that a function of VGAM1963

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1963 include diagnosis, prevention and treatment of viral infection by Camelpox virus. Specific functions, and accordingly utilities, of VGAM1963 correlate with, and may be deduced from, the identity of the host target genes which VGAM1963 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[27449] Nucleotide sequences of the VGAM1963 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1963 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1963 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1963 are further described hereinbelow with reference to Table 1.

[27450] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1963 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[27451] Fig. 1 further provides a conceptual description of another

novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1964 (VGAM1964) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[27452] VGAM1964 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1964 was detected is described hereinabove with reference to Figs. 2-8.

[27453] VGAM1964 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rana tigrina ranavirus. VGAM1964 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[27454] VGAM1964 gene, herein designated VGAM GENE, encodes a VGAM1964 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1964 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1964 precursor RNA is designated SEQ ID:1950, and is provided here-

inbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1950 is located at position 87983 relative to the genome of Rana tigrina ranavirus.

[27455] VGAM1964 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1964 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27456] An enzyme complex designated DICER COMPLEX, dices the VGAM1964 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1964 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM1964 RNA is designated SEQ ID:4675, and

is provided hereinbelow with reference to the sequence listing part.

[27457] VGAM1964 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1964 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1964 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[27458] VGAM1964 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1964 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1964 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites

shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1964 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1964 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[27459] The complementary binding of VGAM1964 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1964 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1964 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1964 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[27460] It is appreciated that VGAM1964 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1964 host target genes. The mRNA of each one of this plurality of VGAM1964 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1964 RNA, herein designated VGAM RNA, and which when bound by VGAM1964 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1964 host target proteins.

[27461] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1964 gene, herein designated VGAM GENE, on one or more VGAM1964 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27462] It is yet further appreciated that a function of VGAM1964 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1964 include diagnosis, prevention and treatment of viral infection by Rana tigrina ranavirus. Specific functions, and accordingly utilities, of VGAM1964 correlate with, and may be deduced from, the identity of the host target genes which VGAM1964 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[27463] Nucleotide sequences of the VGAM1964 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1964 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1964 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1964 are further described hereinbelow with reference to Table 1.

[27464] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1964 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[27465] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1965 (VGAM1965) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[27466] VGAM1965 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1965 was detected is described hereinabove with reference to Figs. 2-8.

[27467] VGAM1965 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rana tigrina ranavirus. VGAM1965 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[27468] VGAM1965 gene, herein designated VGAM GENE, encodes a VGAM1965 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1965 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1965 precur-

sor RNA is designated SEQ ID:1951, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1951 is located at position 100137 relative to the genome of Rana tigrina ranavirus.

[27469] VGAM1965 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1965 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27470] An enzyme complex designated DICER COMPLEX, dices the VGAM1965 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1965 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide se-

quence of VGAM1965 RNA is designated SEQ ID:4676, and is provided hereinbelow with reference to the sequence listing part.

[27471] VGAM1965 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1965 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1965 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[27472] VGAM1965 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1965 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is ap-

preciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1965 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1965 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[27473] The complementary binding of VGAM1965 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1965 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1965 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1965 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[27474] It is appreciated that VGAM1965 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1965 host target genes. The mRNA of

each one of this plurality of VGAM1965 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1965 RNA, herein designated VGAM RNA, and which when bound by VGAM1965 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1965 host target proteins.

[27475] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1965 gene, herein designated VGAM GENE, on one or more VGAM1965 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science

294,779 (2001)).

[27476] It is yet further appreciated that a function of VGAM1965 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of viral infection by Rana tigrina ranavirus. Specific functions, and accordingly utilities, of VGAM1965 correlate with, and may be deduced from, the identity of the host target genes which VGAM1965 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[27477] Nucleotide sequences of the VGAM1965 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1965 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1965 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1965 are further described hereinbelow with reference to Table 1.

[27478] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1965 RNA, herein designated VGAM RNA, are de-

scribed hereinbelow with reference to Table 2.

[27479] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1966 (VGAM1966) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[27480] VGAM1966 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1966 was detected is described hereinabove with reference to Figs. 2-8.

[27481] VGAM1966 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rana tigrina ranavirus. VGAM1966 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[27482] VGAM1966 gene, herein designated VGAM GENE, encodes a VGAM1966 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1966 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly

similar to the nucleotide sequence of VGAM1966 precursor RNA is designated SEQ ID:1952, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1952 is located at position 88719 relative to the genome of Rana tigrina ranavirus.

[27483] VGAM1966 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1966 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27484] An enzyme complex designated DICER COMPLEX, dices the VGAM1966 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1966 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 71%) nucleotide sequence of VGAM1966 RNA is designated SEQ ID:4677, and is provided hereinbelow with reference to the sequence listing part.

[27485] VGAM1966 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1966 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1966 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[27486] VGAM1966 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1966 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1966 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I,

BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1966 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1966 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[27487] The complementary binding of VGAM1966 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1966 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1966 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1966 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[27488] It is appreciated that VGAM1966 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM1966 host target genes. The mRNA of each one of this plurality of VGAM1966 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1966 RNA, herein designated VGAM RNA, and which when bound by VGAM1966 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1966 host target proteins.

[27489] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1966 gene, herein designated VGAM GENE, on one or more VGAM1966 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27490] It is yet further appreciated that a function of VGAM1966 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1966 include diagnosis, prevention and treatment of viral infection by Rana tigrina ranavirus. Specific functions, and accordingly utilities, of VGAM1966 correlate with, and may be deduced from, the identity of the host target genes which VGAM1966 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[27491] Nucleotide sequences of the VGAM1966 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1966 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1966 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1966 are further described hereinbelow with reference to Table 1.

[27492] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites

to VGAM1966 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[27493] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1967 (VGAM1967) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[27494] VGAM1967 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1967 was detected is described hereinabove with reference to Figs. 2-8.

[27495] VGAM1967 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rana tigrina ranavirus. VGAM1967 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[27496] VGAM1967 gene, herein designated VGAM GENE, encodes a VGAM1967 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1967 precursor RNA, herein designated VGAM PRECURSOR RNA, does not en-

code a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1967 precursor RNA is designated SEQ ID:1953, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1953 is located at position 96311 relative to the genome of Rana tigrina ranavirus.

[27497] VGAM1967 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1967 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27498] An enzyme complex designated DICER COMPLEX, dices the VGAM1967 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1967 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 60%) nucleotide sequence of VGAM1967 RNA is designated SEQ ID:4678, and is provided hereinbelow with reference to the sequence listing part.

[27499] VGAM1967 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1967 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1967 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[27500] VGAM1967 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1967 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1967 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3

such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1967 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1967 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[27501] The complementary binding of VGAM1967 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1967 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1967 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1967 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[27502] It is appreciated that VGAM1967 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1967 host target genes. The mRNA of each one of this plurality of VGAM1967 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1967 RNA, herein designated VGAM RNA, and which when bound by VGAM1967 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1967 host target proteins.

[27503] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1967 gene, herein designated VGAM GENE, on one or more VGAM1967 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27504] It is yet further appreciated that a function of VGAM1967 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1967 include diagnosis, prevention and treatment of viral infection by Rana tigrina ranavirus. Specific functions, and accordingly utilities, of VGAM1967 correlate with, and may be deduced from, the identity of the host target genes which VGAM1967 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[27505] Nucleotide sequences of the VGAM1967 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1967 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1967 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1967 are further described hereinbelow with reference to Table 1.

[27506] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the

complementarity of each of these host target binding sites to VGAM1967 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[27507] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1968 (VGAM1968) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[27508] VGAM1968 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1968 was detected is described hereinabove with reference to Figs. 2-8.

[27509] VGAM1968 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rana tigrina ranavirus. VGAM1968 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[27510] VGAM1968 gene, herein designated VGAM GENE, encodes a VGAM1968 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1968 precursor RNA,

herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1968 precursor RNA is designated SEQ ID:1954, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1954 is located at position 97726 relative to the genome of Rana tigrina ranavirus.

[27511] VGAM1968 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1968 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27512] An enzyme complex designated DICER COMPLEX, dices the VGAM1968 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1968 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM1968 RNA is designated SEQ ID:4679, and is provided hereinbelow with reference to the sequence listing part.

[27513] VGAM1968 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1968 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1968 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[27514] VGAM1968 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1968 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host

target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1968 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1968 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[27515] The complementary binding of VGAM1968 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1968 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1968 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1968 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[27516] It is appreciated that VGAM1968 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1968 host target genes. The mRNA of each one of this plurality of VGAM1968 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1968 RNA, herein designated VGAM RNA, and which when bound by VGAM1968 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1968 host target proteins.

[27517] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1968 gene, herein designated VGAM GENE, on one or more VGAM1968 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27518] It is yet further appreciated that a function of VGAM1968 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of viral infection by Rana tigrina ranavirus. Specific functions, and accordingly utilities, of VGAM1968 correlate with, and may be deduced from, the identity of the host target genes which VGAM1968 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[27519] Nucleotide sequences of the VGAM1968 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1968 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1968 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1968 are further described hereinbelow with reference to Table 1.

[27520] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1968 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[27521] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1969 (VGAM1969) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[27522] VGAM1969 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1969 was detected is described hereinabove with reference to Figs. 2-8.

[27523] VGAM1969 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rana tigrina ranavirus. VGAM1969 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[27524] VGAM1969 gene, herein designated VGAM GENE, encodes a VGAM1969 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and un-

like most ordinary genes, VGAM1969 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1969 precursor RNA is designated SEQ ID:1955, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1955 is located at position 88273 relative to the genome of Rana tigrina ranavirus.

[27525] VGAM1969 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1969 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27526] An enzyme complex designated DICER COMPLEX, dices the VGAM1969 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1969 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 62%) nucleotide sequence of VGAM1969 RNA is designated SEQ ID:4680, and is provided hereinbelow with reference to the sequence listing part.

[27527] VGAM1969 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1969 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1969 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[27528] VGAM1969 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1969 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1969 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed

sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1969 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1969 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[27529] The complementary binding of VGAM1969 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1969 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1969 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1969 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target

protein is therefore outlined by a broken line.

[27530] It is appreciated that VGAM1969 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1969 host target genes. The mRNA of each one of this plurality of VGAM1969 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1969 RNA, herein designated VGAM RNA, and which when bound by VGAM1969 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1969 host target proteins.

[27531] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1969 gene, herein designated VGAM GENE, on one or more VGAM1969 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27532] It is yet further appreciated that a function of VGAM1969 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1969 include diagnosis, prevention and treatment of viral infection by Rana tigrina ranavirus. Specific functions, and accordingly utilities, of VGAM1969 correlate with, and may be deduced from, the identity of the host target genes which VGAM1969 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[27533] Nucleotide sequences of the VGAM1969 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1969 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1969 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1969 are further described hereinbelow with reference to Table 1.

[27534] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1969 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[27535] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1970 (VGAM1970) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[27536] VGAM1970 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1970 was detected is described hereinabove with reference to Figs. 2-8.

[27537] VGAM1970 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rana tigrina ranavirus. VGAM1970 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[27538] VGAM1970 gene, herein designated VGAM GENE, encodes a VGAM1970 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1970 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1970 precur-

sor RNA is designated SEQ ID:1956, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1956 is located at position 98318 relative to the genome of Rana tigrina ranavirus.

[27539] VGAM1970 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1970 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27540] An enzyme complex designated DICER COMPLEX, dices the VGAM1970 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1970 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 67%) nucleotide se-

quence of VGAM1970 RNA is designated SEQ ID:4681, and is provided hereinbelow with reference to the sequence listing part.

[27541] VGAM1970 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1970 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1970 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[27542] VGAM1970 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1970 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1970 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is ap-

preciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1970 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1970 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[27543] The complementary binding of VGAM1970 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1970 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1970 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1970 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[27544] It is appreciated that VGAM1970 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1970 host target genes. The mRNA of

each one of this plurality of VGAM1970 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1970 RNA, herein designated VGAM RNA, and which when bound by VGAM1970 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1970 host target proteins.

[27545] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1970 gene, herein designated VGAM GENE, on one or more VGAM1970 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science

294,779 (2001)).

[27546] It is yet further appreciated that a function of VGAM1970 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1970 include diagnosis, prevention and treatment of viral infection by Rana tigrina ranavirus. Specific functions, and accordingly utilities, of VGAM1970 correlate with, and may be deduced from, the identity of the host target genes which VGAM1970 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[27547] Nucleotide sequences of the VGAM1970 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1970 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1970 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1970 are further described hereinbelow with reference to Table 1.

[27548] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1970 RNA, herein designated VGAM RNA, are de-

scribed hereinbelow with reference to Table 2.

[27549] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1971 (VGAM1971) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[27550] VGAM1971 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1971 was detected is described hereinabove with reference to Figs. 2-8.

[27551] VGAM1971 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rana tigrina ranavirus. VGAM1971 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[27552] VGAM1971 gene, herein designated VGAM GENE, encodes a VGAM1971 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1971 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly

similar to the nucleotide sequence of VGAM1971 precursor RNA is designated SEQ ID:1957, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1957 is located at position 90823 relative to the genome of Rana tigrina ranavirus.

[27553] VGAM1971 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1971 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27554] An enzyme complex designated DICER COMPLEX, dices the VGAM1971 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1971 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 42%) nucleotide sequence of VGAM1971 RNA is designated SEQ ID:4682, and is provided hereinbelow with reference to the sequence listing part.

[27555] VGAM1971 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1971 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1971 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[27556] VGAM1971 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1971 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1971 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I,

BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1971 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1971 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[27557] The complementary binding of VGAM1971 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1971 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1971 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1971 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[27558] It is appreciated that VGAM1971 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM1971 host target genes. The mRNA of each one of this plurality of VGAM1971 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1971 RNA, herein designated VGAM RNA, and which when bound by VGAM1971 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1971 host target proteins.

[27559] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1971 gene, herein designated VGAM GENE, on one or more VGAM1971 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27560] It is yet further appreciated that a function of VGAM1971 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1971 include diagnosis, prevention and treatment of viral infection by Rana tigrina ranavirus. Specific functions, and accordingly utilities, of VGAM1971 correlate with, and may be deduced from, the identity of the host target genes which VGAM1971 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[27561] Nucleotide sequences of the VGAM1971 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1971 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1971 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1971 are further described hereinbelow with reference to Table 1.

[27562] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites

to VGAM1971 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[27563] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1972 (VGAM1972) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[27564] VGAM1972 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1972 was detected is described hereinabove with reference to Figs. 2-8.

[27565] VGAM1972 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Bovine herpesvirus 4. VGAM1972 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[27566] VGAM1972 gene, herein designated VGAM GENE, encodes a VGAM1972 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1972 precursor RNA, herein designated VGAM PRECURSOR RNA, does not en-

code a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1972 precursor RNA is designated SEQ ID:1958, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1958 is located at position 10062 relative to the genome of Bovine herpesvirus 4.

[27567] VGAM1972 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1972 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27568] An enzyme complex designated DICER COMPLEX, dices the VGAM1972 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1972 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 84%) nucleotide sequence of VGAM1972 RNA is designated SEQ ID:4683, and is provided hereinbelow with reference to the sequence listing part.

[27569] VGAM1972 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1972 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1972 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[27570] VGAM1972 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1972 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1972 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3

such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1972 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1972 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[27571] The complementary binding of VGAM1972 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1972 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1972 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1972 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[27572] It is appreciated that VGAM1972 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1972 host target genes. The mRNA of each one of this plurality of VGAM1972 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1972 RNA, herein designated VGAM RNA, and which when bound by VGAM1972 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1972 host target proteins.

[27573] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1972 gene, herein designated VGAM GENE, on one or more VGAM1972 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27574] It is yet further appreciated that a function of VGAM1972 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1972 include diagnosis, prevention and treatment of viral infection by Bovine herpesvirus 4. Specific functions, and accordingly utilities, of VGAM1972 correlate with, and may be deduced from, the identity of the host target genes which VGAM1972 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[27575] Nucleotide sequences of the VGAM1972 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1972 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1972 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1972 are further described hereinbelow with reference to Table 1.

[27576] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the

complementarity of each of these host target binding sites to VGAM1972 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[27577] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1973 (VGAM1973) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[27578] VGAM1973 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1973 was detected is described hereinabove with reference to Figs. 2-8.

[27579] VGAM1973 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Bovine herpesvirus 4. VGAM1973 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[27580] VGAM1973 gene, herein designated VGAM GENE, encodes a VGAM1973 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1973 precursor RNA,

herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1973 precursor RNA is designated SEQ ID:1959, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1959 is located at position 5233 relative to the genome of Bovine herpesvirus 4.

[27581] VGAM1973 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1973 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27582] An enzyme complex designated DICER COMPLEX, dices the VGAM1973 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1973 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM1973 RNA is designated SEQ ID:4684, and is provided hereinbelow with reference to the sequence listing part.

[27583] VGAM1973 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1973 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1973 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[27584] VGAM1973 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1973 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1973 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host

target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1973 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1973 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[27585] The complementary binding of VGAM1973 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1973 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1973 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1973 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[27586] It is appreciated that VGAM1973 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1973 host target genes. The mRNA of each one of this plurality of VGAM1973 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1973 RNA, herein designated VGAM RNA, and which when bound by VGAM1973 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1973 host target proteins.

[27587] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1973 gene, herein designated VGAM GENE, on one or more VGAM1973 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27588] It is yet further appreciated that a function of VGAM1973 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1973 include diagnosis, prevention and treatment of viral infection by Bovine herpesvirus 4. Specific functions, and accordingly utilities, of VGAM1973 correlate with, and may be deduced from, the identity of the host target genes which VGAM1973 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[27589] Nucleotide sequences of the VGAM1973 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1973 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1973 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1973 are further described hereinbelow with reference to Table 1.

[27590] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1973 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[27591] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1974 (VGAM1974) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[27592] VGAM1974 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1974 was detected is described hereinabove with reference to Figs. 2-8.

[27593] VGAM1974 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Bovine herpesvirus 4. VGAM1974 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[27594] VGAM1974 gene, herein designated VGAM GENE, encodes a VGAM1974 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and un-

like most ordinary genes, VGAM1974 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1974 precursor RNA is designated SEQ ID:1960, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1960 is located at position 14078 relative to the genome of Bovine herpesvirus 4.

[27595] VGAM1974 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1974 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27596] An enzyme complex designated DICER COMPLEX, dices the VGAM1974 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1974 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM1974 RNA is designated SEQ ID:4685, and is provided hereinbelow with reference to the sequence listing part.

[27597] VGAM1974 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1974 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1974 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[27598] VGAM1974 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1974 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1974 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed

sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1974 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1974 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[27599] The complementary binding of VGAM1974 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1974 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1974 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1974 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target

protein is therefore outlined by a broken line.

[27600] It is appreciated that VGAM1974 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1974 host target genes. The mRNA of each one of this plurality of VGAM1974 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1974 RNA, herein designated VGAM RNA, and which when bound by VGAM1974 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1974 host target proteins.

[27601] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1974 gene, herein designated VGAM GENE, on one or more VGAM1974 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27602] It is yet further appreciated that a function of VGAM1974 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1974 include diagnosis, prevention and treatment of viral infection by Bovine herpesvirus 4. Specific functions, and accordingly utilities, of VGAM1974 correlate with, and may be deduced from, the identity of the host target genes which VGAM1974 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[27603] Nucleotide sequences of the VGAM1974 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1974 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1974 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1974 are further described hereinbelow with reference to Table 1.

[27604] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1974 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[27605] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1975 (VGAM1975) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[27606] VGAM1975 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1975 was detected is described hereinabove with reference to Figs. 2-8.

[27607] VGAM1975 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Bovine herpesvirus 4. VGAM1975 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[27608] VGAM1975 gene, herein designated VGAM GENE, encodes a VGAM1975 precursor RNA, herein designated VGAM

PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1975 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1975 precursor RNA is designated SEQ ID:1961, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1961 is located at position 9804 relative to the genome of Bovine herpesvirus 4.

[27609] VGAM1975 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1975 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27610] An enzyme complex designated DICER COMPLEX, dices the VGAM1975 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1975 RNA, herein designated VGAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM1975 RNA is designated SEQ ID:4686, and is provided hereinbelow with reference to the sequence listing part.

[27611] VGAM1975 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1975 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1975 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[27612] VGAM1975 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1975 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1975 RNA, herein designated

VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1975 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1975 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[27613] The complementary binding of VGAM1975 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1975 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1975 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1975 host target protein, herein desig-

nated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[27614] It is appreciated that VGAM1975 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1975 host target genes. The mRNA of each one of this plurality of VGAM1975 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1975 RNA, herein designated VGAM RNA, and which when bound by VGAM1975 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1975 host target proteins.

[27615] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1975 gene, herein designated VGAM GENE, on one or more VGAM1975 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27616] It is yet further appreciated that a function of VGAM1975 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1975 include diagnosis, prevention and treatment of viral infection by Bovine herpesvirus 4. Specific functions, and accordingly utilities, of VGAM1975 correlate with, and may be deduced from, the identity of the host target genes which VGAM1975 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[27617] Nucleotide sequences of the VGAM1975 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1975 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1975 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1975 are further described hereinbelow with reference to Table 1.

[27618] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1975 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[27619] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1976 (VGAM1976) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[27620] VGAM1976 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1976 was detected is described hereinabove with reference to Figs. 2-8.

[27621] VGAM1976 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Bovine herpesvirus 4. VGAM1976 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[27622] VGAM1976 gene, herein designated VGAM GENE, encodes

a VGAM1976 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1976 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1976 precursor RNA is designated SEQ ID:1962, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1962 is located at position 13694 relative to the genome of Bovine herpesvirus 4.

[27623] VGAM1976 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1976 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27624] An enzyme complex designated DICER COMPLEX, dices the VGAM1976 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1976 RNA,

herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM1976 RNA is designated SEQ ID:4687, and is provided hereinbelow with reference to the sequence listing part.

[27625] VGAM1976 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1976 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1976 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[27626] VGAM1976 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1976 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM1976 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1976 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1976 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[27627] The complementary binding of VGAM1976 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1976 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1976 host target RNA, herein designated VGAM HOST TARGET

RNA, into VGAM1976 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[27628] It is appreciated that VGAM1976 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1976 host target genes. The mRNA of each one of this plurality of VGAM1976 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1976 RNA, herein designated VGAM RNA, and which when bound by VGAM1976 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1976 host target proteins.

[27629] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1976 gene, herein designated VGAM GENE, on one or more VGAM1976 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27630] It is yet further appreciated that a function of VGAM1976 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1976 include diagnosis, prevention and treatment of viral infection by Bovine herpesvirus 4. Specific functions, and accordingly utilities, of VGAM1976 correlate with, and may be deduced from, the identity of the host target genes which VGAM1976 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[27631] Nucleotide sequences of the VGAM1976 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1976 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1976 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1976 are further

described hereinbelow with reference to Table 1.

[27632] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1976 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[27633] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1977 (VGAM1977) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[27634] VGAM1977 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1977 was detected is described hereinabove with reference to Figs. 2-8.

[27635] VGAM1977 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Bovine herpesvirus 4. VGAM1977 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[27636] VGAM1977 gene, herein designated VGAM GENE, encodes a VGAM1977 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1977 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1977 precursor RNA is designated SEQ ID:1963, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1963 is located at position 5340 relative to the genome of Bovine herpesvirus 4.

[27637] VGAM1977 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1977 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27638] An enzyme complex designated DICER COMPLEX, dices the VGAM1977 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, into VGAM1977 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 48%) nucleotide sequence of VGAM1977 RNA is designated SEQ ID:4688, and is provided hereinbelow with reference to the sequence listing part.

[27639] VGAM1977 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1977 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1977 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[27640] VGAM1977 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1977 host target RNA, herein designated VGAM HOST TARGET RNA. This

complementary binding is due to the fact that the nucleotide sequence of VGAM1977 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1977 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1977 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[27641] The complementary binding of VGAM1977 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1977 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1977

host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1977 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[27642] It is appreciated that VGAM1977 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1977 host target genes. The mRNA of each one of this plurality of VGAM1977 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1977 RNA, herein designated VGAM RNA, and which when bound by VGAM1977 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1977 host target proteins.

[27643] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1977 gene, herein designated VGAM GENE, on one or more VGAM1977 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27644] It is yet further appreciated that a function of VGAM1977 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1977 include diagnosis, prevention and treatment of viral infection by Bovine herpesvirus 4. Specific functions, and accordingly utilities, of VGAM1977 correlate with, and may be deduced from, the identity of the host target genes which VGAM1977 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[27645] Nucleotide sequences of the VGAM1977 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1977 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1977 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM1977 are further described hereinbelow with reference to Table 1.

[27646] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1977 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[27647] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1978 (VGAM1978) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[27648] VGAM1978 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1978 was detected is described hereinabove with reference to Figs. 2-8.

[27649] VGAM1978 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Bovine herpesvirus 4. VGAM1978 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the

human genome.

[27650] VGAM1978 gene, herein designated VGAM GENE, encodes a VGAM1978 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1978 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1978 precursor RNA is designated SEQ ID:1964, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1964 is located at position 2128 relative to the genome of Bovine herpesvirus 4.

[27651] VGAM1978 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1978 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27652] An enzyme complex designated DICER COMPLEX, dices

the VGAM1978 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1978 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 82%) nucleotide sequence of VGAM1978 RNA is designated SEQ ID:4689, and is provided hereinbelow with reference to the sequence listing part.

[27653] VGAM1978 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1978 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1978 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[27654] VGAM1978 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1978 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1978 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1978 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1978 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[27655] The complementary binding of VGAM1978 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1978 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM1978 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1978 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[27656] It is appreciated that VGAM1978 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1978 host target genes. The mRNA of each one of this plurality of VGAM1978 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1978 RNA, herein designated VGAM RNA, and which when bound by VGAM1978 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1978 host target proteins.

[27657] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1978 gene, herein designated VGAM GENE, on one or more VGAM1978 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27658] It is yet further appreciated that a function of VGAM1978 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1978 include diagnosis, prevention and treatment of viral infection by Bovine herpesvirus 4. Specific functions, and accordingly utilities, of VGAM1978 correlate with, and may be deduced from, the identity of the host target genes which VGAM1978 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[27659] Nucleotide sequences of the VGAM1978 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1978 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of

VGAM1978 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1978 are further described hereinbelow with reference to Table 1.

[27660] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1978 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[27661] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1979 (VGAM1979) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[27662] VGAM1979 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1979 was detected is described hereinabove with reference to Figs. 2-8.

[27663] VGAM1979 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Bovine herpesvirus 4. VGAM1979 host target gene, herein designated VGAM

HOST TARGET GENE, is a human gene contained in the human genome.

[27664] VGAM1979 gene, herein designated VGAM GENE, encodes a VGAM1979 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1979 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1979 precursor RNA is designated SEQ ID:1965, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1965 is located at position 11708 relative to the genome of Bovine herpesvirus 4.

[27665] VGAM1979 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1979 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27666] An enzyme complex designated DICER COMPLEX, dices the VGAM1979 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1979 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 50%) nucleotide sequence of VGAM1979 RNA is designated SEQ ID:4690, and is provided hereinbelow with reference to the sequence listing part.

[27667] VGAM1979 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1979 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1979 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[27668] VGAM1979 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites

located in untranslated regions of VGAM1979 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1979 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1979 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1979 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[27669] The complementary binding of VGAM1979 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1979 host target RNA, herein designated VGAM

HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1979 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1979 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[27670] It is appreciated that VGAM1979 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1979 host target genes. The mRNA of each one of this plurality of VGAM1979 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1979 RNA, herein designated VGAM RNA, and which when bound by VGAM1979 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1979 host target proteins.

[27671] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1979 gene, herein designated VGAM GENE, on one or more VGAM1979 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove

with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27672] It is yet further appreciated that a function of VGAM1979 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1979 include diagnosis, prevention and treatment of viral infection by Bovine herpesvirus 4. Specific functions, and accordingly utilities, of VGAM1979 correlate with, and may be deduced from, the identity of the host target genes which VGAM1979 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[27673] Nucleotide sequences of the VGAM1979 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1979 RNA, herein designated VGAM RNA, and

a schematic representation of the secondary folding of VGAM1979 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1979 are further described hereinbelow with reference to Table 1.

[27674] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1979 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[27675] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1980 (VGAM1980) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[27676] VGAM1980 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1980 was detected is described hereinabove with reference to Figs. 2-8.

[27677] VGAM1980 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Bovine herpesvirus 4.

VGAM1980 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[27678] VGAM1980 gene, herein designated VGAM GENE, encodes a VGAM1980 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1980 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1980 precursor RNA is designated SEQ ID:1966, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1966 is located at position 9455 relative to the genome of Bovine herpesvirus 4.

[27679] VGAM1980 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1980 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[27680] An enzyme complex designated DICER COMPLEX, dices the VGAM1980 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1980 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM1980 RNA is designated SEQ ID:4691, and is provided hereinbelow with reference to the sequence listing part.

[27681] VGAM1980 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1980 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1980 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[27682] VGAM1980 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM1980 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1980 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1980 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1980 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[27683] The complementary binding of VGAM1980 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM1980 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1980 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1980 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[27684] It is appreciated that VGAM1980 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1980 host target genes. The mRNA of each one of this plurality of VGAM1980 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1980 RNA, herein designated VGAM RNA, and which when bound by VGAM1980 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1980 host target proteins.

[27685] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1980 gene, herein designated VGAM GENE, on one or more VGAM1980 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27686] It is yet further appreciated that a function of VGAM1980 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1980 include diagnosis, prevention and treatment of viral infection by Bovine herpesvirus 4. Specific functions, and accordingly utilities, of VGAM1980 correlate with, and may be deduced from, the identity of the host target genes which VGAM1980 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[27687] Nucleotide sequences of the VGAM1980 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

diced VGAM1980 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1980 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1980 are further described hereinbelow with reference to Table 1.

[27688] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1980 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[27689] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1981 (VGAM1981) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[27690] VGAM1981 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1981 was detected is described hereinabove with reference to Figs. 2-8.

[27691] VGAM1981 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of Hendra virus. VGAM1981 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[27692] VGAM1981 gene, herein designated VGAM GENE, encodes a VGAM1981 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1981 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1981 precursor RNA is designated SEQ ID:1967, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1967 is located at position 10871 relative to the genome of Hendra virus.

[27693] VGAM1981 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1981 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27694] An enzyme complex designated DICER COMPLEX, dices the VGAM1981 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1981 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 61%) nucleotide sequence of VGAM1981 RNA is designated SEQ ID:4692, and is provided hereinbelow with reference to the sequence listing part.

[27695] VGAM1981 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1981 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1981 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[27696] VGAM1981 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1981 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1981 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1981 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1981 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[27697] The complementary binding of VGAM1981 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM1981 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1981 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1981 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[27698] It is appreciated that VGAM1981 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1981 host target genes. The mRNA of each one of this plurality of VGAM1981 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1981 RNA, herein designated VGAM RNA, and which when bound by VGAM1981 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1981 host target proteins.

[27699] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1981 gene, herein designated VGAM GENE, on one or more VGAM1981 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27700] It is yet further appreciated that a function of VGAM1981 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1981 include diagnosis, prevention and treatment of viral infection by Hendra virus. Specific functions, and accordingly utilities, of VGAM1981 correlate with, and may be deduced from, the identity of the host target genes which VGAM1981 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[27701] Nucleotide sequences of the VGAM1981 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the diced VGAM1981 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1981 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1981 are further described hereinbelow with reference to Table 1.

[27702] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1981 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[27703] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1982 (VGAM1982) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[27704] VGAM1982 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1982 was detected is described hereinabove with reference to Figs. 2-8.

[27705] VGAM1982 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Hendra virus.

VGAM1982 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[27706] VGAM1982 gene, herein designated VGAM GENE, encodes a VGAM1982 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1982 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1982 precursor RNA is designated SEQ ID:1968, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1968 is located at position 3780 relative to the genome of Hendra virus.

[27707] VGAM1982 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1982 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27708] An enzyme complex designated DICER COMPLEX, dices the VGAM1982 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1982 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM1982 RNA is designated SEQ ID:4693, and is provided hereinbelow with reference to the sequence listing part.

[27709] VGAM1982 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1982 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1982 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN COD-

ING and 3UTR respectively.

[27710] VGAM1982 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1982 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1982 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1982 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1982 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[27711] The complementary binding of VGAM1982 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1982 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1982 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1982 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[27712] It is appreciated that VGAM1982 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1982 host target genes. The mRNA of each one of this plurality of VGAM1982 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1982 RNA, herein designated VGAM RNA, and which when bound by VGAM1982 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1982 host target proteins.

[27713] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1982 gene, herein designated VGAM GENE, on one

or more VGAM1982 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27714] It is yet further appreciated that a function of VGAM1982 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1982 include diagnosis, prevention and treatment of viral infection by Hendra virus. Specific functions, and accordingly utilities, of VGAM1982 correlate with, and may be deduced from, the identity of the host target genes which VGAM1982 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[27715] Nucleotide sequences of the VGAM1982 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1982 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1982 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1982 are further described hereinbelow with reference to Table 1.

[27716] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1982 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[27717] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1983 (VGAM1983) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[27718] VGAM1983 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1983 was detected is de-

scribed hereinabove with reference to Figs. 2-8.

[27719] VGAM1983 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Hendra virus.
VGAM1983 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[27720] VGAM1983 gene, herein designated VGAM GENE, encodes a VGAM1983 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1983 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1983 precursor RNA is designated SEQ ID:1969, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1969 is located at position 5639 relative to the genome of Hendra virus.

[27721] VGAM1983 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1983 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27722] An enzyme complex designated DICER COMPLEX, dices the VGAM1983 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1983 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 70%) nucleotide sequence of VGAM1983 RNA is designated SEQ ID:4694, and is provided hereinbelow with reference to the sequence listing part.

[27723] VGAM1983 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1983 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1983 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and

a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[27724] VGAM1983 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1983 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1983 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1983 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1983 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both

3UTR and 5UTR regions.

[27725] The complementary binding of VGAM1983 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1983 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1983 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1983 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[27726] It is appreciated that VGAM1983 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1983 host target genes. The mRNA of each one of this plurality of VGAM1983 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1983 RNA, herein designated VGAM RNA, and which when bound by VGAM1983 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1983 host target proteins.

[27727] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM1983 gene, herein designated VGAM GENE, on one or more VGAM1983 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27728] It is yet further appreciated that a function of VGAM1983 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1983 include diagnosis, prevention and treatment of viral infection by Hendra virus. Specific functions, and accordingly utilities, of VGAM1983 correlate with, and may be deduced from, the identity of the host target genes which VGAM1983 binds and inhibits, and the function of these host target genes, as elaborated herein-

below.

[27729] Nucleotide sequences of the VGAM1983 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1983 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1983 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1983 are further described hereinbelow with reference to Table 1.

[27730] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1983 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[27731] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1984 (VGAM1984) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[27732] VGAM1984 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene.

The method by which VGAM1984 was detected is described hereinabove with reference to Figs. 2-8.

[27733] VGAM1984 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Hendra virus.

VGAM1984 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[27734] VGAM1984 gene, herein designated VGAM GENE, encodes a VGAM1984 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1984 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1984 precursor RNA is designated SEQ ID:1970, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1970 is located at position 7867 relative to the genome of Hendra virus.

[27735] VGAM1984 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1984 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27736] An enzyme complex designated DICER COMPLEX, dices the VGAM1984 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1984 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM1984 RNA is designated SEQ ID:4695, and is provided hereinbelow with reference to the sequence listing part.

[27737] VGAM1984 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1984 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1984 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding

gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[27738] VGAM1984 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1984 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1984 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1984 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1984 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be lo-

cated in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[27739] The complementary binding of VGAM1984 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1984 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1984 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1984 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[27740] It is appreciated that VGAM1984 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1984 host target genes. The mRNA of each one of this plurality of VGAM1984 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1984 RNA, herein designated VGAM RNA, and which when bound by VGAM1984 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1984 host target proteins.

[27741] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM1984 gene, herein designated VGAM GENE, on one or more VGAM1984 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27742] It is yet further appreciated that a function of VGAM1984 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1984 include diagnosis, prevention and treatment of viral infection by Hendra virus. Specific functions, and accordingly utilities, of VGAM1984 correlate with, and may be deduced from, the identity of the host target genes which VGAM1984 binds and inhibits, and the

function of these host target genes, as elaborated herein-below.

[27743] Nucleotide sequences of the VGAM1984 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1984 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1984 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1984 are further described hereinbelow with reference to Table 1.

[27744] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1984 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[27745] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1985 (VGAM1985) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[27746] VGAM1985 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1985 was detected is described hereinabove with reference to Figs. 2-8.

[27747] VGAM1985 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Hendra virus. VGAM1985 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[27748] VGAM1985 gene, herein designated VGAM GENE, encodes a VGAM1985 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1985 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1985 precursor RNA is designated SEQ ID:1971, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1971 is located at position 3920 relative to the genome of Hendra virus.

[27749] VGAM1985 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1985 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27750] An enzyme complex designated DICER COMPLEX, dices the VGAM1985 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1985 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM1985 RNA is designated SEQ ID:4696, and is provided hereinbelow with reference to the sequence listing part.

[27751] VGAM1985 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1985 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1985 host target RNA, herein designated VGAM HOST TARGET RNA, comprises

three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[27752] VGAM1985 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1985 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1985 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1985 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1985 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an

example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[27753] The complementary binding of VGAM1985 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1985 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1985 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1985 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[27754] It is appreciated that VGAM1985 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1985 host target genes. The mRNA of each one of this plurality of VGAM1985 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1985 RNA, herein designated VGAM RNA, and which when bound by VGAM1985 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1985 host target proteins.

[27755] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1985 gene, herein designated VGAM GENE, on one or more VGAM1985 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27756] It is yet further appreciated that a function of VGAM1985 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1985 include diagnosis, prevention and treatment of viral infection by Hendra virus. Specific functions, and accordingly utilities, of VGAM1985 correlate with, and may be deduced from, the identity of the host

target genes which VGAM1985 binds and inhibits, and the function of these host target genes, as elaborated herein-below.

[27757] Nucleotide sequences of the VGAM1985 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1985 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1985 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1985 are further described hereinbelow with reference to Table 1.

[27758] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1985 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[27759] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1986 (VGAM1986) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[27760] VGAM1986 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1986 was detected is described hereinabove with reference to Figs. 2-8.

[27761] VGAM1986 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Hendra virus. VGAM1986 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[27762] VGAM1986 gene, herein designated VGAM GENE, encodes a VGAM1986 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1986 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1986 precursor RNA is designated SEQ ID:1972, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1972 is located at position 4500 relative to the genome of Hendra virus.

[27763] VGAM1986 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1986 folded precursor RNA, herein designated VGAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27764] An enzyme complex designated DICER COMPLEX, dices the VGAM1986 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1986 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM1986 RNA is designated SEQ ID:4697, and is provided hereinbelow with reference to the sequence listing part.

[27765] VGAM1986 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1986 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1986 host target RNA,

herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[27766] VGAM1986 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1986 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1986 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1986 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1986 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host tar-

get binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[27767] The complementary binding of VGAM1986 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1986 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1986 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1986 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[27768] It is appreciated that VGAM1986 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1986 host target genes. The mRNA of each one of this plurality of VGAM1986 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1986 RNA, herein designated VGAM RNA, and which when bound by VGAM1986 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1986 host target proteins.

[27769] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1986 gene, herein designated VGAM GENE, on one or more VGAM1986 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27770] It is yet further appreciated that a function of VGAM1986 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1986 include diagnosis, prevention and treatment of viral infection by Hendra virus. Specific functions, and accordingly utilities, of VGAM1986 correlate

with, and may be deduced from, the identity of the host target genes which VGAM1986 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[27771] Nucleotide sequences of the VGAM1986 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1986 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1986 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1986 are further described hereinbelow with reference to Table 1.

[27772] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1986 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[27773] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1987 (VGAM1987) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the

art.

[27774] VGAM1987 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1987 was detected is described hereinabove with reference to Figs. 2-8.

[27775] VGAM1987 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Hendra virus.
VGAM1987 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[27776] VGAM1987 gene, herein designated VGAM GENE, encodes a VGAM1987 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1987 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1987 precursor RNA is designated SEQ ID:1973, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1973 is located at position 11388 relative to the genome of Hendra virus.

[27777] VGAM1987 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1987 folded

precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27778] An enzyme complex designated DICER COMPLEX, dices the VGAM1987 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1987 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 72%) nucleotide sequence of VGAM1987 RNA is designated SEQ ID:4698, and is provided hereinbelow with reference to the sequence listing part.

[27779] VGAM1987 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1987 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM1987 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[27780] VGAM1987 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1987 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1987 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1987 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1987 host target RNA, herein designated VGAM HOST TARGET RNA.

It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[27781] The complementary binding of VGAM1987 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1987 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1987 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1987 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[27782] It is appreciated that VGAM1987 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1987 host target genes. The mRNA of each one of this plurality of VGAM1987 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1987 RNA, herein designated VGAM RNA, and which when bound by VGAM1987 RNA, herein designated VGAM RNA, causes inhibition of translation of

respective one or more VGAM1987 host target proteins.

[27783] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1987 gene, herein designated VGAM GENE, on one or more VGAM1987 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27784] It is yet further appreciated that a function of VGAM1987 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1987 include diagnosis, prevention and treatment of viral infection by Hendra virus. Specific func-

tions, and accordingly utilities, of VGAM1987 correlate with, and may be deduced from, the identity of the host target genes which VGAM1987 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[27785] Nucleotide sequences of the VGAM1987 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1987 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1987 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1987 are further described hereinbelow with reference to Table 1.

[27786] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1987 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[27787] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1988 (VGAM1988) viral gene, which modulates expression of respective host target genes thereof, the func-

tion and utility of which host target genes is known in the art.

[27788] VGAM1988 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1988 was detected is described hereinabove with reference to Figs. 2-8.

[27789] VGAM1988 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Hendra virus.
VGAM1988 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[27790] VGAM1988 gene, herein designated VGAM GENE, encodes a VGAM1988 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1988 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1988 precursor RNA is designated SEQ ID:1974, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1974 is located at position 15383 relative to the genome of Hendra virus.

[27791] VGAM1988 precursor RNA, herein designated VGAM PRE-

CURSOR RNA, folds onto itself, forming VGAM1988 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27792] An enzyme complex designated DICER COMPLEX, dices the VGAM1988 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1988 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 61%) nucleotide sequence of VGAM1988 RNA is designated SEQ ID:4699, and is provided hereinbelow with reference to the sequence listing part.

[27793] VGAM1988 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM1988 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1988 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[27794] VGAM1988 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1988 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1988 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1988 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1988 host

target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[27795] The complementary binding of VGAM1988 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1988 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1988 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1988 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[27796] It is appreciated that VGAM1988 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1988 host target genes. The mRNA of each one of this plurality of VGAM1988 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1988 RNA, herein designated VGAM RNA, and which when bound by VGAM1988 RNA, herein

designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1988 host target proteins.

[27797] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1988 gene, herein designated VGAM GENE, on one or more VGAM1988 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27798] It is yet further appreciated that a function of VGAM1988 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1988 include diagnosis, prevention and

treatment of viral infection by Hendra virus. Specific functions, and accordingly utilities, of VGAM1988 correlate with, and may be deduced from, the identity of the host target genes which VGAM1988 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[27799] Nucleotide sequences of the VGAM1988 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1988 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1988 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1988 are further described hereinbelow with reference to Table 1.

[27800] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1988 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[27801] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1989 (VGAM1989) viral gene, which modulates ex-

pression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[27802] VGAM1989 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1989 was detected is described hereinabove with reference to Figs. 2-8.

[27803] VGAM1989 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Hendra virus. VGAM1989 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[27804] VGAM1989 gene, herein designated VGAM GENE, encodes a VGAM1989 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1989 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1989 precursor RNA is designated SEQ ID:1975, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1975 is located at position 1467 relative to the genome of Hendra virus.

[27805] VGAM1989 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1989 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27806] An enzyme complex designated DICER COMPLEX, dices the VGAM1989 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1989 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 47%) nucleotide sequence of VGAM1989 RNA is designated SEQ ID:4700, and is provided hereinbelow with reference to the sequence listing part.

[27807] VGAM1989 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1989 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1989 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[27808] VGAM1989 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1989 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1989 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1989 RNA, herein designated VGAM RNA, may have a different number of host target

binding sites in untranslated regions of a VGAM1989 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[27809] The complementary binding of VGAM1989 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1989 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1989 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1989 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[27810] It is appreciated that VGAM1989 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1989 host target genes. The mRNA of each one of this plurality of VGAM1989 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1989 RNA, herein designated VGAM

RNA, and which when bound by VGAM1989 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1989 host target proteins.

[27811] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1989 gene, herein designated VGAM GENE, on one or more VGAM1989 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27812] It is yet further appreciated that a function of VGAM1989 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM1989 include diagnosis, prevention and treatment of viral infection by Hendra virus. Specific functions, and accordingly utilities, of VGAM1989 correlate with, and may be deduced from, the identity of the host target genes which VGAM1989 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[27813] Nucleotide sequences of the VGAM1989 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1989 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1989 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1989 are further described hereinbelow with reference to Table 1.

[27814] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1989 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[27815] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Mes-

senger 1990 (VGAM1990) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[27816] VGAM1990 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1990 was detected is described hereinabove with reference to Figs. 2-8.

[27817] VGAM1990 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Nipah virus. VGAM1990 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[27818] VGAM1990 gene, herein designated VGAM GENE, encodes a VGAM1990 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1990 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1990 precursor RNA is designated SEQ ID:1976, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1976 is located at position 7327 relative to the genome of Nipah virus.

[27819] VGAM1990 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1990 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27820] An enzyme complex designated DICER COMPLEX, dices the VGAM1990 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1990 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM1990 RNA is designated SEQ ID:4701, and is provided hereinbelow with reference to the sequence listing part.

[27821] VGAM1990 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1990 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1990 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[27822] VGAM1990 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1990 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1990 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1990 RNA, herein designated VGAM RNA, may have a different number of host target

binding sites in untranslated regions of a VGAM1990 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[27823] The complementary binding of VGAM1990 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1990 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1990 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1990 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[27824] It is appreciated that VGAM1990 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1990 host target genes. The mRNA of each one of this plurality of VGAM1990 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1990 RNA, herein designated VGAM

RNA, and which when bound by VGAM1990 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1990 host target proteins.

[27825] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1990 gene, herein designated VGAM GENE, on one or more VGAM1990 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27826] It is yet further appreciated that a function of VGAM1990 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM1990 include diagnosis, prevention and treatment of viral infection by Nipah virus. Specific functions, and accordingly utilities, of VGAM1990 correlate with, and may be deduced from, the identity of the host target genes which VGAM1990 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[27827] Nucleotide sequences of the VGAM1990 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1990 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1990 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1990 are further described hereinbelow with reference to Table 1.

[27828] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1990 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[27829] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Mes-

senger 1991 (VGAM1991) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[27830] VGAM1991 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1991 was detected is described hereinabove with reference to Figs. 2-8.

[27831] VGAM1991 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Nipah virus. VGAM1991 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[27832] VGAM1991 gene, herein designated VGAM GENE, encodes a VGAM1991 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1991 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1991 precursor RNA is designated SEQ ID:1977, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1977 is located at position 2776 relative to the genome of Nipah virus.

[27833] VGAM1991 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1991 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27834] An enzyme complex designated DICER COMPLEX, dices the VGAM1991 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1991 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM1991 RNA is designated SEQ ID:4702, and is provided hereinbelow with reference to the sequence listing part.

[27835] VGAM1991 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1991 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1991 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[27836] VGAM1991 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1991 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1991 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1991 RNA, herein designated VGAM RNA, may have a different number of host target

binding sites in untranslated regions of a VGAM1991 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[27837] The complementary binding of VGAM1991 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1991 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1991 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1991 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[27838] It is appreciated that VGAM1991 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1991 host target genes. The mRNA of each one of this plurality of VGAM1991 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1991 RNA, herein designated VGAM

RNA, and which when bound by VGAM1991 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1991 host target proteins.

[27839] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1991 gene, herein designated VGAM GENE, on one or more VGAM1991 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27840] It is yet further appreciated that a function of VGAM1991 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM1991 include diagnosis, prevention and treatment of viral infection by Nipah virus. Specific functions, and accordingly utilities, of VGAM1991 correlate with, and may be deduced from, the identity of the host target genes which VGAM1991 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[27841] Nucleotide sequences of the VGAM1991 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1991 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1991 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1991 are further described hereinbelow with reference to Table 1.

[27842] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1991 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[27843] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Mes-

senger 1992 (VGAM1992) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[27844] VGAM1992 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1992 was detected is described hereinabove with reference to Figs. 2-8.

[27845] VGAM1992 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Nipah virus. VGAM1992 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[27846] VGAM1992 gene, herein designated VGAM GENE, encodes a VGAM1992 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1992 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1992 precursor RNA is designated SEQ ID:1978, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1978 is located at position 12009 relative to the genome of Nipah virus.

[27847] VGAM1992 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1992 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27848] An enzyme complex designated DICER COMPLEX, dices the VGAM1992 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1992 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 54%) nucleotide sequence of VGAM1992 RNA is designated SEQ ID:4703, and is provided hereinbelow with reference to the sequence listing part.

[27849] VGAM1992 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1992 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1992 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[27850] VGAM1992 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1992 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1992 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1992 RNA, herein designated VGAM RNA, may have a different number of host target

binding sites in untranslated regions of a VGAM1992 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[27851] The complementary binding of VGAM1992 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1992 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1992 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1992 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[27852] It is appreciated that VGAM1992 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1992 host target genes. The mRNA of each one of this plurality of VGAM1992 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1992 RNA, herein designated VGAM

RNA, and which when bound by VGAM1992 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1992 host target proteins.

[27853] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1992 gene, herein designated VGAM GENE, on one or more VGAM1992 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27854] It is yet further appreciated that a function of VGAM1992 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM1992 include diagnosis, prevention and treatment of viral infection by Nipah virus. Specific functions, and accordingly utilities, of VGAM1992 correlate with, and may be deduced from, the identity of the host target genes which VGAM1992 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[27855] Nucleotide sequences of the VGAM1992 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1992 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1992 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1992 are further described hereinbelow with reference to Table 1.

[27856] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1992 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[27857] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Mes-

senger 1993 (VGAM1993) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[27858] VGAM1993 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1993 was detected is described hereinabove with reference to Figs. 2-8.

[27859] VGAM1993 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Nipah virus. VGAM1993 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[27860] VGAM1993 gene, herein designated VGAM GENE, encodes a VGAM1993 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1993 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1993 precursor RNA is designated SEQ ID:1979, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1979 is located at position 17946 relative to the genome of Nipah virus.

[27861] VGAM1993 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1993 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27862] An enzyme complex designated DICER COMPLEX, dices the VGAM1993 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1993 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 60%) nucleotide sequence of VGAM1993 RNA is designated SEQ ID:4704, and is provided hereinbelow with reference to the sequence listing part.

[27863] VGAM1993 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1993 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1993 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[27864] VGAM1993 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1993 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1993 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1993 RNA, herein designated VGAM RNA, may have a different number of host target

binding sites in untranslated regions of a VGAM1993 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[27865] The complementary binding of VGAM1993 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1993 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1993 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1993 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[27866] It is appreciated that VGAM1993 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1993 host target genes. The mRNA of each one of this plurality of VGAM1993 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1993 RNA, herein designated VGAM

RNA, and which when bound by VGAM1993 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1993 host target proteins.

[27867] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1993 gene, herein designated VGAM GENE, on one or more VGAM1993 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27868] It is yet further appreciated that a function of VGAM1993 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM1993 include diagnosis, prevention and treatment of viral infection by Nipah virus. Specific functions, and accordingly utilities, of VGAM1993 correlate with, and may be deduced from, the identity of the host target genes which VGAM1993 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[27869] Nucleotide sequences of the VGAM1993 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1993 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1993 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1993 are further described hereinbelow with reference to Table 1.

[27870] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1993 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[27871] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Mes-

senger 1994 (VGAM1994) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[27872] VGAM1994 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1994 was detected is described hereinabove with reference to Figs. 2-8.

[27873] VGAM1994 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Nipah virus. VGAM1994 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[27874] VGAM1994 gene, herein designated VGAM GENE, encodes a VGAM1994 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1994 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1994 precursor RNA is designated SEQ ID:1980, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1980 is located at position 17237 relative to the genome of Nipah virus.

[27875] VGAM1994 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1994 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27876] An enzyme complex designated DICER COMPLEX, dices the VGAM1994 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1994 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 67%) nucleotide sequence of VGAM1994 RNA is designated SEQ ID:4705, and is provided hereinbelow with reference to the sequence listing part.

[27877] VGAM1994 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1994 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1994 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[27878] VGAM1994 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1994 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1994 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1994 RNA, herein designated VGAM RNA, may have a different number of host target

binding sites in untranslated regions of a VGAM1994 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[27879] The complementary binding of VGAM1994 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1994 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1994 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1994 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[27880] It is appreciated that VGAM1994 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1994 host target genes. The mRNA of each one of this plurality of VGAM1994 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1994 RNA, herein designated VGAM

RNA, and which when bound by VGAM1994 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1994 host target proteins.

[27881] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1994 gene, herein designated VGAM GENE, on one or more VGAM1994 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27882] It is yet further appreciated that a function of VGAM1994 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM1994 include diagnosis, prevention and treatment of viral infection by Nipah virus. Specific functions, and accordingly utilities, of VGAM1994 correlate with, and may be deduced from, the identity of the host target genes which VGAM1994 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[27883] Nucleotide sequences of the VGAM1994 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1994 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1994 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1994 are further described hereinbelow with reference to Table 1.

[27884] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1994 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[27885] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Mes-

senger 1995 (VGAM1995) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[27886] VGAM1995 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1995 was detected is described hereinabove with reference to Figs. 2-8.

[27887] VGAM1995 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Nipah virus. VGAM1995 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[27888] VGAM1995 gene, herein designated VGAM GENE, encodes a VGAM1995 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1995 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1995 precursor RNA is designated SEQ ID:1981, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1981 is located at position 9693 relative to the genome of Nipah virus.

[27889] VGAM1995 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1995 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27890] An enzyme complex designated DICER COMPLEX, dices the VGAM1995 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1995 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM1995 RNA is designated SEQ ID:4706, and is provided hereinbelow with reference to the sequence listing part.

[27891] VGAM1995 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1995 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1995 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[27892] VGAM1995 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1995 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1995 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1995 RNA, herein designated VGAM RNA, may have a different number of host target

binding sites in untranslated regions of a VGAM1995 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[27893] The complementary binding of VGAM1995 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1995 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1995 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1995 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[27894] It is appreciated that VGAM1995 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1995 host target genes. The mRNA of each one of this plurality of VGAM1995 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1995 RNA, herein designated VGAM

RNA, and which when bound by VGAM1995 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1995 host target proteins.

[27895] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1995 gene, herein designated VGAM GENE, on one or more VGAM1995 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27896] It is yet further appreciated that a function of VGAM1995 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM1995 include diagnosis, prevention and treatment of viral infection by Nipah virus. Specific functions, and accordingly utilities, of VGAM1995 correlate with, and may be deduced from, the identity of the host target genes which VGAM1995 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[27897] Nucleotide sequences of the VGAM1995 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1995 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1995 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1995 are further described hereinbelow with reference to Table 1.

[27898] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1995 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[27899] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Mes-

senger 1996 (VGAM1996) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[27900] VGAM1996 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1996 was detected is described hereinabove with reference to Figs. 2-8.

[27901] VGAM1996 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Nipah virus. VGAM1996 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[27902] VGAM1996 gene, herein designated VGAM GENE, encodes a VGAM1996 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1996 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1996 precursor RNA is designated SEQ ID:1982, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1982 is located at position 8558 relative to the genome of Nipah virus.

[27903] VGAM1996 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1996 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27904] An enzyme complex designated DICER COMPLEX, dices the VGAM1996 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1996 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide sequence of VGAM1996 RNA is designated SEQ ID:4707, and is provided hereinbelow with reference to the sequence listing part.

[27905] VGAM1996 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1996 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1996 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[27906] VGAM1996 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1996 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1996 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1996 RNA, herein designated VGAM RNA, may have a different number of host target

binding sites in untranslated regions of a VGAM1996 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[27907] The complementary binding of VGAM1996 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1996 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1996 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1996 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[27908] It is appreciated that VGAM1996 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1996 host target genes. The mRNA of each one of this plurality of VGAM1996 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1996 RNA, herein designated VGAM

RNA, and which when bound by VGAM1996 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1996 host target proteins.

[27909] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1996 gene, herein designated VGAM GENE, on one or more VGAM1996 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27910] It is yet further appreciated that a function of VGAM1996 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM1996 include diagnosis, prevention and treatment of viral infection by Nipah virus. Specific functions, and accordingly utilities, of VGAM1996 correlate with, and may be deduced from, the identity of the host target genes which VGAM1996 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[27911] Nucleotide sequences of the VGAM1996 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1996 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1996 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1996 are further described hereinbelow with reference to Table 1.

[27912] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1996 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[27913] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Mes-

senger 1997 (VGAM1997) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[27914] VGAM1997 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1997 was detected is described hereinabove with reference to Figs. 2-8.

[27915] VGAM1997 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Nipah virus. VGAM1997 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[27916] VGAM1997 gene, herein designated VGAM GENE, encodes a VGAM1997 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1997 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1997 precursor RNA is designated SEQ ID:1983, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1983 is located at position 1708 relative to the genome of Nipah virus.

[27917] VGAM1997 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1997 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27918] An enzyme complex designated DICER COMPLEX, dices the VGAM1997 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1997 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 51%) nucleotide sequence of VGAM1997 RNA is designated SEQ ID:4708, and is provided hereinbelow with reference to the sequence listing part.

[27919] VGAM1997 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1997 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1997 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[27920] VGAM1997 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1997 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1997 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1997 RNA, herein designated VGAM RNA, may have a different number of host target

binding sites in untranslated regions of a VGAM1997 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[27921] The complementary binding of VGAM1997 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1997 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1997 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1997 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[27922] It is appreciated that VGAM1997 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1997 host target genes. The mRNA of each one of this plurality of VGAM1997 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1997 RNA, herein designated VGAM

RNA, and which when bound by VGAM1997 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1997 host target proteins.

[27923] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1997 gene, herein designated VGAM GENE, on one or more VGAM1997 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27924] It is yet further appreciated that a function of VGAM1997 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM1997 include diagnosis, prevention and treatment of viral infection by Nipah virus. Specific functions, and accordingly utilities, of VGAM1997 correlate with, and may be deduced from, the identity of the host target genes which VGAM1997 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[27925] Nucleotide sequences of the VGAM1997 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1997 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1997 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1997 are further described hereinbelow with reference to Table 1.

[27926] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1997 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[27927] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Mes-

senger 1998 (VGAM1998) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[27928] VGAM1998 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1998 was detected is described hereinabove with reference to Figs. 2-8.

[27929] VGAM1998 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Nipah virus. VGAM1998 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[27930] VGAM1998 gene, herein designated VGAM GENE, encodes a VGAM1998 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1998 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1998 precursor RNA is designated SEQ ID:1984, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1984 is located at position 15895 relative to the genome of Nipah virus.

[27931] VGAM1998 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1998 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27932] An enzyme complex designated DICER COMPLEX, dices the VGAM1998 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1998 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM1998 RNA is designated SEQ ID:4709, and is provided hereinbelow with reference to the sequence listing part.

[27933] VGAM1998 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1998 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1998 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[27934] VGAM1998 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1998 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1998 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1998 RNA, herein designated VGAM RNA, may have a different number of host target

binding sites in untranslated regions of a VGAM1998 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[27935] The complementary binding of VGAM1998 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1998 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1998 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1998 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[27936] It is appreciated that VGAM1998 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1998 host target genes. The mRNA of each one of this plurality of VGAM1998 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1998 RNA, herein designated VGAM

RNA, and which when bound by VGAM1998 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1998 host target proteins.

[27937] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1998 gene, herein designated VGAM GENE, on one or more VGAM1998 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27938] It is yet further appreciated that a function of VGAM1998 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM1998 include diagnosis, prevention and treatment of viral infection by Nipah virus. Specific functions, and accordingly utilities, of VGAM1998 correlate with, and may be deduced from, the identity of the host target genes which VGAM1998 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[27939] Nucleotide sequences of the VGAM1998 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1998 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1998 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1998 are further described hereinbelow with reference to Table 1.

[27940] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1998 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[27941] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Mes-

senger 1999 (VGAM1999) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[27942] VGAM1999 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1999 was detected is described hereinabove with reference to Figs. 2-8.

[27943] VGAM1999 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Nipah virus. VGAM1999 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[27944] VGAM1999 gene, herein designated VGAM GENE, encodes a VGAM1999 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1999 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1999 precursor RNA is designated SEQ ID:1985, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1985 is located at position 11709 relative to the genome of Nipah virus.

[27945] VGAM1999 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM1999 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27946] An enzyme complex designated DICER COMPLEX, dices the VGAM1999 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM1999 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 51%) nucleotide sequence of VGAM1999 RNA is designated SEQ ID:4710, and is provided hereinbelow with reference to the sequence listing part.

[27947] VGAM1999 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1999 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1999 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[27948] VGAM1999 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1999 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1999 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM1999 RNA, herein designated VGAM RNA, may have a different number of host target

binding sites in untranslated regions of a VGAM1999 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[27949] The complementary binding of VGAM1999 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1999 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1999 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM1999 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[27950] It is appreciated that VGAM1999 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1999 host target genes. The mRNA of each one of this plurality of VGAM1999 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1999 RNA, herein designated VGAM

RNA, and which when bound by VGAM1999 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM1999 host target proteins.

[27951] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1999 gene, herein designated VGAM GENE, on one or more VGAM1999 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27952] It is yet further appreciated that a function of VGAM1999 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM1999 include diagnosis, prevention and treatment of viral infection by Nipah virus. Specific functions, and accordingly utilities, of VGAM1999 correlate with, and may be deduced from, the identity of the host target genes which VGAM1999 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[27953] Nucleotide sequences of the VGAM1999 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM1999 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1999 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1999 are further described hereinbelow with reference to Table 1.

[27954] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM1999 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[27955] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Mes-

senger 2000 (VGAM2000) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[27956] VGAM2000 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2000 was detected is described hereinabove with reference to Figs. 2-8.

[27957] VGAM2000 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Nipah virus. VGAM2000 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[27958] VGAM2000 gene, herein designated VGAM GENE, encodes a VGAM2000 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2000 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2000 precursor RNA is designated SEQ ID:1986, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1986 is located at position 10918 relative to the genome of Nipah virus.

[27959] VGAM2000 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2000 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27960] An enzyme complex designated DICER COMPLEX, dices the VGAM2000 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2000 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide sequence of VGAM2000 RNA is designated SEQ ID:4711, and is provided hereinbelow with reference to the sequence listing part.

[27961] VGAM2000 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2000 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2000 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[27962] VGAM2000 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2000 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2000 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2000 RNA, herein designated VGAM RNA, may have a different number of host target

binding sites in untranslated regions of a VGAM2000 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[27963] The complementary binding of VGAM2000 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2000 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2000 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2000 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[27964] It is appreciated that VGAM2000 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2000 host target genes. The mRNA of each one of this plurality of VGAM2000 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2000 RNA, herein designated VGAM

RNA, and which when bound by VGAM2000 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2000 host target proteins.

[27965] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2000 gene, herein designated VGAM GENE, on one or more VGAM2000 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27966] It is yet further appreciated that a function of VGAM2000 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM2000 include diagnosis, prevention and treatment of viral infection by Nipah virus. Specific functions, and accordingly utilities, of VGAM2000 correlate with, and may be deduced from, the identity of the host target genes which VGAM2000 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[27967] Nucleotide sequences of the VGAM2000 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2000 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2000 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2000 are further described hereinbelow with reference to Table 1.

[27968] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2000 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[27969] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Mes-

senger 2001 (VGAM2001) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[27970] VGAM2001 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2001 was detected is described hereinabove with reference to Figs. 2-8.

[27971] VGAM2001 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Nipah virus. VGAM2001 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[27972] VGAM2001 gene, herein designated VGAM GENE, encodes a VGAM2001 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2001 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2001 precursor RNA is designated SEQ ID:1987, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1987 is located at position 2273 relative to the genome of Nipah virus.

[27973] VGAM2001 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2001 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27974] An enzyme complex designated DICER COMPLEX, dices the VGAM2001 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2001 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 76%) nucleotide sequence of VGAM2001 RNA is designated SEQ ID:4712, and is provided hereinbelow with reference to the sequence listing part.

[27975] VGAM2001 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2001 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2001 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[27976] VGAM2001 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2001 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2001 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2001 RNA, herein designated VGAM RNA, may have a different number of host target

binding sites in untranslated regions of a VGAM2001 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[27977] The complementary binding of VGAM2001 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2001 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2001 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2001 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[27978] It is appreciated that VGAM2001 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2001 host target genes. The mRNA of each one of this plurality of VGAM2001 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2001 RNA, herein designated VGAM

RNA, and which when bound by VGAM2001 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2001 host target proteins.

[27979] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2001 gene, herein designated VGAM GENE, on one or more VGAM2001 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27980] It is yet further appreciated that a function of VGAM2001 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM2001 include diagnosis, prevention and treatment of viral infection by Nipah virus. Specific functions, and accordingly utilities, of VGAM2001 correlate with, and may be deduced from, the identity of the host target genes which VGAM2001 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[27981] Nucleotide sequences of the VGAM2001 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2001 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2001 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2001 are further described hereinbelow with reference to Table 1.

[27982] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2001 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[27983] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Mes-

senger 2002 (VGAM2002) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[27984] VGAM2002 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2002 was detected is described hereinabove with reference to Figs. 2-8.

[27985] VGAM2002 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Nipah virus. VGAM2002 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[27986] VGAM2002 gene, herein designated VGAM GENE, encodes a VGAM2002 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2002 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2002 precursor RNA is designated SEQ ID:1988, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1988 is located at position 1516 relative to the genome of Nipah virus.

[27987] VGAM2002 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2002 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27988] An enzyme complex designated DICER COMPLEX, dices the VGAM2002 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2002 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 63%) nucleotide sequence of VGAM2002 RNA is designated SEQ ID:4713, and is provided hereinbelow with reference to the sequence listing part.

[27989] VGAM2002 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2002 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2002 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[27990] VGAM2002 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2002 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2002 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2002 RNA, herein designated VGAM RNA, may have a different number of host target

binding sites in untranslated regions of a VGAM2002 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[27991] The complementary binding of VGAM2002 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2002 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2002 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2002 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[27992] It is appreciated that VGAM2002 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2002 host target genes. The mRNA of each one of this plurality of VGAM2002 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2002 RNA, herein designated VGAM

RNA, and which when bound by VGAM2002 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2002 host target proteins.

[27993] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2002 gene, herein designated VGAM GENE, on one or more VGAM2002 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27994] It is yet further appreciated that a function of VGAM2002 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM2002 include diagnosis, prevention and treatment of viral infection by Nipah virus. Specific functions, and accordingly utilities, of VGAM2002 correlate with, and may be deduced from, the identity of the host target genes which VGAM2002 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[27995] Nucleotide sequences of the VGAM2002 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2002 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2002 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2002 are further described hereinbelow with reference to Table 1.

[27996] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2002 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[27997] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Mes-

senger 2003 (VGAM2003) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[27998] VGAM2003 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2003 was detected is described hereinabove with reference to Figs. 2-8.

[27999] VGAM2003 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Nipah virus. VGAM2003 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[28000] VGAM2003 gene, herein designated VGAM GENE, encodes a VGAM2003 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2003 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2003 precursor RNA is designated SEQ ID:1989, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1989 is located at position 5319 relative to the genome of Nipah virus.

[28001] VGAM2003 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2003 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[28002] An enzyme complex designated DICER COMPLEX, dices the VGAM2003 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2003 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2003 RNA is designated SEQ ID:4714, and is provided hereinbelow with reference to the sequence listing part.

[28003] VGAM2003 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2003 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2003 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[28004] VGAM2003 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2003 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2003 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2003 RNA, herein designated VGAM RNA, may have a different number of host target

binding sites in untranslated regions of a VGAM2003 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[28005] The complementary binding of VGAM2003 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2003 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2003 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2003 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[28006] It is appreciated that VGAM2003 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2003 host target genes. The mRNA of each one of this plurality of VGAM2003 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2003 RNA, herein designated VGAM

RNA, and which when bound by VGAM2003 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2003 host target proteins.

[28007] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2003 gene, herein designated VGAM GENE, on one or more VGAM2003 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[28008] It is yet further appreciated that a function of VGAM2003 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM2003 include diagnosis, prevention and treatment of viral infection by Nipah virus. Specific functions, and accordingly utilities, of VGAM2003 correlate with, and may be deduced from, the identity of the host target genes which VGAM2003 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[28009] Nucleotide sequences of the VGAM2003 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2003 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2003 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2003 are further described hereinbelow with reference to Table 1.

[28010] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2003 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[28011] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Mes-

senger 2004 (VGAM2004) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[28012] VGAM2004 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2004 was detected is described hereinabove with reference to Figs. 2-8.

[28013] VGAM2004 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Chimpanzee cytomegalovirus. VGAM2004 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[28014] VGAM2004 gene, herein designated VGAM GENE, encodes a VGAM2004 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2004 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2004 precursor RNA is designated SEQ ID:1990, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1990 is located at position

177784 relative to the genome of Chimpanzee cytomegalovirus.

[28015] VGAM2004 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2004 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[28016] An enzyme complex designated DICER COMPLEX, dices the VGAM2004 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2004 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2004 RNA is designated SEQ ID:4715, and is provided hereinbelow with reference to the sequence

listing part.

[28017] VGAM2004 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2004 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2004 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[28018] VGAM2004 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2004 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2004 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not

meant to be limiting VGAM2004 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2004 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[28019] The complementary binding of VGAM2004 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2004 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2004 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2004 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[28020] It is appreciated that VGAM2004 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2004 host target genes. The mRNA of each one of this plurality of VGAM2004 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2004 RNA, herein designated VGAM RNA, and which when bound by VGAM2004 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2004 host target proteins.

[28021] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2004 gene, herein designated VGAM GENE, on one or more VGAM2004 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[28022] It is yet further appreciated that a function of VGAM2004

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2004 include diagnosis, prevention and treatment of viral infection by Chimpanzee cytomegalovirus. Specific functions, and accordingly utilities, of VGAM2004 correlate with, and may be deduced from, the identity of the host target genes which VGAM2004 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[28023] Nucleotide sequences of the VGAM2004 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2004 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2004 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2004 are further described hereinbelow with reference to Table 1.

[28024] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2004 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[28025] Fig. 1 further provides a conceptual description of another

novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2005 (VGAM2005) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[28026] VGAM2005 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2005 was detected is described hereinabove with reference to Figs. 2-8.

[28027] VGAM2005 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Chimpanzee cytomegalovirus. VGAM2005 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[28028] VGAM2005 gene, herein designated VGAM GENE, encodes a VGAM2005 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2005 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2005 precursor RNA is designated SEQ ID:1991, and is provided here-

inbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1991 is located at position 177914 relative to the genome of Chimpanzee cytomegalovirus.

[28029] VGAM2005 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2005 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[28030] An enzyme complex designated DICER COMPLEX, dices the VGAM2005 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2005 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide se-

quence of VGAM2005 RNA is designated SEQ ID:4716, and is provided hereinbelow with reference to the sequence listing part.

[28031] VGAM2005 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2005 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2005 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[28032] VGAM2005 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2005 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2005 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is ap-

preciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2005 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2005 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[28033] The complementary binding of VGAM2005 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2005 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2005 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2005 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[28034] It is appreciated that VGAM2005 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2005 host target genes. The mRNA of

each one of this plurality of VGAM2005 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2005 RNA, herein designated VGAM RNA, and which when bound by VGAM2005 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2005 host target proteins.

[28035] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2005 gene, herein designated VGAM GENE, on one or more VGAM2005 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science

294,779 (2001)).

[28036] It is yet further appreciated that a function of VGAM2005 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2005 include diagnosis, prevention and treatment of viral infection by Chimpanzee cytomegalovirus. Specific functions, and accordingly utilities, of VGAM2005 correlate with, and may be deduced from, the identity of the host target genes which VGAM2005 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[28037] Nucleotide sequences of the VGAM2005 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2005 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2005 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2005 are further described hereinbelow with reference to Table 1.

[28038] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2005 RNA, herein designated VGAM RNA, are de-

scribed hereinbelow with reference to Table 2.

[28039] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2006 (VGAM2006) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[28040] VGAM2006 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2006 was detected is described hereinabove with reference to Figs. 2-8.

[28041] VGAM2006 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Chimpanzee cytomegalovirus. VGAM2006 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[28042] VGAM2006 gene, herein designated VGAM GENE, encodes a VGAM2006 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2006 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly

similar to the nucleotide sequence of VGAM2006 precursor RNA is designated SEQ ID:1992, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1992 is located at position 191561 relative to the genome of Chimpanzee cytomegalovirus.

[28043] VGAM2006 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2006 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[28044] An enzyme complex designated DICER COMPLEX, dices the VGAM2006 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2006 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 71%) nucleotide sequence of VGAM2006 RNA is designated SEQ ID:4717, and is provided hereinbelow with reference to the sequence listing part.

[28045] VGAM2006 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2006 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2006 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[28046] VGAM2006 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2006 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2006 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3

such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2006 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2006 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[28047] The complementary binding of VGAM2006 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2006 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2006 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2006 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[28048] It is appreciated that VGAM2006 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2006 host target genes. The mRNA of each one of this plurality of VGAM2006 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2006 RNA, herein designated VGAM RNA, and which when bound by VGAM2006 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2006 host target proteins.

[28049] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2006 gene, herein designated VGAM GENE, on one or more VGAM2006 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[28050] It is yet further appreciated that a function of VGAM2006 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2006 include diagnosis, prevention and treatment of viral infection by Chimpanzee cytomegalovirus. Specific functions, and accordingly utilities, of VGAM2006 correlate with, and may be deduced from, the identity of the host target genes which VGAM2006 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[28051] Nucleotide sequences of the VGAM2006 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2006 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2006 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2006 are further described hereinbelow with reference to Table 1.

[28052] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the

complementarity of each of these host target binding sites to VGAM2006 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[28053] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2007 (VGAM2007) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[28054] VGAM2007 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2007 was detected is described hereinabove with reference to Figs. 2-8.

[28055] VGAM2007 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Reston Ebola virus (REBOV). VGAM2007 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[28056] VGAM2007 gene, herein designated VGAM GENE, encodes a VGAM2007 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2007 precursor RNA,

herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2007 precursor RNA is designated SEQ ID:1993, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1993 is located at position 5965 relative to the genome of Reston Ebola virus (REBOV).

[28057] VGAM2007 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2007 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[28058] An enzyme complex designated DICER COMPLEX, dices the VGAM2007 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2007 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of VGAM2007 RNA is designated SEQ ID:4718, and is provided hereinbelow with reference to the sequence listing part.

[28059] VGAM2007 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2007 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2007 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[28060] VGAM2007 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2007 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2007 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host

target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2007 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2007 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[28061] The complementary binding of VGAM2007 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2007 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2007 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2007 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[28062] It is appreciated that VGAM2007 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2007 host target genes. The mRNA of each one of this plurality of VGAM2007 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2007 RNA, herein designated VGAM RNA, and which when bound by VGAM2007 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2007 host target proteins.

[28063] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2007 gene, herein designated VGAM GENE, on one or more VGAM2007 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[28064] It is yet further appreciated that a function of VGAM2007 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2007 include diagnosis, prevention and treatment of viral infection by Reston Ebola virus (REBOV). Specific functions, and accordingly utilities, of VGAM2007 correlate with, and may be deduced from, the identity of the host target genes which VGAM2007 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[28065] Nucleotide sequences of the VGAM2007 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2007 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2007 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2007 are further described hereinbelow with reference to Table 1.

[28066] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2007 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[28067] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2008 (VGAM2008) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[28068] VGAM2008 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2008 was detected is described hereinabove with reference to Figs. 2-8.

[28069] VGAM2008 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Reston Ebola virus (REBOV). VGAM2008 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[28070] VGAM2008 gene, herein designated VGAM GENE, encodes a VGAM2008 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and un-

like most ordinary genes, VGAM2008 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2008 precursor RNA is designated SEQ ID:1994, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1994 is located at position 11658 relative to the genome of Reston Ebola virus (REBOV).

[28071] VGAM2008 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2008 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[28072] An enzyme complex designated DICER COMPLEX, dices the VGAM2008 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2008 RNA, herein designated VGAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2008 RNA is designated SEQ ID:4719, and is provided hereinbelow with reference to the sequence listing part.

[28073] VGAM2008 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2008 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2008 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[28074] VGAM2008 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2008 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2008 RNA, herein designated

VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2008 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2008 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[28075] The complementary binding of VGAM2008 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2008 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2008 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2008 host target protein, herein desig-

nated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[28076] It is appreciated that VGAM2008 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2008 host target genes. The mRNA of each one of this plurality of VGAM2008 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2008 RNA, herein designated VGAM RNA, and which when bound by VGAM2008 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2008 host target proteins.

[28077] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2008 gene, herein designated VGAM GENE, on one or more VGAM2008 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[28078] It is yet further appreciated that a function of VGAM2008 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2008 include diagnosis, prevention and treatment of viral infection by Reston Ebola virus (REBOV). Specific functions, and accordingly utilities, of VGAM2008 correlate with, and may be deduced from, the identity of the host target genes which VGAM2008 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[28079] Nucleotide sequences of the VGAM2008 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2008 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2008 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2008 are further described hereinbelow with reference to Table 1.

[28080] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2008 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[28081] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2009 (VGAM2009) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[28082] VGAM2009 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2009 was detected is described hereinabove with reference to Figs. 2-8.

[28083] VGAM2009 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Reston Ebola virus (REBOV). VGAM2009 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[28084] VGAM2009 gene, herein designated VGAM GENE, encodes

a VGAM2009 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2009 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2009 precursor RNA is designated SEQ ID:1995, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1995 is located at position 12590 relative to the genome of Reston Ebola virus (REBOV).

[28085] VGAM2009 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2009 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[28086] An enzyme complex designated DICER COMPLEX, dices the VGAM2009 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, into VGAM2009 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2009 RNA is designated SEQ ID:4720, and is provided hereinbelow with reference to the sequence listing part.

[28087] VGAM2009 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2009 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2009 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[28088] VGAM2009 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2009 host target RNA, herein designated VGAM HOST TARGET RNA. This

complementary binding is due to the fact that the nucleotide sequence of VGAM2009 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2009 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2009 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[28089] The complementary binding of VGAM2009 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2009 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2009

host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2009 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[28090] It is appreciated that VGAM2009 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2009 host target genes. The mRNA of each one of this plurality of VGAM2009 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2009 RNA, herein designated VGAM RNA, and which when bound by VGAM2009 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2009 host target proteins.

[28091] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2009 gene, herein designated VGAM GENE, on one or more VGAM2009 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[28092] It is yet further appreciated that a function of VGAM2009 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2009 include diagnosis, prevention and treatment of viral infection by Reston Ebola virus (REBOV). Specific functions, and accordingly utilities, of VGAM2009 correlate with, and may be deduced from, the identity of the host target genes which VGAM2009 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[28093] Nucleotide sequences of the VGAM2009 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2009 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2009 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM2009 are further described hereinbelow with reference to Table 1.

[28094] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2009 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[28095] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2010 (VGAM2010) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[28096] VGAM2010 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2010 was detected is described hereinabove with reference to Figs. 2-8.

[28097] VGAM2010 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Reston Ebola virus (REBOV). VGAM2010 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in

the human genome.

[28098] VGAM2010 gene, herein designated VGAM GENE, encodes a VGAM2010 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2010 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2010 precursor RNA is designated SEQ ID:1996, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1996 is located at position 17622 relative to the genome of Reston Ebola virus (REBOV).

[28099] VGAM2010 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2010 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[28100] An enzyme complex designated DICER COMPLEX, dices the VGAM2010 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2010 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 61%) nucleotide sequence of VGAM2010 RNA is designated SEQ ID:4721, and is provided hereinbelow with reference to the sequence listing part.

[28101] VGAM2010 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2010 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2010 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[28102] VGAM2010 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites

located in untranslated regions of VGAM2010 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2010 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2010 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2010 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[28103] The complementary binding of VGAM2010 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2010 host target RNA, herein designated VGAM

HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2010 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2010 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[28104] It is appreciated that VGAM2010 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2010 host target genes. The mRNA of each one of this plurality of VGAM2010 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2010 RNA, herein designated VGAM RNA, and which when bound by VGAM2010 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2010 host target proteins.

[28105] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2010 gene, herein designated VGAM GENE, on one or more VGAM2010 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove

with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[28106] It is yet further appreciated that a function of VGAM2010 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2010 include diagnosis, prevention and treatment of viral infection by Reston Ebola virus (REBOV). Specific functions, and accordingly utilities, of VGAM2010 correlate with, and may be deduced from, the identity of the host target genes which VGAM2010 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[28107] Nucleotide sequences of the VGAM2010 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2010 RNA, herein designated VGAM RNA, and

a schematic representation of the secondary folding of VGAM2010 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2010 are further described hereinbelow with reference to Table 1.

[28108] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2010 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[28109] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2011 (VGAM2011) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[28110] VGAM2011 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2011 was detected is described hereinabove with reference to Figs. 2-8.

[28111] VGAM2011 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Reston Ebola virus

(REBOV). VGAM2011 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[28112] VGAM2011 gene, herein designated VGAM GENE, encodes a VGAM2011 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2011 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2011 precursor RNA is designated SEQ ID:1997, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1997 is located at position 4098 relative to the genome of Reston Ebola virus (REBOV).

[28113] VGAM2011 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2011 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[28114] An enzyme complex designated DICER COMPLEX, dices the VGAM2011 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2011 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 52%) nucleotide sequence of VGAM2011 RNA is designated SEQ ID:4722, and is provided hereinbelow with reference to the sequence listing part.

[28115] VGAM2011 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2011 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2011 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[28116] VGAM2011 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM2011 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2011 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2011 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2011 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[28117] The complementary binding of VGAM2011 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM2011 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2011 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2011 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[28118] It is appreciated that VGAM2011 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2011 host target genes. The mRNA of each one of this plurality of VGAM2011 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2011 RNA, herein designated VGAM RNA, and which when bound by VGAM2011 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2011 host target proteins.

[28119] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2011 gene, herein designated VGAM GENE, on one or more VGAM2011 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[28120] It is yet further appreciated that a function of VGAM2011 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2011 include diagnosis, prevention and treatment of viral infection by Reston Ebola virus (REBOV). Specific functions, and accordingly utilities, of VGAM2011 correlate with, and may be deduced from, the identity of the host target genes which VGAM2011 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[28121] Nucleotide sequences of the VGAM2011 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

diced VGAM2011 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2011 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2011 are further described hereinbelow with reference to Table 1.

[28122] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2011 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[28123] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2012 (VGAM2012) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[28124] VGAM2012 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2012 was detected is described hereinabove with reference to Figs. 2-8.

[28125] VGAM2012 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of Reston Ebola virus (REBOV). VGAM2012 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[28126] VGAM2012 gene, herein designated VGAM GENE, encodes a VGAM2012 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2012 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2012 precursor RNA is designated SEQ ID:1998, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1998 is located at position 16890 relative to the genome of Reston Ebola virus (REBOV).

[28127] VGAM2012 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2012 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[28128] An enzyme complex designated DICER COMPLEX, dices the VGAM2012 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2012 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2012 RNA is designated SEQ ID:4723, and is provided hereinbelow with reference to the sequence listing part.

[28129] VGAM2012 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2012 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2012 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN COD-

ING and 3UTR respectively.

[28130] VGAM2012 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2012 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2012 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2012 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2012 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[28131] The complementary binding of VGAM2012 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2012 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2012 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2012 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[28132] It is appreciated that VGAM2012 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2012 host target genes. The mRNA of each one of this plurality of VGAM2012 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2012 RNA, herein designated VGAM RNA, and which when bound by VGAM2012 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2012 host target proteins.

[28133] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2012 gene, herein designated VGAM GENE, on one

or more VGAM2012 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[28134] It is yet further appreciated that a function of VGAM2012 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2012 include diagnosis, prevention and treatment of viral infection by Reston Ebola virus (REBOV). Specific functions, and accordingly utilities, of VGAM2012 correlate with, and may be deduced from, the identity of the host target genes which VGAM2012 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[28135] Nucleotide sequences of the VGAM2012 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2012 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2012 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2012 are further described hereinbelow with reference to Table 1.

[28136] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2012 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[28137] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2013 (VGAM2013) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[28138] VGAM2013 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2013 was detected is de-

scribed hereinabove with reference to Figs. 2-8.

[28139] VGAM2013 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Reston Ebola virus (REBOV). VGAM2013 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[28140] VGAM2013 gene, herein designated VGAM GENE, encodes a VGAM2013 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2013 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2013 precursor RNA is designated SEQ ID:1999, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1999 is located at position 12733 relative to the genome of Reston Ebola virus (REBOV).

[28141] VGAM2013 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2013 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[28142] An enzyme complex designated DICER COMPLEX, dices the VGAM2013 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2013 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2013 RNA is designated SEQ ID:4724, and is provided hereinbelow with reference to the sequence listing part.

[28143] VGAM2013 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2013 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2013 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding

gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[28144] VGAM2013 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2013 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2013 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2013 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2013 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be lo-

cated in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[28145] The complementary binding of VGAM2013 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2013 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2013 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2013 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[28146] It is appreciated that VGAM2013 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2013 host target genes. The mRNA of each one of this plurality of VGAM2013 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2013 RNA, herein designated VGAM RNA, and which when bound by VGAM2013 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2013 host target proteins.

[28147] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM2013 gene, herein designated VGAM GENE, on one or more VGAM2013 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[28148] It is yet further appreciated that a function of VGAM2013 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2013 include diagnosis, prevention and treatment of viral infection by Reston Ebola virus (REBOV). Specific functions, and accordingly utilities, of VGAM2013 correlate with, and may be deduced from, the identity of the host target genes which VGAM2013 binds and in-

hibits, and the function of these host target genes, as elaborated hereinbelow.

[28149] Nucleotide sequences of the VGAM2013 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2013 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2013 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2013 are further described hereinbelow with reference to Table 1.

[28150] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2013 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[28151] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2014 (VGAM2014) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[28152] VGAM2014 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2014 was detected is described hereinabove with reference to Figs. 2-8.

[28153] VGAM2014 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Reston Ebola virus (REBOV). VGAM2014 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[28154] VGAM2014 gene, herein designated VGAM GENE, encodes a VGAM2014 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2014 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2014 precursor RNA is designated SEQ ID:2000, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2000 is located at position 13026 relative to the genome of Reston Ebola virus (REBOV).

[28155] VGAM2014 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2014 folded precursor RNA, herein designated VGAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[28156] An enzyme complex designated DICER COMPLEX, dices the VGAM2014 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2014 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2014 RNA is designated SEQ ID:4725, and is provided hereinbelow with reference to the sequence listing part.

[28157] VGAM2014 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2014 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2014 host target RNA,

herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[28158] VGAM2014 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2014 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2014 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2014 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2014 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host tar-

get binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[28159] The complementary binding of VGAM2014 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2014 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2014 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2014 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[28160] It is appreciated that VGAM2014 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2014 host target genes. The mRNA of each one of this plurality of VGAM2014 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2014 RNA, herein designated VGAM RNA, and which when bound by VGAM2014 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2014 host target proteins.

[28161] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2014 gene, herein designated VGAM GENE, on one or more VGAM2014 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[28162] It is yet further appreciated that a function of VGAM2014 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2014 include diagnosis, prevention and treatment of viral infection by Reston Ebola virus (REBOV). Specific functions, and accordingly utilities, of VGAM2014

correlate with, and may be deduced from, the identity of the host target genes which VGAM2014 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[28163] Nucleotide sequences of the VGAM2014 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2014 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2014 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2014 are further described hereinbelow with reference to Table 1.

[28164] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2014 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[28165] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2015 (VGAM2015) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the

art.

[28166] VGAM2015 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2015 was detected is described hereinabove with reference to Figs. 2-8.

[28167] VGAM2015 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Kyuri green mottle mosaic virus. VGAM2015 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[28168] VGAM2015 gene, herein designated VGAM GENE, encodes a VGAM2015 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2015 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2015 precursor RNA is designated SEQ ID:2001, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2001 is located at position 4081 relative to the genome of Kyuri green mottle mosaic virus.

[28169] VGAM2015 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2015 folded

precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[28170] An enzyme complex designated DICER COMPLEX, dices the VGAM2015 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2015 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 58%) nucleotide sequence of VGAM2015 RNA is designated SEQ ID:4726, and is provided hereinbelow with reference to the sequence listing part.

[28171] VGAM2015 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2015 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM2015 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[28172] VGAM2015 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2015 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2015 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2015 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2015 host target RNA, herein designated VGAM HOST TARGET RNA.

It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[28173] The complementary binding of VGAM2015 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2015 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2015 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2015 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[28174] It is appreciated that VGAM2015 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2015 host target genes. The mRNA of each one of this plurality of VGAM2015 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2015 RNA, herein designated VGAM RNA, and which when bound by VGAM2015 RNA, herein designated VGAM RNA, causes inhibition of translation of

respective one or more VGAM2015 host target proteins.

[28175] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2015 gene, herein designated VGAM GENE, on one or more VGAM2015 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[28176] It is yet further appreciated that a function of VGAM2015 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2015 include diagnosis, prevention and treatment of viral infection by Kyuri green mottle mosaic

virus. Specific functions, and accordingly utilities, of VGAM2015 correlate with, and may be deduced from, the identity of the host target genes which VGAM2015 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[28177] Nucleotide sequences of the VGAM2015 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2015 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2015 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2015 are further described hereinbelow with reference to Table 1.

[28178] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2015 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[28179] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2016 (VGAM2016) viral gene, which modulates expression of respective host target genes thereof, the func-

tion and utility of which host target genes is known in the art.

[28180] VGAM2016 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2016 was detected is described hereinabove with reference to Figs. 2-8.

[28181] VGAM2016 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Kyuri green mottle mosaic virus. VGAM2016 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[28182] VGAM2016 gene, herein designated VGAM GENE, encodes a VGAM2016 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2016 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2016 precursor RNA is designated SEQ ID:2002, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2002 is located at position 1496 relative to the genome of Kyuri green mottle mosaic virus.

[28183] VGAM2016 precursor RNA, herein designated VGAM PRE-

CURSOR RNA, folds onto itself, forming VGAM2016 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[28184] An enzyme complex designated DICER COMPLEX, dices the VGAM2016 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2016 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2016 RNA is designated SEQ ID:4727, and is provided hereinbelow with reference to the sequence listing part.

[28185] VGAM2016 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM2016 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2016 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[28186] VGAM2016 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2016 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2016 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2016 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2016 host

target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[28187] The complementary binding of VGAM2016 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2016 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2016 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2016 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[28188] It is appreciated that VGAM2016 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2016 host target genes. The mRNA of each one of this plurality of VGAM2016 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2016 RNA, herein designated VGAM RNA, and which when bound by VGAM2016 RNA, herein

designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2016 host target proteins.

[28189] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2016 gene, herein designated VGAM GENE, on one or more VGAM2016 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[28190] It is yet further appreciated that a function of VGAM2016 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2016 include diagnosis, prevention and

treatment of viral infection by Kyuri green mottle mosaic virus. Specific functions, and accordingly utilities, of VGAM2016 correlate with, and may be deduced from, the identity of the host target genes which VGAM2016 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[28191] Nucleotide sequences of the VGAM2016 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2016 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2016 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2016 are further described hereinbelow with reference to Table 1.

[28192] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2016 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[28193] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2017 (VGAM2017) viral gene, which modulates ex-

pression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[28194] VGAM2017 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2017 was detected is described hereinabove with reference to Figs. 2-8.

[28195] VGAM2017 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Zaire Ebola virus (ZEBOV). VGAM2017 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[28196] VGAM2017 gene, herein designated VGAM GENE, encodes a VGAM2017 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2017 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2017 precursor RNA is designated SEQ ID:2003, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2003 is located at position 15595 relative to the genome of Zaire Ebola virus (ZEBOV).

[28197] VGAM2017 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2017 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[28198] An enzyme complex designated DICER COMPLEX, dices the VGAM2017 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2017 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 61%) nucleotide sequence of VGAM2017 RNA is designated SEQ ID:4728, and is provided hereinbelow with reference to the sequence listing part.

[28199] VGAM2017 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2017 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2017 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[28200] VGAM2017 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2017 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2017 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2017 RNA, herein designated VGAM RNA, may have a different number of host target

binding sites in untranslated regions of a VGAM2017 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[28201] The complementary binding of VGAM2017 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2017 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2017 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2017 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[28202] It is appreciated that VGAM2017 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2017 host target genes. The mRNA of each one of this plurality of VGAM2017 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2017 RNA, herein designated VGAM

RNA, and which when bound by VGAM2017 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2017 host target proteins.

[28203] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2017 gene, herein designated VGAM GENE, on one or more VGAM2017 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[28204] It is yet further appreciated that a function of VGAM2017 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM2017 include diagnosis, prevention and treatment of viral infection by Zaire Ebola virus (ZEBOV). Specific functions, and accordingly utilities, of VGAM2017 correlate with, and may be deduced from, the identity of the host target genes which VGAM2017 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[28205] Nucleotide sequences of the VGAM2017 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2017 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2017 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2017 are further described hereinbelow with reference to Table 1.

[28206] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2017 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[28207] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Mes-

senger 2018 (VGAM2018) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[28208] VGAM2018 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2018 was detected is described hereinabove with reference to Figs. 2-8.

[28209] VGAM2018 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Zaire Ebola virus (ZEBOV). VGAM2018 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[28210] VGAM2018 gene, herein designated VGAM GENE, encodes a VGAM2018 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2018 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2018 precursor RNA is designated SEQ ID:2004, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2004 is located at position

13583 relative to the genome of Zaire Ebola virus (ZEBOV).

[28211] VGAM2018 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2018 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[28212] An enzyme complex designated DICER COMPLEX, dices the VGAM2018 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2018 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 75%) nucleotide sequence of VGAM2018 RNA is designated SEQ ID:4729, and is provided hereinbelow with reference to the sequence listing part.

[28213] VGAM2018 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2018 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2018 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[28214] VGAM2018 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2018 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2018 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2018 RNA, herein designated

VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2018 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[28215] The complementary binding of VGAM2018 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2018 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2018 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2018 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[28216] It is appreciated that VGAM2018 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2018 host target genes. The mRNA of each one of this plurality of VGAM2018 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM2018 RNA, herein designated VGAM RNA, and which when bound by VGAM2018 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2018 host target proteins.

[28217] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2018 gene, herein designated VGAM GENE, on one or more VGAM2018 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[28218] It is yet further appreciated that a function of VGAM2018 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2018 include diagnosis, prevention and treatment of viral infection by Zaire Ebola virus (ZEBOV). Specific functions, and accordingly utilities, of VGAM2018 correlate with, and may be deduced from, the identity of the host target genes which VGAM2018 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[28219] Nucleotide sequences of the VGAM2018 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2018 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2018 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2018 are further described hereinbelow with reference to Table 1.

[28220] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2018 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[28221] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present

invention, referred to here as Viral Genomic Address Messenger 2019 (VGAM2019) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[28222] VGAM2019 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2019 was detected is described hereinabove with reference to Figs. 2-8.

[28223] VGAM2019 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Kyuri green mottle mosaic virus. VGAM2019 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[28224] VGAM2019 gene, herein designated VGAM GENE, encodes a VGAM2019 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2019 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2019 precursor RNA is designated SEQ ID:2005, and is provided hereinbelow with reference to the sequence listing part. Nu-

cleotide sequence SEQ ID:2005 is located at position 3691 relative to the genome of Kyuri green mottle mosaic virus.

[28225] VGAM2019 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2019 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[28226] An enzyme complex designated DICER COMPLEX, dices the VGAM2019 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2019 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 66%) nucleotide sequence of VGAM2019 RNA is designated SEQ ID:4730, and is provided hereinbelow with reference to the sequence

listing part.

[28227] VGAM2019 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2019 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2019 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[28228] VGAM2019 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2019 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2019 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not

meant to be limiting VGAM2019 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2019 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[28229] The complementary binding of VGAM2019 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2019 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2019 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2019 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[28230] It is appreciated that VGAM2019 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2019 host target genes. The mRNA of each one of this plurality of VGAM2019 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2019 RNA, herein designated VGAM RNA, and which when bound by VGAM2019 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2019 host target proteins.

[28231] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2019 gene, herein designated VGAM GENE, on one or more VGAM2019 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[28232] It is yet further appreciated that a function of VGAM2019

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2019 include diagnosis, prevention and treatment of viral infection by Kyuri green mottle mosaic virus. Specific functions, and accordingly utilities, of VGAM2019 correlate with, and may be deduced from, the identity of the host target genes which VGAM2019 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[28233] Nucleotide sequences of the VGAM2019 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2019 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2019 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2019 are further described hereinbelow with reference to Table 1.

[28234] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2019 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[28235] Fig. 1 further provides a conceptual description of another

novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2020 (VGAM2020) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[28236] VGAM2020 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2020 was detected is described hereinabove with reference to Figs. 2-8.

[28237] VGAM2020 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Zaire Ebola virus (ZEBOV). VGAM2020 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[28238] VGAM2020 gene, herein designated VGAM GENE, encodes a VGAM2020 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2020 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2020 precursor RNA is designated SEQ ID:2006, and is provided here-

inbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2006 is located at position 8150 relative to the genome of Zaire Ebola virus (ZEBOV).

[28239] VGAM2020 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2020 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[28240] An enzyme complex designated DICER COMPLEX, dices the VGAM2020 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2020 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 72%) nucleotide sequence of VGAM2020 RNA is designated SEQ ID:4731, and

is provided hereinbelow with reference to the sequence listing part.

[28241] VGAM2020 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2020 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2020 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[28242] VGAM2020 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2020 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2020 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites

shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2020 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2020 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[28243] The complementary binding of VGAM2020 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2020 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2020 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2020 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[28244] It is appreciated that VGAM2020 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2020 host target genes. The mRNA of each one of this plurality of VGAM2020 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2020 RNA, herein designated VGAM RNA, and which when bound by VGAM2020 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2020 host target proteins.

[28245] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2020 gene, herein designated VGAM GENE, on one or more VGAM2020 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[28246] It is yet further appreciated that a function of VGAM2020 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2020 include diagnosis, prevention and treatment of viral infection by Zaire Ebola virus (ZEBOV). Specific functions, and accordingly utilities, of VGAM2020 correlate with, and may be deduced from, the identity of the host target genes which VGAM2020 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[28247] Nucleotide sequences of the VGAM2020 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2020 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2020 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2020 are further described hereinbelow with reference to Table 1.

[28248] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2020 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[28249] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2021 (VGAM2021) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[28250] VGAM2021 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2021 was detected is described hereinabove with reference to Figs. 2-8.

[28251] VGAM2021 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Zaire Ebola virus (ZEBOV). VGAM2021 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[28252] VGAM2021 gene, herein designated VGAM GENE, encodes a VGAM2021 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2021 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2021 precur-

sor RNA is designated SEQ ID:2007, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2007 is located at position 11857 relative to the genome of Zaire Ebola virus (ZEBOV).

[28253] VGAM2021 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2021 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[28254] An enzyme complex designated DICER COMPLEX, dices the VGAM2021 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2021 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide se-

quence of VGAM2021 RNA is designated SEQ ID:4732, and is provided hereinbelow with reference to the sequence listing part.

[28255] VGAM2021 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2021 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2021 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[28256] VGAM2021 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2021 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2021 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is ap-

preciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2021 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2021 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[28257] The complementary binding of VGAM2021 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2021 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2021 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2021 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[28258] It is appreciated that VGAM2021 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2021 host target genes. The mRNA of

each one of this plurality of VGAM2021 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2021 RNA, herein designated VGAM RNA, and which when bound by VGAM2021 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2021 host target proteins.

[28259] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2021 gene, herein designated VGAM GENE, on one or more VGAM2021 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science

294,779 (2001)).

[28260] It is yet further appreciated that a function of VGAM2021 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2021 include diagnosis, prevention and treatment of viral infection by Zaire Ebola virus (ZEBOV). Specific functions, and accordingly utilities, of VGAM2021 correlate with, and may be deduced from, the identity of the host target genes which VGAM2021 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[28261] Nucleotide sequences of the VGAM2021 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2021 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2021 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2021 are further described hereinbelow with reference to Table 1.

[28262] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2021 RNA, herein designated VGAM RNA, are de-

scribed hereinbelow with reference to Table 2.

[28263] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2022 (VGAM2022) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[28264] VGAM2022 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2022 was detected is described hereinabove with reference to Figs. 2-8.

[28265] VGAM2022 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Zaire Ebola virus (ZEBOV). VGAM2022 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[28266] VGAM2022 gene, herein designated VGAM GENE, encodes a VGAM2022 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2022 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly

similar to the nucleotide sequence of VGAM2022 precursor RNA is designated SEQ ID:2008, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2008 is located at position 4390 relative to the genome of Zaire Ebola virus (ZEBOV).

[28267] VGAM2022 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2022 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[28268] An enzyme complex designated DICER COMPLEX, dices the VGAM2022 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2022 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2022 RNA is designated SEQ ID:4733, and is provided hereinbelow with reference to the sequence listing part.

[28269] VGAM2022 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2022 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2022 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[28270] VGAM2022 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2022 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2022 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I,

BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2022 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2022 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[28271] The complementary binding of VGAM2022 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2022 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2022 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2022 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[28272] It is appreciated that VGAM2022 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM2022 host target genes. The mRNA of each one of this plurality of VGAM2022 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2022 RNA, herein designated VGAM RNA, and which when bound by VGAM2022 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2022 host target proteins.

[28273] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2022 gene, herein designated VGAM GENE, on one or more VGAM2022 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[28274] It is yet further appreciated that a function of VGAM2022 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2022 include diagnosis, prevention and treatment of viral infection by Zaire Ebola virus (ZEBOV). Specific functions, and accordingly utilities, of VGAM2022 correlate with, and may be deduced from, the identity of the host target genes which VGAM2022 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[28275] Nucleotide sequences of the VGAM2022 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2022 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2022 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2022 are further described hereinbelow with reference to Table 1.

[28276] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites

to VGAM2022 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[28277] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2023 (VGAM2023) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[28278] VGAM2023 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2023 was detected is described hereinabove with reference to Figs. 2-8.

[28279] VGAM2023 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Zaire Ebola virus (ZEBOV). VGAM2023 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[28280] VGAM2023 gene, herein designated VGAM GENE, encodes a VGAM2023 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2023 precursor RNA, herein designated VGAM PRECURSOR RNA, does not en-

code a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2023 precursor RNA is designated SEQ ID:2009, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2009 is located at position 11139 relative to the genome of Zaire Ebola virus (ZEBOV).

[28281] VGAM2023 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2023 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[28282] An enzyme complex designated DICER COMPLEX, dices the VGAM2023 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2023 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 73%) nucleotide sequence of VGAM2023 RNA is designated SEQ ID:4734, and is provided hereinbelow with reference to the sequence listing part.

[28283] VGAM2023 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2023 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2023 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[28284] VGAM2023 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2023 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2023 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3

such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2023 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2023 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[28285] The complementary binding of VGAM2023 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2023 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2023 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2023 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[28286] It is appreciated that VGAM2023 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2023 host target genes. The mRNA of each one of this plurality of VGAM2023 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2023 RNA, herein designated VGAM RNA, and which when bound by VGAM2023 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2023 host target proteins.

[28287] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2023 gene, herein designated VGAM GENE, on one or more VGAM2023 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[28288] It is yet further appreciated that a function of VGAM2023 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2023 include diagnosis, prevention and treatment of viral infection by Zaire Ebola virus (ZEBOV). Specific functions, and accordingly utilities, of VGAM2023 correlate with, and may be deduced from, the identity of the host target genes which VGAM2023 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[28289] Nucleotide sequences of the VGAM2023 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2023 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2023 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2023 are further described hereinbelow with reference to Table 1.

[28290] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the

complementarity of each of these host target binding sites to VGAM2023 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[28291] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2024 (VGAM2024) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[28292] VGAM2024 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2024 was detected is described hereinabove with reference to Figs. 2-8.

[28293] VGAM2024 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Kyuri green mottle mosaic virus. VGAM2024 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[28294] VGAM2024 gene, herein designated VGAM GENE, encodes a VGAM2024 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2024 precursor RNA,

herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2024 precursor RNA is designated SEQ ID:2010, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2010 is located at position 332 relative to the genome of Kyuri green mottle mosaic virus.

[28295] VGAM2024 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2024 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[28296] An enzyme complex designated DICER COMPLEX, dices the VGAM2024 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2024 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 72%) nucleotide sequence of VGAM2024 RNA is designated SEQ ID:4735, and is provided hereinbelow with reference to the sequence listing part.

[28297] VGAM2024 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2024 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2024 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[28298] VGAM2024 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2024 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2024 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host

target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2024 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2024 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[28299] The complementary binding of VGAM2024 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2024 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2024 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2024 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[28300] It is appreciated that VGAM2024 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2024 host target genes. The mRNA of each one of this plurality of VGAM2024 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2024 RNA, herein designated VGAM RNA, and which when bound by VGAM2024 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2024 host target proteins.

[28301] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2024 gene, herein designated VGAM GENE, on one or more VGAM2024 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[28302] It is yet further appreciated that a function of VGAM2024 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2024 include diagnosis, prevention and treatment of viral infection by Kyuri green mottle mosaic virus. Specific functions, and accordingly utilities, of VGAM2024 correlate with, and may be deduced from, the identity of the host target genes which VGAM2024 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[28303] Nucleotide sequences of the VGAM2024 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2024 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2024 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2024 are further described hereinbelow with reference to Table 1.

[28304] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2024 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[28305] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2025 (VGAM2025) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[28306] VGAM2025 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2025 was detected is described hereinabove with reference to Figs. 2-8.

[28307] VGAM2025 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Kyuri green mottle mosaic virus. VGAM2025 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[28308] VGAM2025 gene, herein designated VGAM GENE, encodes a VGAM2025 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and un-

like most ordinary genes, VGAM2025 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2025 precursor RNA is designated SEQ ID:2011, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2011 is located at position 4374 relative to the genome of Kyuri green mottle mosaic virus.

[28309] VGAM2025 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2025 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[28310] An enzyme complex designated DICER COMPLEX, dices the VGAM2025 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2025 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2025 RNA is designated SEQ ID:4736, and is provided hereinbelow with reference to the sequence listing part.

[28311] VGAM2025 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2025 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2025 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[28312] VGAM2025 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2025 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2025 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed

sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2025 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2025 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[28313] The complementary binding of VGAM2025 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2025 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2025 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2025 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target

protein is therefore outlined by a broken line.

[28314] It is appreciated that VGAM2025 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2025 host target genes. The mRNA of each one of this plurality of VGAM2025 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2025 RNA, herein designated VGAM RNA, and which when bound by VGAM2025 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2025 host target proteins.

[28315] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2025 gene, herein designated VGAM GENE, on one or more VGAM2025 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[28316] It is yet further appreciated that a function of VGAM2025 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2025 include diagnosis, prevention and treatment of viral infection by Kyuri green mottle mosaic virus. Specific functions, and accordingly utilities, of VGAM2025 correlate with, and may be deduced from, the identity of the host target genes which VGAM2025 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[28317] Nucleotide sequences of the VGAM2025 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2025 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2025 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2025 are further described hereinbelow with reference to Table 1.

[28318] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2025 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[28319] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2026 (VGAM2026) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[28320] VGAM2026 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2026 was detected is described hereinabove with reference to Figs. 2-8.

[28321] VGAM2026 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Zaire Ebola virus (ZEBOV). VGAM2026 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[28322] VGAM2026 gene, herein designated VGAM GENE, encodes a VGAM2026 precursor RNA, herein designated VGAM

PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2026 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2026 precursor RNA is designated SEQ ID:2012, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2012 is located at position 18253 relative to the genome of Zaire Ebola virus (ZEBOV).

[28323] VGAM2026 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2026 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[28324] An enzyme complex designated DICER COMPLEX, dices the VGAM2026 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2026 RNA, herein designated VGAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 52%) nucleotide sequence of VGAM2026 RNA is designated SEQ ID:4737, and is provided hereinbelow with reference to the sequence listing part.

[28325] VGAM2026 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2026 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2026 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[28326] VGAM2026 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2026 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2026 RNA, herein designated

VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2026 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2026 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[28327] The complementary binding of VGAM2026 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2026 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2026 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2026 host target protein, herein desig-

nated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[28328] It is appreciated that VGAM2026 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2026 host target genes. The mRNA of each one of this plurality of VGAM2026 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2026 RNA, herein designated VGAM RNA, and which when bound by VGAM2026 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2026 host target proteins.

[28329] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2026 gene, herein designated VGAM GENE, on one or more VGAM2026 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[28330] It is yet further appreciated that a function of VGAM2026 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2026 include diagnosis, prevention and treatment of viral infection by Zaire Ebola virus (ZEBOV). Specific functions, and accordingly utilities, of VGAM2026 correlate with, and may be deduced from, the identity of the host target genes which VGAM2026 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[28331] Nucleotide sequences of the VGAM2026 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2026 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2026 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2026 are further described hereinbelow with reference to Table 1.

[28332] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2026 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[28333] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2027 (VGAM2027) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[28334] VGAM2027 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2027 was detected is described hereinabove with reference to Figs. 2-8.

[28335] VGAM2027 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Kyuri green mottle mosaic virus. VGAM2027 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[28336] VGAM2027 gene, herein designated VGAM GENE, encodes

a VGAM2027 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2027 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2027 precursor RNA is designated SEQ ID:2013, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2013 is located at position 4198 relative to the genome of Kyuri green mottle mosaic virus.

[28337] VGAM2027 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2027 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[28338] An enzyme complex designated DICER COMPLEX, dices the VGAM2027 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2027 RNA,

herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2027 RNA is designated SEQ ID:4738, and is provided hereinbelow with reference to the sequence listing part.

[28339] VGAM2027 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2027 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2027 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[28340] VGAM2027 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2027 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM2027 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2027 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2027 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[28341] The complementary binding of VGAM2027 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2027 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2027 host target RNA, herein designated VGAM HOST TARGET

RNA, into VGAM2027 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[28342] It is appreciated that VGAM2027 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2027 host target genes. The mRNA of each one of this plurality of VGAM2027 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2027 RNA, herein designated VGAM RNA, and which when bound by VGAM2027 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2027 host target proteins.

[28343] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2027 gene, herein designated VGAM GENE, on one or more VGAM2027 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[28344] It is yet further appreciated that a function of VGAM2027 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2027 include diagnosis, prevention and treatment of viral infection by Kyuri green mottle mosaic virus. Specific functions, and accordingly utilities, of VGAM2027 correlate with, and may be deduced from, the identity of the host target genes which VGAM2027 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[28345] Nucleotide sequences of the VGAM2027 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2027 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2027 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2027 are further

described hereinbelow with reference to Table 1.

[28346] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2027 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[28347] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2028 (VGAM2028) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[28348] VGAM2028 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2028 was detected is described hereinabove with reference to Figs. 2-8.

[28349] VGAM2028 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Zaire Ebola virus (ZEBOV). VGAM2028 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[28350] VGAM2028 gene, herein designated VGAM GENE, encodes a VGAM2028 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2028 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2028 precursor RNA is designated SEQ ID:2014, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2014 is located at position 16037 relative to the genome of Zaire Ebola virus (ZEBOV).

[28351] VGAM2028 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2028 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[28352] An enzyme complex designated DICER COMPLEX, dices the VGAM2028 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, into VGAM2028 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 50%) nucleotide sequence of VGAM2028 RNA is designated SEQ ID:4739, and is provided hereinbelow with reference to the sequence listing part.

[28353] VGAM2028 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2028 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2028 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[28354] VGAM2028 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2028 host target RNA, herein designated VGAM HOST TARGET RNA. This

complementary binding is due to the fact that the nucleotide sequence of VGAM2028 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2028 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2028 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[28355] The complementary binding of VGAM2028 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2028 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2028

host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2028 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[28356] It is appreciated that VGAM2028 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2028 host target genes. The mRNA of each one of this plurality of VGAM2028 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2028 RNA, herein designated VGAM RNA, and which when bound by VGAM2028 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2028 host target proteins.

[28357] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2028 gene, herein designated VGAM GENE, on one or more VGAM2028 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[28358] It is yet further appreciated that a function of VGAM2028 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2028 include diagnosis, prevention and treatment of viral infection by Zaire Ebola virus (ZEBOV). Specific functions, and accordingly utilities, of VGAM2028 correlate with, and may be deduced from, the identity of the host target genes which VGAM2028 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[28359] Nucleotide sequences of the VGAM2028 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2028 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2028 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM2028 are further described hereinbelow with reference to Table 1.

[28360] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2028 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[28361] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2029 (VGAM2029) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[28362] VGAM2029 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2029 was detected is described hereinabove with reference to Figs. 2-8.

[28363] VGAM2029 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Zaire Ebola virus (ZEBOV). VGAM2029 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in

the human genome.

[28364] VGAM2029 gene, herein designated VGAM GENE, encodes a VGAM2029 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2029 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2029 precursor RNA is designated SEQ ID:2015, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2015 is located at position 17355 relative to the genome of Zaire Ebola virus (ZEBOV).

[28365] VGAM2029 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2029 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[28366] An enzyme complex designated DICER COMPLEX, dices

the VGAM2029 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2029 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2029 RNA is designated SEQ ID:4740, and is provided hereinbelow with reference to the sequence listing part.

[28367] VGAM2029 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2029 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2029 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[28368] VGAM2029 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2029 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2029 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2029 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2029 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[28369] The complementary binding of VGAM2029 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2029 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM2029 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2029 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[28370] It is appreciated that VGAM2029 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2029 host target genes. The mRNA of each one of this plurality of VGAM2029 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2029 RNA, herein designated VGAM RNA, and which when bound by VGAM2029 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2029 host target proteins.

[28371] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2029 gene, herein designated VGAM GENE, on one or more VGAM2029 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[28372] It is yet further appreciated that a function of VGAM2029 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2029 include diagnosis, prevention and treatment of viral infection by Zaire Ebola virus (ZEBOV). Specific functions, and accordingly utilities, of VGAM2029 correlate with, and may be deduced from, the identity of the host target genes which VGAM2029 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[28373] Nucleotide sequences of the VGAM2029 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2029 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of

VGAM2029 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2029 are further described hereinbelow with reference to Table 1.

[28374] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2029 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[28375] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2030 (VGAM2030) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[28376] VGAM2030 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2030 was detected is described hereinabove with reference to Figs. 2-8.

[28377] VGAM2030 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Zaire Ebola virus (ZEBOV). VGAM2030 host target gene, herein designated

VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[28378] VGAM2030 gene, herein designated VGAM GENE, encodes a VGAM2030 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2030 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2030 precursor RNA is designated SEQ ID:2016, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2016 is located at position 12693 relative to the genome of Zaire Ebola virus (ZEBOV).

[28379] VGAM2030 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2030 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[28380] An enzyme complex designated DICER COMPLEX, dices the VGAM2030 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2030 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2030 RNA is designated SEQ ID:4741, and is provided hereinbelow with reference to the sequence listing part.

[28381] VGAM2030 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2030 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2030 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[28382] VGAM2030 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites

located in untranslated regions of VGAM2030 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2030 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2030 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2030 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[28383] The complementary binding of VGAM2030 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2030 host target RNA, herein designated VGAM

HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2030 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2030 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[28384] It is appreciated that VGAM2030 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2030 host target genes. The mRNA of each one of this plurality of VGAM2030 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2030 RNA, herein designated VGAM RNA, and which when bound by VGAM2030 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2030 host target proteins.

[28385] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2030 gene, herein designated VGAM GENE, on one or more VGAM2030 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove

with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[28386] It is yet further appreciated that a function of VGAM2030 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2030 include diagnosis, prevention and treatment of viral infection by Zaire Ebola virus (ZEBOV). Specific functions, and accordingly utilities, of VGAM2030 correlate with, and may be deduced from, the identity of the host target genes which VGAM2030 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[28387] Nucleotide sequences of the VGAM2030 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2030 RNA, herein designated VGAM RNA, and

a schematic representation of the secondary folding of VGAM2030 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2030 are further described hereinbelow with reference to Table 1.

[28388] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2030 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[28389] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2031 (VGAM2031) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[28390] VGAM2031 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2031 was detected is described hereinabove with reference to Figs. 2-8.

[28391] VGAM2031 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Zaire Ebola virus

(ZEBOV). VGAM2031 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[28392] VGAM2031 gene, herein designated VGAM GENE, encodes a VGAM2031 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2031 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2031 precursor RNA is designated SEQ ID:2017, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2017 is located at position 9873 relative to the genome of Zaire Ebola virus (ZEBOV).

[28393] VGAM2031 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2031 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[28394] An enzyme complex designated DICER COMPLEX, dices the VGAM2031 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2031 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 66%) nucleotide sequence of VGAM2031 RNA is designated SEQ ID:4742, and is provided hereinbelow with reference to the sequence listing part.

[28395] VGAM2031 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2031 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2031 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[28396] VGAM2031 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM2031 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2031 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2031 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2031 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[28397] The complementary binding of VGAM2031 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM2031 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2031 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2031 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[28398] It is appreciated that VGAM2031 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2031 host target genes. The mRNA of each one of this plurality of VGAM2031 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2031 RNA, herein designated VGAM RNA, and which when bound by VGAM2031 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2031 host target proteins.

[28399] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2031 gene, herein designated VGAM GENE, on one or more VGAM2031 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[28400] It is yet further appreciated that a function of VGAM2031 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2031 include diagnosis, prevention and treatment of viral infection by Zaire Ebola virus (ZEBOV). Specific functions, and accordingly utilities, of VGAM2031 correlate with, and may be deduced from, the identity of the host target genes which VGAM2031 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[28401] Nucleotide sequences of the VGAM2031 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

diced VGAM2031 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2031 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2031 are further described hereinbelow with reference to Table 1.

[28402] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2031 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[28403] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2032 (VGAM2032) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[28404] VGAM2032 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2032 was detected is described hereinabove with reference to Figs. 2-8.

[28405] VGAM2032 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of Kyuri green mottle mosaic virus. VGAM2032 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[28406] VGAM2032 gene, herein designated VGAM GENE, encodes a VGAM2032 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2032 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2032 precursor RNA is designated SEQ ID:2018, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2018 is located at position 2336 relative to the genome of Kyuri green mottle mosaic virus.

[28407] VGAM2032 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2032 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[28408] An enzyme complex designated DICER COMPLEX, dices the VGAM2032 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2032 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2032 RNA is designated SEQ ID:4743, and is provided hereinbelow with reference to the sequence listing part.

[28409] VGAM2032 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2032 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2032 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[28410] VGAM2032 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2032 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2032 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2032 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2032 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[28411] The complementary binding of VGAM2032 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM2032 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2032 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2032 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[28412] It is appreciated that VGAM2032 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2032 host target genes. The mRNA of each one of this plurality of VGAM2032 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2032 RNA, herein designated VGAM RNA, and which when bound by VGAM2032 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2032 host target proteins.

[28413] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2032 gene, herein designated VGAM GENE, on one or more VGAM2032 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[28414] It is yet further appreciated that a function of VGAM2032 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2032 include diagnosis, prevention and treatment of viral infection by Kyuri green mottle mosaic virus. Specific functions, and accordingly utilities, of VGAM2032 correlate with, and may be deduced from, the identity of the host target genes which VGAM2032 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[28415] Nucleotide sequences of the VGAM2032 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the diced VGAM2032 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2032 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2032 are further described hereinbelow with reference to Table 1.

[28416] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2032 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[28417] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2033 (VGAM2033) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[28418] VGAM2033 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2033 was detected is described hereinabove with reference to Figs. 2-8.

[28419] VGAM2033 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Zaire Ebola virus (ZEBOV). VGAM2033 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[28420] VGAM2033 gene, herein designated VGAM GENE, encodes a VGAM2033 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2033 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2033 precursor RNA is designated SEQ ID:2019, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2019 is located at position 4726 relative to the genome of Zaire Ebola virus (ZEBOV).

[28421] VGAM2033 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2033 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[28422] An enzyme complex designated DICER COMPLEX, dices the VGAM2033 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2033 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2033 RNA is designated SEQ ID:4744, and is provided hereinbelow with reference to the sequence listing part.

[28423] VGAM2033 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2033 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2033 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN COD-

ING and 3UTR respectively.

[28424] VGAM2033 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2033 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2033 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2033 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2033 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[28425] The complementary binding of VGAM2033 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2033 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2033 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2033 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[28426] It is appreciated that VGAM2033 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2033 host target genes. The mRNA of each one of this plurality of VGAM2033 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2033 RNA, herein designated VGAM RNA, and which when bound by VGAM2033 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2033 host target proteins.

[28427] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2033 gene, herein designated VGAM GENE, on one

or more VGAM2033 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[28428] It is yet further appreciated that a function of VGAM2033 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2033 include diagnosis, prevention and treatment of viral infection by Zaire Ebola virus (ZEBOV). Specific functions, and accordingly utilities, of VGAM2033 correlate with, and may be deduced from, the identity of the host target genes which VGAM2033 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[28429] Nucleotide sequences of the VGAM2033 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2033 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2033 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2033 are further described hereinbelow with reference to Table 1.

[28430] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2033 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[28431] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2034 (VGAM2034) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[28432] VGAM2034 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2034 was detected is de-

scribed hereinabove with reference to Figs. 2-8.

[28433] VGAM2034 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Kyuri green mottle mosaic virus. VGAM2034 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[28434] VGAM2034 gene, herein designated VGAM GENE, encodes a VGAM2034 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2034 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2034 precursor RNA is designated SEQ ID:2020, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2020 is located at position 3084 relative to the genome of Kyuri green mottle mosaic virus.

[28435] VGAM2034 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2034 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[28436] An enzyme complex designated DICER COMPLEX, dices the VGAM2034 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2034 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2034 RNA is designated SEQ ID:4745, and is provided hereinbelow with reference to the sequence listing part.

[28437] VGAM2034 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2034 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2034 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and

a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[28438] VGAM2034 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2034 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2034 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2034 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2034 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both

3UTR and 5UTR regions.

[28439] The complementary binding of VGAM2034 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2034 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2034 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2034 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[28440] It is appreciated that VGAM2034 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2034 host target genes. The mRNA of each one of this plurality of VGAM2034 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2034 RNA, herein designated VGAM RNA, and which when bound by VGAM2034 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2034 host target proteins.

[28441] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM2034 gene, herein designated VGAM GENE, on one or more VGAM2034 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[28442] It is yet further appreciated that a function of VGAM2034 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2034 include diagnosis, prevention and treatment of viral infection by Kyuri green mottle mosaic virus. Specific functions, and accordingly utilities, of VGAM2034 correlate with, and may be deduced from, the identity of the host target genes which VGAM2034 binds and inhibits, and the function of these host target genes,

as elaborated hereinbelow.

[28443] Nucleotide sequences of the VGAM2034 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2034 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2034 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2034 are further described hereinbelow with reference to Table 1.

[28444] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2034 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[28445] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2035 (VGAM2035) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[28446] VGAM2035 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene.

The method by which VGAM2035 was detected is described hereinabove with reference to Figs. 2-8.

[28447] VGAM2035 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Zaire Ebola virus (ZEBOV). VGAM2035 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[28448] VGAM2035 gene, herein designated VGAM GENE, encodes a VGAM2035 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2035 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2035 precursor RNA is designated SEQ ID:2021, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2021 is located at position 12837 relative to the genome of Zaire Ebola virus (ZEBOV).

[28449] VGAM2035 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2035 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[28450] An enzyme complex designated DICER COMPLEX, dices the VGAM2035 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2035 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 57%) nucleotide sequence of VGAM2035 RNA is designated SEQ ID:4746, and is provided hereinbelow with reference to the sequence listing part.

[28451] VGAM2035 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2035 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2035 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding

gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[28452] VGAM2035 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2035 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2035 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2035 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2035 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be lo-

cated in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[28453] The complementary binding of VGAM2035 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2035 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2035 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2035 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[28454] It is appreciated that VGAM2035 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2035 host target genes. The mRNA of each one of this plurality of VGAM2035 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2035 RNA, herein designated VGAM RNA, and which when bound by VGAM2035 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2035 host target proteins.

[28455] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM2035 gene, herein designated VGAM GENE, on one or more VGAM2035 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[28456] It is yet further appreciated that a function of VGAM2035 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2035 include diagnosis, prevention and treatment of viral infection by Zaire Ebola virus (ZEBOV). Specific functions, and accordingly utilities, of VGAM2035 correlate with, and may be deduced from, the identity of the host target genes which VGAM2035 binds and in-

hibits, and the function of these host target genes, as elaborated hereinbelow.

[28457] Nucleotide sequences of the VGAM2035 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2035 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2035 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2035 are further described hereinbelow with reference to Table 1.

[28458] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2035 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[28459] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2036 (VGAM2036) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[28460] VGAM2036 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2036 was detected is described hereinabove with reference to Figs. 2-8.

[28461] VGAM2036 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Marburg virus. VGAM2036 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[28462] VGAM2036 gene, herein designated VGAM GENE, encodes a VGAM2036 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2036 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2036 precursor RNA is designated SEQ ID:2022, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2022 is located at position 4709 relative to the genome of Marburg virus.

[28463] VGAM2036 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2036 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[28464] An enzyme complex designated DICER COMPLEX, dices the VGAM2036 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2036 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2036 RNA is designated SEQ ID:4747, and is provided hereinbelow with reference to the sequence listing part.

[28465] VGAM2036 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2036 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2036 host target RNA, herein designated VGAM HOST TARGET RNA, comprises

three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[28466] VGAM2036 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2036 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2036 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2036 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2036 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an

example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[28467] The complementary binding of VGAM2036 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2036 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2036 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2036 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[28468] It is appreciated that VGAM2036 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2036 host target genes. The mRNA of each one of this plurality of VGAM2036 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2036 RNA, herein designated VGAM RNA, and which when bound by VGAM2036 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2036 host target proteins.

[28469] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2036 gene, herein designated VGAM GENE, on one or more VGAM2036 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[28470] It is yet further appreciated that a function of VGAM2036 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2036 include diagnosis, prevention and treatment of viral infection by Marburg virus. Specific functions, and accordingly utilities, of VGAM2036 correlate with, and may be deduced from, the identity of the

host target genes which VGAM2036 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[28471] Nucleotide sequences of the VGAM2036 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2036 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2036 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2036 are further described hereinbelow with reference to Table 1.

[28472] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2036 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[28473] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2037 (VGAM2037) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[28474] VGAM2037 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2037 was detected is described hereinabove with reference to Figs. 2-8.

[28475] VGAM2037 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Marburg virus. VGAM2037 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[28476] VGAM2037 gene, herein designated VGAM GENE, encodes a VGAM2037 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2037 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2037 precursor RNA is designated SEQ ID:2023, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2023 is located at position 17431 relative to the genome of Marburg virus.

[28477] VGAM2037 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2037 folded precursor RNA, herein designated VGAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[28478] An enzyme complex designated DICER COMPLEX, dices the VGAM2037 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2037 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2037 RNA is designated SEQ ID:4748, and is provided hereinbelow with reference to the sequence listing part.

[28479] VGAM2037 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2037 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2037 host target RNA,

herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[28480] VGAM2037 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2037 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2037 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2037 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2037 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host tar-

get binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[28481] The complementary binding of VGAM2037 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2037 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2037 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2037 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[28482] It is appreciated that VGAM2037 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2037 host target genes. The mRNA of each one of this plurality of VGAM2037 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2037 RNA, herein designated VGAM RNA, and which when bound by VGAM2037 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2037 host target proteins.

[28483] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2037 gene, herein designated VGAM GENE, on one or more VGAM2037 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[28484] It is yet further appreciated that a function of VGAM2037 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2037 include diagnosis, prevention and treatment of viral infection by Marburg virus. Specific functions, and accordingly utilities, of VGAM2037 corre-

late with, and may be deduced from, the identity of the host target genes which VGAM2037 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[28485] Nucleotide sequences of the VGAM2037 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2037 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2037 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2037 are further described hereinbelow with reference to Table 1.

[28486] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2037 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[28487] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2038 (VGAM2038) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the

art.

[28488] VGAM2038 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2038 was detected is described hereinabove with reference to Figs. 2-8.

[28489] VGAM2038 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Kyuri green mottle mosaic virus. VGAM2038 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[28490] VGAM2038 gene, herein designated VGAM GENE, encodes a VGAM2038 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2038 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2038 precursor RNA is designated SEQ ID:2024, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2024 is located at position 2310 relative to the genome of Kyuri green mottle mosaic virus.

[28491] VGAM2038 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2038 folded

precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[28492] An enzyme complex designated DICER COMPLEX, dices the VGAM2038 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2038 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2038 RNA is designated SEQ ID:4749, and is provided hereinbelow with reference to the sequence listing part.

[28493] VGAM2038 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2038 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM2038 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[28494] VGAM2038 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2038 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2038 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2038 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2038 host target RNA, herein designated VGAM HOST TARGET RNA.

It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[28495] The complementary binding of VGAM2038 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2038 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2038 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2038 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[28496] It is appreciated that VGAM2038 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2038 host target genes. The mRNA of each one of this plurality of VGAM2038 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2038 RNA, herein designated VGAM RNA, and which when bound by VGAM2038 RNA, herein designated VGAM RNA, causes inhibition of translation of

respective one or more VGAM2038 host target proteins.

[28497] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2038 gene, herein designated VGAM GENE, on one or more VGAM2038 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[28498] It is yet further appreciated that a function of VGAM2038 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2038 include diagnosis, prevention and treatment of viral infection by Kyuri green mottle mosaic

virus. Specific functions, and accordingly utilities, of VGAM2038 correlate with, and may be deduced from, the identity of the host target genes which VGAM2038 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[28499] Nucleotide sequences of the VGAM2038 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2038 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2038 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2038 are further described hereinbelow with reference to Table 1.

[28500] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2038 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[28501] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2039 (VGAM2039) viral gene, which modulates expression of respective host target genes thereof, the func-

tion and utility of which host target genes is known in the art.

[28502] VGAM2039 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2039 was detected is described hereinabove with reference to Figs. 2-8.

[28503] VGAM2039 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Marburg virus. VGAM2039 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[28504] VGAM2039 gene, herein designated VGAM GENE, encodes a VGAM2039 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2039 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2039 precursor RNA is designated SEQ ID:2025, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2025 is located at position 2481 relative to the genome of Marburg virus.

[28505] VGAM2039 precursor RNA, herein designated VGAM PRE-

CURSOR RNA, folds onto itself, forming VGAM2039 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[28506] An enzyme complex designated DICER COMPLEX, dices the VGAM2039 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2039 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2039 RNA is designated SEQ ID:4750, and is provided hereinbelow with reference to the sequence listing part.

[28507] VGAM2039 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM2039 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2039 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[28508] VGAM2039 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2039 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2039 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2039 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2039 host

target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[28509] The complementary binding of VGAM2039 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2039 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2039 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2039 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[28510] It is appreciated that VGAM2039 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2039 host target genes. The mRNA of each one of this plurality of VGAM2039 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2039 RNA, herein designated VGAM RNA, and which when bound by VGAM2039 RNA, herein

designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2039 host target proteins.

[28511] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2039 gene, herein designated VGAM GENE, on one or more VGAM2039 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[28512] It is yet further appreciated that a function of VGAM2039 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2039 include diagnosis, prevention and

treatment of viral infection by Marburg virus. Specific functions, and accordingly utilities, of VGAM2039 correlate with, and may be deduced from, the identity of the host target genes which VGAM2039 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[28513] Nucleotide sequences of the VGAM2039 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2039 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2039 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2039 are further described hereinbelow with reference to Table 1.

[28514] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2039 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[28515] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2040 (VGAM2040) viral gene, which modulates ex-

pression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[28516] VGAM2040 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2040 was detected is described hereinabove with reference to Figs. 2-8.

[28517] VGAM2040 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Marburg virus. VGAM2040 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[28518] VGAM2040 gene, herein designated VGAM GENE, encodes a VGAM2040 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2040 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2040 precursor RNA is designated SEQ ID:2026, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2026 is located at position 5679 relative to the genome of Marburg virus.

[28519] VGAM2040 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2040 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[28520] An enzyme complex designated DICER COMPLEX, dices the VGAM2040 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2040 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2040 RNA is designated SEQ ID:4751, and is provided hereinbelow with reference to the sequence listing part.

[28521] VGAM2040 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2040 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2040 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[28522] VGAM2040 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2040 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2040 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2040 RNA, herein designated VGAM RNA, may have a different number of host target

binding sites in untranslated regions of a VGAM2040 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[28523] The complementary binding of VGAM2040 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2040 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2040 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2040 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[28524] It is appreciated that VGAM2040 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2040 host target genes. The mRNA of each one of this plurality of VGAM2040 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2040 RNA, herein designated VGAM

RNA, and which when bound by VGAM2040 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2040 host target proteins.

[28525] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2040 gene, herein designated VGAM GENE, on one or more VGAM2040 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[28526] It is yet further appreciated that a function of VGAM2040 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM2040 include diagnosis, prevention and treatment of viral infection by Marburg virus. Specific functions, and accordingly utilities, of VGAM2040 correlate with, and may be deduced from, the identity of the host target genes which VGAM2040 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[28527] Nucleotide sequences of the VGAM2040 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2040 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2040 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2040 are further described hereinbelow with reference to Table 1.

[28528] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2040 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[28529] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Mes-

senger 2041 (VGAM2041) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[28530] VGAM2041 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2041 was detected is described hereinabove with reference to Figs. 2-8.

[28531] VGAM2041 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Marburg virus. VGAM2041 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[28532] VGAM2041 gene, herein designated VGAM GENE, encodes a VGAM2041 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2041 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2041 precursor RNA is designated SEQ ID:2027, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2027 is located at position 9817

relative to the genome of Marburg virus.

[28533] VGAM2041 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2041 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[28534] An enzyme complex designated DICER COMPLEX, dices the VGAM2041 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2041 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of VGAM2041 RNA is designated SEQ ID:4752, and is provided hereinbelow with reference to the sequence listing part.

[28535] VGAM2041 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2041 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2041 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[28536] VGAM2041 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2041 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2041 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2041 RNA, herein designated

VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2041 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[28537] The complementary binding of VGAM2041 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2041 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2041 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2041 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[28538] It is appreciated that VGAM2041 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2041 host target genes. The mRNA of each one of this plurality of VGAM2041 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM2041 RNA, herein designated VGAM RNA, and which when bound by VGAM2041 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2041 host target proteins.

[28539] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2041 gene, herein designated VGAM GENE, on one or more VGAM2041 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[28540] It is yet further appreciated that a function of VGAM2041 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2041 include diagnosis, prevention and treatment of viral infection by Marburg virus. Specific functions, and accordingly utilities, of VGAM2041 correlate with, and may be deduced from, the identity of the host target genes which VGAM2041 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[28541] Nucleotide sequences of the VGAM2041 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2041 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2041 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2041 are further described hereinbelow with reference to Table 1.

[28542] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2041 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[28543] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present

invention, referred to here as Viral Genomic Address Messenger 2042 (VGAM2042) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[28544] VGAM2042 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2042 was detected is described hereinabove with reference to Figs. 2-8.

[28545] VGAM2042 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human herpesvirus 5. VGAM2042 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[28546] VGAM2042 gene, herein designated VGAM GENE, encodes a VGAM2042 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2042 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2042 precursor RNA is designated SEQ ID:2028, and is provided hereinbelow with reference to the sequence listing part. Nu-

cleotide sequence SEQ ID:2028 is located at position 207065 relative to the genome of Human herpesvirus 5.

[28547] VGAM2042 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2042 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[28548] An enzyme complex designated DICER COMPLEX, dices the VGAM2042 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2042 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 50%) nucleotide sequence of VGAM2042 RNA is designated SEQ ID:4753, and is provided hereinbelow with reference to the sequence

listing part.

[28549] VGAM2042 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2042 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2042 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[28550] VGAM2042 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2042 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2042 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not

meant to be limiting VGAM2042 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2042 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[28551] The complementary binding of VGAM2042 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2042 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2042 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2042 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[28552] It is appreciated that VGAM2042 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2042 host target genes. The mRNA of each one of this plurality of VGAM2042 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2042 RNA, herein designated VGAM RNA, and which when bound by VGAM2042 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2042 host target proteins.

[28553] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2042 gene, herein designated VGAM GENE, on one

or more VGAM2042 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[28554] It is yet further appreciated that a function of VGAM2042 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2042 include diagnosis, prevention and treatment of viral infection by Human herpesvirus 5. Specific functions, and accordingly utilities, of VGAM2042 correlate with, and may be deduced from, the identity of the host target genes which VGAM2042 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[28555] Nucleotide sequences of the VGAM2042 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2042 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2042 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2042 are further described hereinbelow with reference to Table 1.

[28556] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2042 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[28557] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2043 (VGAM2043) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[28558] VGAM2043 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2043 was detected is de-

scribed hereinabove with reference to Figs. 2-8.

[28559] VGAM2043 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human herpesvirus 5. VGAM2043 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[28560] VGAM2043 gene, herein designated VGAM GENE, encodes a VGAM2043 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2043 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2043 precursor RNA is designated SEQ ID:2029, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2029 is located at position 200386 relative to the genome of Human herpesvirus 5.

[28561] VGAM2043 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2043 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[28562] An enzyme complex designated DICER COMPLEX, dices the VGAM2043 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2043 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of VGAM2043 RNA is designated SEQ ID:4754, and is provided hereinbelow with reference to the sequence listing part.

[28563] VGAM2043 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2043 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2043 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and

a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[28564] VGAM2043 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2043 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2043 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2043 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2043 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both

3UTR and 5UTR regions.

[28565] The complementary binding of VGAM2043 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2043 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2043 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2043 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[28566] It is appreciated that VGAM2043 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2043 host target genes. The mRNA of each one of this plurality of VGAM2043 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2043 RNA, herein designated VGAM RNA, and which when bound by VGAM2043 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2043 host target proteins.

[28567] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM2043 gene, herein designated VGAM GENE, on one or more VGAM2043 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[28568] It is yet further appreciated that a function of VGAM2043 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2043 include diagnosis, prevention and treatment of viral infection by Human herpesvirus 5. Specific functions, and accordingly utilities, of VGAM2043 correlate with, and may be deduced from, the identity of the host target genes which VGAM2043 binds and inhibits, and the function of these host target genes, as

elaborated hereinbelow.

[28569] Nucleotide sequences of the VGAM2043 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2043 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2043 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2043 are further described hereinbelow with reference to Table 1.

[28570] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2043 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[28571] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2044 (VGAM2044) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[28572] VGAM2044 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene.

The method by which VGAM2044 was detected is described hereinabove with reference to Figs. 2-8.

[28573] VGAM2044 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human herpesvirus 5. VGAM2044 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[28574] VGAM2044 gene, herein designated VGAM GENE, encodes a VGAM2044 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2044 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2044 precursor RNA is designated SEQ ID:2030, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2030 is located at position 212421 relative to the genome of Human herpesvirus 5.

[28575] VGAM2044 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2044 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[28576] An enzyme complex designated DICER COMPLEX, dices the VGAM2044 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2044 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 56%) nucleotide sequence of VGAM2044 RNA is designated SEQ ID:4755, and is provided hereinbelow with reference to the sequence listing part.

[28577] VGAM2044 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2044 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2044 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding

gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[28578] VGAM2044 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2044 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2044 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2044 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2044 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be lo-

cated in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[28579] The complementary binding of VGAM2044 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2044 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2044 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2044 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[28580] It is appreciated that VGAM2044 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2044 host target genes. The mRNA of each one of this plurality of VGAM2044 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2044 RNA, herein designated VGAM RNA, and which when bound by VGAM2044 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2044 host target proteins.

[28581] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM2044 gene, herein designated VGAM GENE, on one or more VGAM2044 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[28582] It is yet further appreciated that a function of VGAM2044 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2044 include diagnosis, prevention and treatment of viral infection by Human herpesvirus 5. Specific functions, and accordingly utilities, of VGAM2044 correlate with, and may be deduced from, the identity of the host target genes which VGAM2044 binds and in-

hibits, and the function of these host target genes, as elaborated hereinbelow.

[28583] Nucleotide sequences of the VGAM2044 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2044 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2044 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2044 are further described hereinbelow with reference to Table 1.

[28584] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2044 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[28585] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2045 (VGAM2045) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[28586] VGAM2045 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2045 was detected is described hereinabove with reference to Figs. 2-8.

[28587] VGAM2045 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human herpesvirus 5. VGAM2045 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[28588] VGAM2045 gene, herein designated VGAM GENE, encodes a VGAM2045 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2045 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2045 precursor RNA is designated SEQ ID:2031, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2031 is located at position 196544 relative to the genome of Human herpesvirus 5.

[28589] VGAM2045 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2045 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[28590] An enzyme complex designated DICER COMPLEX, dices the VGAM2045 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2045 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2045 RNA is designated SEQ ID:4756, and is provided hereinbelow with reference to the sequence listing part.

[28591] VGAM2045 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2045 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2045 host target RNA, herein designated VGAM HOST TARGET RNA, comprises

three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[28592] VGAM2045 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2045 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2045 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2045 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2045 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an

example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[28593] The complementary binding of VGAM2045 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2045 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2045 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2045 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[28594] It is appreciated that VGAM2045 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2045 host target genes. The mRNA of each one of this plurality of VGAM2045 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2045 RNA, herein designated VGAM RNA, and which when bound by VGAM2045 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2045 host target proteins.

[28595] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2045 gene, herein designated VGAM GENE, on one or more VGAM2045 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[28596] It is yet further appreciated that a function of VGAM2045 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2045 include diagnosis, prevention and treatment of viral infection by Human herpesvirus 5. Specific functions, and accordingly utilities, of VGAM2045 correlate with, and may be deduced from, the identity of

the host target genes which VGAM2045 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[28597] Nucleotide sequences of the VGAM2045 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2045 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2045 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2045 are further described hereinbelow with reference to Table 1.

[28598] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2045 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[28599] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2046 (VGAM2046) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[28600] VGAM2046 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2046 was detected is described hereinabove with reference to Figs. 2-8.

[28601] VGAM2046 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human herpesvirus 5. VGAM2046 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[28602] VGAM2046 gene, herein designated VGAM GENE, encodes a VGAM2046 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2046 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2046 precursor RNA is designated SEQ ID:2032, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2032 is located at position 209917 relative to the genome of Human herpesvirus 5.

[28603] VGAM2046 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2046 folded precursor RNA, herein designated VGAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[28604] An enzyme complex designated DICER COMPLEX, dices the VGAM2046 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2046 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 53%) nucleotide sequence of VGAM2046 RNA is designated SEQ ID:4757, and is provided hereinbelow with reference to the sequence listing part.

[28605] VGAM2046 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2046 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2046 host target RNA,

herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[28606] VGAM2046 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2046 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2046 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2046 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2046 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host tar-

get binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[28607] The complementary binding of VGAM2046 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2046 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2046 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2046 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[28608] It is appreciated that VGAM2046 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2046 host target genes. The mRNA of each one of this plurality of VGAM2046 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2046 RNA, herein designated VGAM RNA, and which when bound by VGAM2046 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2046 host target proteins.

[28609] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2046 gene, herein designated VGAM GENE, on one or more VGAM2046 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[28610] It is yet further appreciated that a function of VGAM2046 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2046 include diagnosis, prevention and treatment of viral infection by Human herpesvirus 5. Specific functions, and accordingly utilities, of VGAM2046

correlate with, and may be deduced from, the identity of the host target genes which VGAM2046 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[28611] Nucleotide sequences of the VGAM2046 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2046 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2046 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2046 are further described hereinbelow with reference to Table 1.

[28612] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2046 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[28613] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2047 (VGAM2047) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the

art.

[28614] VGAM2047 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2047 was detected is described hereinabove with reference to Figs. 2-8.

[28615] VGAM2047 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human herpesvirus 5. VGAM2047 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[28616] VGAM2047 gene, herein designated VGAM GENE, encodes a VGAM2047 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2047 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2047 precursor RNA is designated SEQ ID:2033, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2033 is located at position 202249 relative to the genome of Human herpesvirus 5.

[28617] VGAM2047 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2047 folded

precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[28618] An enzyme complex designated DICER COMPLEX, dices the VGAM2047 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2047 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2047 RNA is designated SEQ ID:4758, and is provided hereinbelow with reference to the sequence listing part.

[28619] VGAM2047 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2047 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM2047 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[28620] VGAM2047 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2047 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2047 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2047 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2047 host target RNA, herein designated VGAM HOST TARGET RNA.

It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[28621] The complementary binding of VGAM2047 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2047 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2047 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2047 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[28622] It is appreciated that VGAM2047 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2047 host target genes. The mRNA of each one of this plurality of VGAM2047 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2047 RNA, herein designated VGAM RNA, and which when bound by VGAM2047 RNA, herein designated VGAM RNA, causes inhibition of translation of

respective one or more VGAM2047 host target proteins.

[28623] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2047 gene, herein designated VGAM GENE, on one or more VGAM2047 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[28624] It is yet further appreciated that a function of VGAM2047 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2047 include diagnosis, prevention and treatment of viral infection by Human herpesvirus 5. Spe-

cific functions, and accordingly utilities, of VGAM2047 correlate with, and may be deduced from, the identity of the host target genes which VGAM2047 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[28625] Nucleotide sequences of the VGAM2047 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2047 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2047 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2047 are further described hereinbelow with reference to Table 1.

[28626] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2047 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[28627] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2048 (VGAM2048) viral gene, which modulates expression of respective host target genes thereof, the func-

tion and utility of which host target genes is known in the art.

[28628] VGAM2048 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2048 was detected is described hereinabove with reference to Figs. 2-8.

[28629] VGAM2048 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human herpesvirus 5. VGAM2048 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[28630] VGAM2048 gene, herein designated VGAM GENE, encodes a VGAM2048 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2048 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2048 precursor RNA is designated SEQ ID:2034, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2034 is located at position 207766 relative to the genome of Human herpesvirus 5.

[28631] VGAM2048 precursor RNA, herein designated VGAM PRE-

CURSOR RNA, folds onto itself, forming VGAM2048 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[28632] An enzyme complex designated DICER COMPLEX, dices the VGAM2048 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2048 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2048 RNA is designated SEQ ID:4759, and is provided hereinbelow with reference to the sequence listing part.

[28633] VGAM2048 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM2048 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2048 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[28634] VGAM2048 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2048 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2048 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2048 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2048 host

target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[28635] The complementary binding of VGAM2048 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2048 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2048 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2048 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[28636] It is appreciated that VGAM2048 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2048 host target genes. The mRNA of each one of this plurality of VGAM2048 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2048 RNA, herein designated VGAM RNA, and which when bound by VGAM2048 RNA, herein

designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2048 host target proteins.

[28637] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2048 gene, herein designated VGAM GENE, on one or more VGAM2048 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[28638] It is yet further appreciated that a function of VGAM2048 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2048 include diagnosis, prevention and

treatment of viral infection by Human herpesvirus 5. Specific functions, and accordingly utilities, of VGAM2048 correlate with, and may be deduced from, the identity of the host target genes which VGAM2048 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[28639] Nucleotide sequences of the VGAM2048 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2048 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2048 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2048 are further described hereinbelow with reference to Table 1.

[28640] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2048 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[28641] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2049 (VGAM2049) viral gene, which modulates ex-

pression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[28642] VGAM2049 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2049 was detected is described hereinabove with reference to Figs. 2-8.

[28643] VGAM2049 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human herpesvirus 5. VGAM2049 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[28644] VGAM2049 gene, herein designated VGAM GENE, encodes a VGAM2049 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2049 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2049 precursor RNA is designated SEQ ID:2035, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2035 is located at position 196060 relative to the genome of Human herpesvirus 5.

[28645] VGAM2049 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2049 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[28646] An enzyme complex designated DICER COMPLEX, dices the VGAM2049 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2049 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of VGAM2049 RNA is designated SEQ ID:4760, and is provided hereinbelow with reference to the sequence listing part.

[28647] VGAM2049 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2049 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2049 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[28648] VGAM2049 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2049 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2049 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2049 RNA, herein designated VGAM RNA, may have a different number of host target

binding sites in untranslated regions of a VGAM2049 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[28649] The complementary binding of VGAM2049 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2049 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2049 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2049 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[28650] It is appreciated that VGAM2049 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2049 host target genes. The mRNA of each one of this plurality of VGAM2049 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2049 RNA, herein designated VGAM

RNA, and which when bound by VGAM2049 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2049 host target proteins.

[28651] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2049 gene, herein designated VGAM GENE, on one or more VGAM2049 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[28652] It is yet further appreciated that a function of VGAM2049 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM2049 include diagnosis, prevention and treatment of viral infection by Human herpesvirus 5. Specific functions, and accordingly utilities, of VGAM2049 correlate with, and may be deduced from, the identity of the host target genes which VGAM2049 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[28653] Nucleotide sequences of the VGAM2049 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2049 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2049 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2049 are further described hereinbelow with reference to Table 1.

[28654] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2049 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[28655] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Mes-

senger 2050 (VGAM2050) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[28656] VGAM2050 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2050 was detected is described hereinabove with reference to Figs. 2-8.

[28657] VGAM2050 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ovine adenovirus A. VGAM2050 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[28658] VGAM2050 gene, herein designated VGAM GENE, encodes a VGAM2050 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2050 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2050 precursor RNA is designated SEQ ID:2036, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2036 is located at position

13096 relative to the genome of Ovine adenovirus A.

[28659] VGAM2050 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2050 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[28660] An enzyme complex designated DICER COMPLEX, dices the VGAM2050 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2050 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 50%) nucleotide sequence of VGAM2050 RNA is designated SEQ ID:4761, and is provided hereinbelow with reference to the sequence listing part.

[28661] VGAM2050 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2050 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2050 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[28662] VGAM2050 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2050 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2050 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2050 RNA, herein designated

VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2050 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[28663] The complementary binding of VGAM2050 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2050 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2050 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2050 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[28664] It is appreciated that VGAM2050 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2050 host target genes. The mRNA of each one of this plurality of VGAM2050 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM2050 RNA, herein designated VGAM RNA, and which when bound by VGAM2050 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2050 host target proteins.

[28665] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2050 gene, herein designated VGAM GENE, on one or more VGAM2050 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[28666] It is yet further appreciated that a function of VGAM2050 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2050 include diagnosis, prevention and treatment of viral infection by Ovine adenovirus A. Specific functions, and accordingly utilities, of VGAM2050 correlate with, and may be deduced from, the identity of the host target genes which VGAM2050 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[28667] Nucleotide sequences of the VGAM2050 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2050 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2050 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2050 are further described hereinbelow with reference to Table 1.

[28668] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2050 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[28669] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present

invention, referred to here as Viral Genomic Address Messenger 2051 (VGAM2051) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[28670] VGAM2051 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2051 was detected is described hereinabove with reference to Figs. 2-8.

[28671] VGAM2051 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ovine adenovirus A. VGAM2051 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[28672] VGAM2051 gene, herein designated VGAM GENE, encodes a VGAM2051 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2051 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2051 precursor RNA is designated SEQ ID:2037, and is provided hereinbelow with reference to the sequence listing part. Nu-

cleotide sequence SEQ ID:2037 is located at position 24505 relative to the genome of Ovine adenovirus A.

[28673] VGAM2051 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2051 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[28674] An enzyme complex designated DICER COMPLEX, dices the VGAM2051 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2051 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 81%) nucleotide sequence of VGAM2051 RNA is designated SEQ ID:4762, and is provided hereinbelow with reference to the sequence

listing part.

[28675] VGAM2051 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2051 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2051 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[28676] VGAM2051 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2051 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2051 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not

meant to be limiting VGAM2051 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2051 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[28677] The complementary binding of VGAM2051 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2051 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2051 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2051 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[28678] It is appreciated that VGAM2051 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2051 host target genes. The mRNA of each one of this plurality of VGAM2051 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2051 RNA, herein designated VGAM RNA, and which when bound by VGAM2051 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2051 host target proteins.

[28679] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2051 gene, herein designated VGAM GENE, on one or more VGAM2051 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[28680] It is yet further appreciated that a function of VGAM2051

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2051 include diagnosis, prevention and treatment of viral infection by Ovine adenovirus A. Specific functions, and accordingly utilities, of VGAM2051 correlate with, and may be deduced from, the identity of the host target genes which VGAM2051 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[28681] Nucleotide sequences of the VGAM2051 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2051 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2051 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2051 are further described hereinbelow with reference to Table 1.

[28682] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2051 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[28683] Fig. 1 further provides a conceptual description of another

novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2052 (VGAM2052) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[28684] VGAM2052 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2052 was detected is described hereinabove with reference to Figs. 2-8.

[28685] VGAM2052 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ovine adenovirus A. VGAM2052 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[28686] VGAM2052 gene, herein designated VGAM GENE, encodes a VGAM2052 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2052 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2052 precursor RNA is designated SEQ ID:2038, and is provided here-

inbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2038 is located at position 28963 relative to the genome of Ovine adenovirus A.

[28687] VGAM2052 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2052 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[28688] An enzyme complex designated DICER COMPLEX, dices the VGAM2052 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2052 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 58%) nucleotide sequence of VGAM2052 RNA is designated SEQ ID:4763, and

is provided hereinbelow with reference to the sequence listing part.

[28689] VGAM2052 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2052 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2052 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[28690] VGAM2052 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2052 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2052 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites

shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2052 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2052 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[28691] The complementary binding of VGAM2052 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2052 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2052 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2052 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[28692] It is appreciated that VGAM2052 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2052 host target genes. The mRNA of each one of this plurality of VGAM2052 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2052 RNA, herein designated VGAM RNA, and which when bound by VGAM2052 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2052 host target proteins.

[28693] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2052 gene, herein designated VGAM GENE, on one or more VGAM2052 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[28694] It is yet further appreciated that a function of VGAM2052 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2052 include diagnosis, prevention and treatment of viral infection by Ovine adenovirus A. Specific functions, and accordingly utilities, of VGAM2052 correlate with, and may be deduced from, the identity of the host target genes which VGAM2052 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[28695] Nucleotide sequences of the VGAM2052 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2052 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2052 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2052 are further described hereinbelow with reference to Table 1.

[28696] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2052 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[28697] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2053 (VGAM2053) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[28698] VGAM2053 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2053 was detected is described hereinabove with reference to Figs. 2-8.

[28699] VGAM2053 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ovine adenovirus A. VGAM2053 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[28700] VGAM2053 gene, herein designated VGAM GENE, encodes a VGAM2053 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2053 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2053 precur-

sor RNA is designated SEQ ID:2039, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2039 is located at position 25948 relative to the genome of Ovine adenovirus A.

[28701] VGAM2053 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2053 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[28702] An enzyme complex designated DICER COMPLEX, dices the VGAM2053 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2053 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 50%) nucleotide se-

quence of VGAM2053 RNA is designated SEQ ID:4764, and is provided hereinbelow with reference to the sequence listing part.

[28703] VGAM2053 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2053 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2053 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[28704] VGAM2053 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2053 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2053 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is ap-

preciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2053 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2053 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[28705] The complementary binding of VGAM2053 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2053 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2053 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2053 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[28706] It is appreciated that VGAM2053 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2053 host target genes. The mRNA of

each one of this plurality of VGAM2053 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2053 RNA, herein designated VGAM RNA, and which when bound by VGAM2053 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2053 host target proteins.

[28707] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2053 gene, herein designated VGAM GENE, on one or more VGAM2053 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science

294,779 (2001)).

[28708] It is yet further appreciated that a function of VGAM2053 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2053 include diagnosis, prevention and treatment of viral infection by Ovine adenovirus A. Specific functions, and accordingly utilities, of VGAM2053 correlate with, and may be deduced from, the identity of the host target genes which VGAM2053 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[28709] Nucleotide sequences of the VGAM2053 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2053 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2053 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2053 are further described hereinbelow with reference to Table 1.

[28710] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2053 RNA, herein designated VGAM RNA, are de-

scribed hereinbelow with reference to Table 2.

[28711] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2054 (VGAM2054) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[28712] VGAM2054 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2054 was detected is described hereinabove with reference to Figs. 2-8.

[28713] VGAM2054 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia virus. VGAM2054 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[28714] VGAM2054 gene, herein designated VGAM GENE, encodes a VGAM2054 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2054 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly

similar to the nucleotide sequence of VGAM2054 precursor RNA is designated SEQ ID:2040, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2040 is located at position 2713 relative to the genome of Ectromelia virus.

[28715] VGAM2054 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2054 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[28716] An enzyme complex designated DICER COMPLEX, dices the VGAM2054 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2054 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 48%) nucleotide sequence of VGAM2054 RNA is designated SEQ ID:4765, and is provided hereinbelow with reference to the sequence listing part.

[28717] VGAM2054 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2054 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2054 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[28718] VGAM2054 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2054 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2054 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I,

BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2054 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2054 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[28719] The complementary binding of VGAM2054 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2054 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2054 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2054 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[28720] It is appreciated that VGAM2054 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM2054 host target genes. The mRNA of each one of this plurality of VGAM2054 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2054 RNA, herein designated VGAM RNA, and which when bound by VGAM2054 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2054 host target proteins.

[28721] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2054 gene, herein designated VGAM GENE, on one or more VGAM2054 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[28722] It is yet further appreciated that a function of VGAM2054 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2054 include diagnosis, prevention and treatment of viral infection by Ectromelia virus. Specific functions, and accordingly utilities, of VGAM2054 correlate with, and may be deduced from, the identity of the host target genes which VGAM2054 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[28723] Nucleotide sequences of the VGAM2054 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2054 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2054 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2054 are further described hereinbelow with reference to Table 1.

[28724] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites

to VGAM2054 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[28725] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2055 (VGAM2055) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[28726] VGAM2055 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2055 was detected is described hereinabove with reference to Figs. 2-8.

[28727] VGAM2055 gene, herein designated VGAM GENE, is a viral gene contained in the genome of peanut bud necrosis virus. VGAM2055 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[28728] VGAM2055 gene, herein designated VGAM GENE, encodes a VGAM2055 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2055 precursor RNA, herein designated VGAM PRECURSOR RNA, does not en-

code a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2055 precursor RNA is designated SEQ ID:2041, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2041 is located at position 6690 relative to the genome of peanut bud necrosis virus.

[28729] VGAM2055 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2055 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[28730] An enzyme complex designated DICER COMPLEX, dices the VGAM2055 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2055 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2055 RNA is designated SEQ ID:4766, and is provided hereinbelow with reference to the sequence listing part.

[28731] VGAM2055 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2055 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2055 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[28732] VGAM2055 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2055 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2055 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3

such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2055 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2055 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[28733] The complementary binding of VGAM2055 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2055 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2055 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2055 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[28734] It is appreciated that VGAM2055 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2055 host target genes. The mRNA of each one of this plurality of VGAM2055 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2055 RNA, herein designated VGAM RNA, and which when bound by VGAM2055 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2055 host target proteins.

[28735] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2055 gene, herein designated VGAM GENE, on one or more VGAM2055 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[28736] It is yet further appreciated that a function of VGAM2055 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2055 include diagnosis, prevention and treatment of viral infection by peanut bud necrosis virus. Specific functions, and accordingly utilities, of VGAM2055 correlate with, and may be deduced from, the identity of the host target genes which VGAM2055 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[28737] Nucleotide sequences of the VGAM2055 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2055 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2055 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2055 are further described hereinbelow with reference to Table 1.

[28738] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the

complementarity of each of these host target binding sites to VGAM2055 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[28739] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2056 (VGAM2056) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[28740] VGAM2056 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2056 was detected is described hereinabove with reference to Figs. 2-8.

[28741] VGAM2056 gene, herein designated VGAM GENE, is a viral gene contained in the genome of peanut bud necrosis virus. VGAM2056 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[28742] VGAM2056 gene, herein designated VGAM GENE, encodes a VGAM2056 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2056 precursor RNA,

herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2056 precursor RNA is designated SEQ ID:2042, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2042 is located at position 5281 relative to the genome of peanut bud necrosis virus.

[28743] VGAM2056 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2056 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[28744] An enzyme complex designated DICER COMPLEX, dices the VGAM2056 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2056 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2056 RNA is designated SEQ ID:4767, and is provided hereinbelow with reference to the sequence listing part.

[28745] VGAM2056 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2056 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2056 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[28746] VGAM2056 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2056 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2056 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host

target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2056 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2056 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[28747] The complementary binding of VGAM2056 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2056 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2056 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2056 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[28748] It is appreciated that VGAM2056 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2056 host target genes. The mRNA of each one of this plurality of VGAM2056 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2056 RNA, herein designated VGAM RNA, and which when bound by VGAM2056 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2056 host target proteins.

[28749] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2056 gene, herein designated VGAM GENE, on one or more VGAM2056 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[28750] It is yet further appreciated that a function of VGAM2056 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2056 include diagnosis, prevention and treatment of viral infection by peanut bud necrosis virus. Specific functions, and accordingly utilities, of VGAM2056 correlate with, and may be deduced from, the identity of the host target genes which VGAM2056 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[28751] Nucleotide sequences of the VGAM2056 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2056 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2056 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2056 are further described hereinbelow with reference to Table 1.

[28752] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2056 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[28753] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2057 (VGAM2057) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[28754] VGAM2057 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2057 was detected is described hereinabove with reference to Figs. 2-8.

[28755] VGAM2057 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia virus. VGAM2057 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[28756] VGAM2057 gene, herein designated VGAM GENE, encodes a VGAM2057 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and un-

like most ordinary genes, VGAM2057 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2057 precursor RNA is designated SEQ ID:2043, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2043 is located at position 3968 relative to the genome of Ectromelia virus.

[28757] VGAM2057 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2057 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[28758] An enzyme complex designated DICER COMPLEX, dices the VGAM2057 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2057 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 69%) nucleotide sequence of VGAM2057 RNA is designated SEQ ID:4768, and is provided hereinbelow with reference to the sequence listing part.

[28759] VGAM2057 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2057 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2057 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[28760] VGAM2057 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2057 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2057 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed

sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2057 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2057 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[28761] The complementary binding of VGAM2057 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2057 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2057 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2057 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target

protein is therefore outlined by a broken line.

[28762] It is appreciated that VGAM2057 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2057 host target genes. The mRNA of each one of this plurality of VGAM2057 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2057 RNA, herein designated VGAM RNA, and which when bound by VGAM2057 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2057 host target proteins.

[28763] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2057 gene, herein designated VGAM GENE, on one or more VGAM2057 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[28764] It is yet further appreciated that a function of VGAM2057 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2057 include diagnosis, prevention and treatment of viral infection by Ectromelia virus. Specific functions, and accordingly utilities, of VGAM2057 correlate with, and may be deduced from, the identity of the host target genes which VGAM2057 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[28765] Nucleotide sequences of the VGAM2057 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2057 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2057 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2057 are further described hereinbelow with reference to Table 1.

[28766] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2057 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[28767] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2058 (VGAM2058) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[28768] VGAM2058 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2058 was detected is described hereinabove with reference to Figs. 2-8.

[28769] VGAM2058 gene, herein designated VGAM GENE, is a viral gene contained in the genome of peanut bud necrosis virus. VGAM2058 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[28770] VGAM2058 gene, herein designated VGAM GENE, encodes a VGAM2058 precursor RNA, herein designated VGAM

PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2058 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2058 precursor RNA is designated SEQ ID:2044, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2044 is located at position 4967 relative to the genome of peanut bud necrosis virus.

[28771] VGAM2058 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2058 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[28772] An enzyme complex designated DICER COMPLEX, dices the VGAM2058 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2058 RNA, herein designated VGAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 66%) nucleotide sequence of VGAM2058 RNA is designated SEQ ID:4769, and is provided hereinbelow with reference to the sequence listing part.

[28773] VGAM2058 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2058 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2058 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[28774] VGAM2058 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2058 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2058 RNA, herein designated

VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2058 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2058 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[28775] The complementary binding of VGAM2058 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2058 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2058 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2058 host target protein, herein desig-

nated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[28776] It is appreciated that VGAM2058 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2058 host target genes. The mRNA of each one of this plurality of VGAM2058 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2058 RNA, herein designated VGAM RNA, and which when bound by VGAM2058 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2058 host target proteins.

[28777] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2058 gene, herein designated VGAM GENE, on one or more VGAM2058 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[28778] It is yet further appreciated that a function of VGAM2058 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2058 include diagnosis, prevention and treatment of viral infection by peanut bud necrosis virus. Specific functions, and accordingly utilities, of VGAM2058 correlate with, and may be deduced from, the identity of the host target genes which VGAM2058 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[28779] Nucleotide sequences of the VGAM2058 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2058 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2058 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2058 are further described hereinbelow with reference to Table 1.

[28780] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2058 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[28781] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2059 (VGAM2059) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[28782] VGAM2059 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2059 was detected is described hereinabove with reference to Figs. 2-8.

[28783] VGAM2059 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia virus. VGAM2059 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[28784] VGAM2059 gene, herein designated VGAM GENE, encodes

a VGAM2059 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2059 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2059 precursor RNA is designated SEQ ID:2045, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2045 is located at position 15250 relative to the genome of Ectromelia virus.

[28785] VGAM2059 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2059 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[28786] An enzyme complex designated DICER COMPLEX, dices the VGAM2059 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2059 RNA,

herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2059 RNA is designated SEQ ID:4770, and is provided hereinbelow with reference to the sequence listing part.

[28787] VGAM2059 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2059 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2059 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[28788] VGAM2059 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2059 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM2059 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2059 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2059 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[28789] The complementary binding of VGAM2059 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2059 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2059 host target RNA, herein designated VGAM HOST TARGET

RNA, into VGAM2059 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[28790] It is appreciated that VGAM2059 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2059 host target genes. The mRNA of each one of this plurality of VGAM2059 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2059 RNA, herein designated VGAM RNA, and which when bound by VGAM2059 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2059 host target proteins.

[28791] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2059 gene, herein designated VGAM GENE, on one or more VGAM2059 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[28792] It is yet further appreciated that a function of VGAM2059 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2059 include diagnosis, prevention and treatment of viral infection by Ectromelia virus. Specific functions, and accordingly utilities, of VGAM2059 correlate with, and may be deduced from, the identity of the host target genes which VGAM2059 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[28793] Nucleotide sequences of the VGAM2059 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2059 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2059 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2059 are further

described hereinbelow with reference to Table 1.

[28794] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2059 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[28795] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2060 (VGAM2060) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[28796] VGAM2060 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2060 was detected is described hereinabove with reference to Figs. 2-8.

[28797] VGAM2060 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia virus. VGAM2060 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[28798] VGAM2060 gene, herein designated VGAM GENE, encodes a VGAM2060 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2060 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2060 precursor RNA is designated SEQ ID:2046, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2046 is located at position 3202 relative to the genome of Ectromelia virus.

[28799] VGAM2060 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2060 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[28800] An enzyme complex designated DICER COMPLEX, dices the VGAM2060 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, into VGAM2060 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 70%) nucleotide sequence of VGAM2060 RNA is designated SEQ ID:4771, and is provided hereinbelow with reference to the sequence listing part.

[28801] VGAM2060 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2060 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2060 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[28802] VGAM2060 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2060 host target RNA, herein designated VGAM HOST TARGET RNA. This

complementary binding is due to the fact that the nucleotide sequence of VGAM2060 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2060 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2060 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[28803] The complementary binding of VGAM2060 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2060 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2060

host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2060 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[28804] It is appreciated that VGAM2060 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2060 host target genes. The mRNA of each one of this plurality of VGAM2060 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2060 RNA, herein designated VGAM RNA, and which when bound by VGAM2060 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2060 host target proteins.

[28805] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2060 gene, herein designated VGAM GENE, on one or more VGAM2060 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[28806] It is yet further appreciated that a function of VGAM2060 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2060 include diagnosis, prevention and treatment of viral infection by Ectromelia virus. Specific functions, and accordingly utilities, of VGAM2060 correlate with, and may be deduced from, the identity of the host target genes which VGAM2060 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[28807] Nucleotide sequences of the VGAM2060 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2060 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2060 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM2060 are further described hereinbelow with reference to Table 1.

[28808] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2060 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[28809] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2061 (VGAM2061) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[28810] VGAM2061 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2061 was detected is described hereinabove with reference to Figs. 2-8.

[28811] VGAM2061 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia virus. VGAM2061 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the

human genome.

[28812] VGAM2061 gene, herein designated VGAM GENE, encodes a VGAM2061 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2061 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2061 precursor RNA is designated SEQ ID:2047, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2047 is located at position 132 relative to the genome of Ectromelia virus.

[28813] VGAM2061 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2061 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[28814] An enzyme complex designated DICER COMPLEX, dices

the VGAM2061 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2061 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2061 RNA is designated SEQ ID:4772, and is provided hereinbelow with reference to the sequence listing part.

[28815] VGAM2061 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2061 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2061 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[28816] VGAM2061 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2061 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2061 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2061 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2061 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[28817] The complementary binding of VGAM2061 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2061 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM2061 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2061 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[28818] It is appreciated that VGAM2061 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2061 host target genes. The mRNA of each one of this plurality of VGAM2061 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2061 RNA, herein designated VGAM RNA, and which when bound by VGAM2061 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2061 host target proteins.

[28819] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2061 gene, herein designated VGAM GENE, on one or more VGAM2061 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[28820] It is yet further appreciated that a function of VGAM2061 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2061 include diagnosis, prevention and treatment of viral infection by Ectromelia virus. Specific functions, and accordingly utilities, of VGAM2061 correlate with, and may be deduced from, the identity of the host target genes which VGAM2061 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[28821] Nucleotide sequences of the VGAM2061 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2061 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of

VGAM2061 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2061 are further described hereinbelow with reference to Table 1.

[28822] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2061 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[28823] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2062 (VGAM2062) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[28824] VGAM2062 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2062 was detected is described hereinabove with reference to Figs. 2-8.

[28825] VGAM2062 gene, herein designated VGAM GENE, is a viral gene contained in the genome of peanut bud necrosis virus. VGAM2062 host target gene, herein designated

VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[28826] VGAM2062 gene, herein designated VGAM GENE, encodes a VGAM2062 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2062 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2062 precursor RNA is designated SEQ ID:2048, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2048 is located at position 345 relative to the genome of peanut bud necrosis virus.

[28827] VGAM2062 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2062 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[28828] An enzyme complex designated DICER COMPLEX, dices the VGAM2062 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2062 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2062 RNA is designated SEQ ID:4773, and is provided hereinbelow with reference to the sequence listing part.

[28829] VGAM2062 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2062 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2062 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[28830] VGAM2062 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites

located in untranslated regions of VGAM2062 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2062 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2062 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2062 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[28831] The complementary binding of VGAM2062 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2062 host target RNA, herein designated VGAM

HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2062 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2062 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[28832] It is appreciated that VGAM2062 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2062 host target genes. The mRNA of each one of this plurality of VGAM2062 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2062 RNA, herein designated VGAM RNA, and which when bound by VGAM2062 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2062 host target proteins.

[28833] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2062 gene, herein designated VGAM GENE, on one or more VGAM2062 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove

with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[28834] It is yet further appreciated that a function of VGAM2062 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2062 include diagnosis, prevention and treatment of viral infection by peanut bud necrosis virus. Specific functions, and accordingly utilities, of VGAM2062 correlate with, and may be deduced from, the identity of the host target genes which VGAM2062 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[28835] Nucleotide sequences of the VGAM2062 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2062 RNA, herein designated VGAM RNA, and

a schematic representation of the secondary folding of VGAM2062 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2062 are further described hereinbelow with reference to Table 1.

[28836] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2062 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[28837] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2063 (VGAM2063) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[28838] VGAM2063 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2063 was detected is described hereinabove with reference to Figs. 2-8.

[28839] VGAM2063 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia virus.

VGAM2063 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[28840] VGAM2063 gene, herein designated VGAM GENE, encodes a VGAM2063 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2063 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2063 precursor RNA is designated SEQ ID:2049, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2049 is located at position 7074 relative to the genome of Ectromelia virus.

[28841] VGAM2063 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2063 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[28842] An enzyme complex designated DICER COMPLEX, dices the VGAM2063 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2063 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of VGAM2063 RNA is designated SEQ ID:4774, and is provided hereinbelow with reference to the sequence listing part.

[28843] VGAM2063 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2063 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2063 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[28844] VGAM2063 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM2063 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2063 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2063 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2063 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[28845] The complementary binding of VGAM2063 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM2063 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2063 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2063 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[28846] It is appreciated that VGAM2063 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2063 host target genes. The mRNA of each one of this plurality of VGAM2063 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2063 RNA, herein designated VGAM RNA, and which when bound by VGAM2063 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2063 host target proteins.

[28847] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2063 gene, herein designated VGAM GENE, on one or more VGAM2063 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[28848] It is yet further appreciated that a function of VGAM2063 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2063 include diagnosis, prevention and treatment of viral infection by Ectromelia virus. Specific functions, and accordingly utilities, of VGAM2063 correlate with, and may be deduced from, the identity of the host target genes which VGAM2063 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[28849] Nucleotide sequences of the VGAM2063 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

diced VGAM2063 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2063 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2063 are further described hereinbelow with reference to Table 1.

[28850] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2063 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[28851] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2064 (VGAM2064) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[28852] VGAM2064 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2064 was detected is described hereinabove with reference to Figs. 2-8.

[28853] VGAM2064 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of peanut bud necrosis virus. VGAM2064 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[28854] VGAM2064 gene, herein designated VGAM GENE, encodes a VGAM2064 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2064 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2064 precursor RNA is designated SEQ ID:2050, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2050 is located at position 3726 relative to the genome of peanut bud necrosis virus.

[28855] VGAM2064 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2064 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[28856] An enzyme complex designated DICER COMPLEX, dices the VGAM2064 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2064 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide sequence of VGAM2064 RNA is designated SEQ ID:4775, and is provided hereinbelow with reference to the sequence listing part.

[28857] VGAM2064 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2064 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2064 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[28858] VGAM2064 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2064 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2064 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2064 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2064 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[28859] The complementary binding of VGAM2064 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM2064 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2064 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2064 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[28860] It is appreciated that VGAM2064 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2064 host target genes. The mRNA of each one of this plurality of VGAM2064 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2064 RNA, herein designated VGAM RNA, and which when bound by VGAM2064 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2064 host target proteins.

[28861] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2064 gene, herein designated VGAM GENE, on one or more VGAM2064 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[28862] It is yet further appreciated that a function of VGAM2064 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2064 include diagnosis, prevention and treatment of viral infection by peanut bud necrosis virus. Specific functions, and accordingly utilities, of VGAM2064 correlate with, and may be deduced from, the identity of the host target genes which VGAM2064 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[28863] Nucleotide sequences of the VGAM2064 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the diced VGAM2064 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2064 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2064 are further described hereinbelow with reference to Table 1.

[28864] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2064 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[28865] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2065 (VGAM2065) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[28866] VGAM2065 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2065 was detected is described hereinabove with reference to Figs. 2-8.

[28867] VGAM2065 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia virus. VGAM2065 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[28868] VGAM2065 gene, herein designated VGAM GENE, encodes a VGAM2065 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2065 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2065 precursor RNA is designated SEQ ID:2051, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2051 is located at position 18973 relative to the genome of Ectromelia virus.

[28869] VGAM2065 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2065 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[28870] An enzyme complex designated DICER COMPLEX, dices the VGAM2065 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2065 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 82%) nucleotide sequence of VGAM2065 RNA is designated SEQ ID:4776, and is provided hereinbelow with reference to the sequence listing part.

[28871] VGAM2065 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2065 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2065 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN COD-

ING and 3UTR respectively.

[28872] VGAM2065 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2065 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2065 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2065 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2065 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[28873] The complementary binding of VGAM2065 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2065 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2065 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2065 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[28874] It is appreciated that VGAM2065 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2065 host target genes. The mRNA of each one of this plurality of VGAM2065 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2065 RNA, herein designated VGAM RNA, and which when bound by VGAM2065 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2065 host target proteins.

[28875] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2065 gene, herein designated VGAM GENE, on one

or more VGAM2065 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[28876] It is yet further appreciated that a function of VGAM2065 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2065 include diagnosis, prevention and treatment of viral infection by Ectromelia virus. Specific functions, and accordingly utilities, of VGAM2065 correlate with, and may be deduced from, the identity of the host target genes which VGAM2065 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[28877] Nucleotide sequences of the VGAM2065 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2065 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2065 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2065 are further described hereinbelow with reference to Table 1.

[28878] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2065 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[28879] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2066 (VGAM2066) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[28880] VGAM2066 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2066 was detected is de-

scribed hereinabove with reference to Figs. 2-8.

[28881] VGAM2066 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia virus. VGAM2066 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[28882] VGAM2066 gene, herein designated VGAM GENE, encodes a VGAM2066 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2066 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2066 precursor RNA is designated SEQ ID:2052, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2052 is located at position 9912 relative to the genome of Ectromelia virus.

[28883] VGAM2066 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2066 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[28884] An enzyme complex designated DICER COMPLEX, dices the VGAM2066 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2066 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2066 RNA is designated SEQ ID:4777, and is provided hereinbelow with reference to the sequence listing part.

[28885] VGAM2066 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2066 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2066 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and

a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[28886] VGAM2066 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2066 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2066 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2066 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2066 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both

3UTR and 5UTR regions.

[28887] The complementary binding of VGAM2066 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2066 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2066 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2066 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[28888] It is appreciated that VGAM2066 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2066 host target genes. The mRNA of each one of this plurality of VGAM2066 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2066 RNA, herein designated VGAM RNA, and which when bound by VGAM2066 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2066 host target proteins.

[28889] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM2066 gene, herein designated VGAM GENE, on one or more VGAM2066 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[28890] It is yet further appreciated that a function of VGAM2066 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2066 include diagnosis, prevention and treatment of viral infection by Ectromelia virus. Specific functions, and accordingly utilities, of VGAM2066 correlate with, and may be deduced from, the identity of the host target genes which VGAM2066 binds and inhibits, and the function of these host target genes, as elaborated

hereinbelow.

[28891] Nucleotide sequences of the VGAM2066 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2066 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2066 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2066 are further described hereinbelow with reference to Table 1.

[28892] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2066 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[28893] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2067 (VGAM2067) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[28894] VGAM2067 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene.

The method by which VGAM2067 was detected is described hereinabove with reference to Figs. 2-8.

[28895] VGAM2067 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia virus. VGAM2067 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[28896] VGAM2067 gene, herein designated VGAM GENE, encodes a VGAM2067 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2067 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2067 precursor RNA is designated SEQ ID:2053, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2053 is located at position 7556 relative to the genome of Ectromelia virus.

[28897] VGAM2067 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2067 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[28898] An enzyme complex designated DICER COMPLEX, dices the VGAM2067 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2067 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2067 RNA is designated SEQ ID:4778, and is provided hereinbelow with reference to the sequence listing part.

[28899] VGAM2067 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2067 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2067 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding

gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[28900] VGAM2067 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2067 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2067 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2067 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2067 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be lo-

cated in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[28901] The complementary binding of VGAM2067 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2067 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2067 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2067 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[28902] It is appreciated that VGAM2067 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2067 host target genes. The mRNA of each one of this plurality of VGAM2067 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2067 RNA, herein designated VGAM RNA, and which when bound by VGAM2067 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2067 host target proteins.

[28903] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM2067 gene, herein designated VGAM GENE, on one or more VGAM2067 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[28904] It is yet further appreciated that a function of VGAM2067 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2067 include diagnosis, prevention and treatment of viral infection by Ectromelia virus. Specific functions, and accordingly utilities, of VGAM2067 correlate with, and may be deduced from, the identity of the host target genes which VGAM2067 binds and inhibits,

and the function of these host target genes, as elaborated hereinbelow.

[28905] Nucleotide sequences of the VGAM2067 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2067 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2067 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2067 are further described hereinbelow with reference to Table 1.

[28906] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2067 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[28907] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2068 (VGAM2068) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[28908] VGAM2068 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2068 was detected is described hereinabove with reference to Figs. 2-8.

[28909] VGAM2068 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Monkeypox virus. VGAM2068 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[28910] VGAM2068 gene, herein designated VGAM GENE, encodes a VGAM2068 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2068 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2068 precursor RNA is designated SEQ ID:2054, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2054 is located at position 18952 relative to the genome of Monkeypox virus.

[28911] VGAM2068 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2068 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[28912] An enzyme complex designated DICER COMPLEX, dices the VGAM2068 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2068 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2068 RNA is designated SEQ ID:4779, and is provided hereinbelow with reference to the sequence listing part.

[28913] VGAM2068 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2068 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2068 host target RNA, herein designated VGAM HOST TARGET RNA, comprises

three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[28914] VGAM2068 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2068 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2068 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2068 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2068 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an

example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[28915] The complementary binding of VGAM2068 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2068 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2068 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2068 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[28916] It is appreciated that VGAM2068 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2068 host target genes. The mRNA of each one of this plurality of VGAM2068 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2068 RNA, herein designated VGAM RNA, and which when bound by VGAM2068 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2068 host target proteins.

[28917] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2068 gene, herein designated VGAM GENE, on one or more VGAM2068 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[28918] It is yet further appreciated that a function of VGAM2068 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2068 include diagnosis, prevention and treatment of viral infection by Monkeypox virus. Specific functions, and accordingly utilities, of VGAM2068 correlate with, and may be deduced from, the identity of the

host target genes which VGAM2068 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[28919] Nucleotide sequences of the VGAM2068 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2068 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2068 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2068 are further described hereinbelow with reference to Table 1.

[28920] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2068 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[28921] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2069 (VGAM2069) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[28922] VGAM2069 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2069 was detected is described hereinabove with reference to Figs. 2-8.

[28923] VGAM2069 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Monkeypox virus. VGAM2069 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[28924] VGAM2069 gene, herein designated VGAM GENE, encodes a VGAM2069 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2069 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2069 precursor RNA is designated SEQ ID:2055, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2055 is located at position 20862 relative to the genome of Monkeypox virus.

[28925] VGAM2069 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2069 folded precursor RNA, herein designated VGAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[28926] An enzyme complex designated DICER COMPLEX, dices the VGAM2069 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2069 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2069 RNA is designated SEQ ID:4780, and is provided hereinbelow with reference to the sequence listing part.

[28927] VGAM2069 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2069 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2069 host target RNA,

herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[28928] VGAM2069 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2069 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2069 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2069 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2069 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host tar-

get binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[28929] The complementary binding of VGAM2069 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2069 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2069 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2069 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[28930] It is appreciated that VGAM2069 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2069 host target genes. The mRNA of each one of this plurality of VGAM2069 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2069 RNA, herein designated VGAM RNA, and which when bound by VGAM2069 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2069 host target proteins.

[28931] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2069 gene, herein designated VGAM GENE, on one or more VGAM2069 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[28932] It is yet further appreciated that a function of VGAM2069 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2069 include diagnosis, prevention and treatment of viral infection by Monkeypox virus. Specific functions, and accordingly utilities, of VGAM2069 corre-

late with, and may be deduced from, the identity of the host target genes which VGAM2069 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[28933] Nucleotide sequences of the VGAM2069 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2069 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2069 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2069 are further described hereinbelow with reference to Table 1.

[28934] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2069 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[28935] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2070 (VGAM2070) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the

art.

[28936] VGAM2070 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2070 was detected is described hereinabove with reference to Figs. 2-8.

[28937] VGAM2070 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Monkeypox virus. VGAM2070 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[28938] VGAM2070 gene, herein designated VGAM GENE, encodes a VGAM2070 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2070 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2070 precursor RNA is designated SEQ ID:2056, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2056 is located at position 20302 relative to the genome of Monkeypox virus.

[28939] VGAM2070 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2070 folded

precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[28940] An enzyme complex designated DICER COMPLEX, dices the VGAM2070 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2070 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2070 RNA is designated SEQ ID:4781, and is provided hereinbelow with reference to the sequence listing part.

[28941] VGAM2070 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2070 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM2070 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[28942] VGAM2070 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2070 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2070 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2070 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2070 host target RNA, herein designated VGAM HOST TARGET RNA.

It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[28943] The complementary binding of VGAM2070 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2070 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2070 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2070 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[28944] It is appreciated that VGAM2070 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2070 host target genes. The mRNA of each one of this plurality of VGAM2070 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2070 RNA, herein designated VGAM RNA, and which when bound by VGAM2070 RNA, herein designated VGAM RNA, causes inhibition of translation of

respective one or more VGAM2070 host target proteins.

[28945] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2070 gene, herein designated VGAM GENE, on one or more VGAM2070 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[28946] It is yet further appreciated that a function of VGAM2070 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2070 include diagnosis, prevention and treatment of viral infection by Monkeypox virus. Specific

functions, and accordingly utilities, of VGAM2070 correlate with, and may be deduced from, the identity of the host target genes which VGAM2070 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[28947] Nucleotide sequences of the VGAM2070 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2070 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2070 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2070 are further described hereinbelow with reference to Table 1.

[28948] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2070 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[28949] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2071 (VGAM2071) viral gene, which modulates expression of respective host target genes thereof, the func-

tion and utility of which host target genes is known in the art.

[28950] VGAM2071 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2071 was detected is described hereinabove with reference to Figs. 2-8.

[28951] VGAM2071 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Monkeypox virus. VGAM2071 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[28952] VGAM2071 gene, herein designated VGAM GENE, encodes a VGAM2071 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2071 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2071 precursor RNA is designated SEQ ID:2057, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2057 is located at position 28091 relative to the genome of Monkeypox virus.

[28953] VGAM2071 precursor RNA, herein designated VGAM PRE-

CURSOR RNA, folds onto itself, forming VGAM2071 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[28954] An enzyme complex designated DICER COMPLEX, dices the VGAM2071 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2071 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 75%) nucleotide sequence of VGAM2071 RNA is designated SEQ ID:4782, and is provided hereinbelow with reference to the sequence listing part.

[28955] VGAM2071 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM2071 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2071 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[28956] VGAM2071 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2071 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2071 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2071 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2071 host

target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[28957] The complementary binding of VGAM2071 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2071 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2071 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2071 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[28958] It is appreciated that VGAM2071 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2071 host target genes. The mRNA of each one of this plurality of VGAM2071 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2071 RNA, herein designated VGAM RNA, and which when bound by VGAM2071 RNA, herein

designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2071 host target proteins.

[28959] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2071 gene, herein designated VGAM GENE, on one or more VGAM2071 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[28960] It is yet further appreciated that a function of VGAM2071 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2071 include diagnosis, prevention and

treatment of viral infection by Monkeypox virus. Specific functions, and accordingly utilities, of VGAM2071 correlate with, and may be deduced from, the identity of the host target genes which VGAM2071 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[28961] Nucleotide sequences of the VGAM2071 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2071 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2071 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2071 are further described hereinbelow with reference to Table 1.

[28962] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2071 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[28963] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2072 (VGAM2072) viral gene, which modulates ex-

pression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[28964] VGAM2072 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2072 was detected is described hereinabove with reference to Figs. 2-8.

[28965] VGAM2072 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia virus. VGAM2072 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[28966] VGAM2072 gene, herein designated VGAM GENE, encodes a VGAM2072 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2072 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2072 precursor RNA is designated SEQ ID:2058, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2058 is located at position 23821 relative to the genome of Ectromelia virus.

[28967] VGAM2072 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2072 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[28968] An enzyme complex designated DICER COMPLEX, dices the VGAM2072 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2072 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 64%) nucleotide sequence of VGAM2072 RNA is designated SEQ ID:4783, and is provided hereinbelow with reference to the sequence listing part.

[28969] VGAM2072 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2072 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2072 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[28970] VGAM2072 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2072 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2072 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2072 RNA, herein designated VGAM RNA, may have a different number of host target

binding sites in untranslated regions of a VGAM2072 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[28971] The complementary binding of VGAM2072 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2072 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2072 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2072 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[28972] It is appreciated that VGAM2072 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2072 host target genes. The mRNA of each one of this plurality of VGAM2072 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2072 RNA, herein designated VGAM

RNA, and which when bound by VGAM2072 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2072 host target proteins.

[28973] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2072 gene, herein designated VGAM GENE, on one or more VGAM2072 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[28974] It is yet further appreciated that a function of VGAM2072 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM2072 include diagnosis, prevention and treatment of viral infection by Ectromelia virus. Specific functions, and accordingly utilities, of VGAM2072 correlate with, and may be deduced from, the identity of the host target genes which VGAM2072 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[28975] Nucleotide sequences of the VGAM2072 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2072 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2072 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2072 are further described hereinbelow with reference to Table 1.

[28976] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2072 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[28977] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Mes-

senger 2073 (VGAM2073) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[28978] VGAM2073 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2073 was detected is described hereinabove with reference to Figs. 2-8.

[28979] VGAM2073 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Monkeypox virus. VGAM2073 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[28980] VGAM2073 gene, herein designated VGAM GENE, encodes a VGAM2073 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2073 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2073 precursor RNA is designated SEQ ID:2059, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2059 is located at position

16020 relative to the genome of Monkeypox virus.

[28981] VGAM2073 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2073 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[28982] An enzyme complex designated DICER COMPLEX, dices the VGAM2073 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2073 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2073 RNA is designated SEQ ID:4784, and is provided hereinbelow with reference to the sequence listing part.

[28983] VGAM2073 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2073 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2073 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[28984] VGAM2073 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2073 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2073 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2073 RNA, herein designated

VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2073 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[28985] The complementary binding of VGAM2073 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2073 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2073 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2073 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[28986] It is appreciated that VGAM2073 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2073 host target genes. The mRNA of each one of this plurality of VGAM2073 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM2073 RNA, herein designated VGAM RNA, and which when bound by VGAM2073 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2073 host target proteins.

[28987] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2073 gene, herein designated VGAM GENE, on one or more VGAM2073 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[28988] It is yet further appreciated that a function of VGAM2073 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2073 include diagnosis, prevention and treatment of viral infection by Monkeypox virus. Specific functions, and accordingly utilities, of VGAM2073 correlate with, and may be deduced from, the identity of the host target genes which VGAM2073 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[28989] Nucleotide sequences of the VGAM2073 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2073 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2073 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2073 are further described hereinbelow with reference to Table 1.

[28990] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2073 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[28991] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present

invention, referred to here as Viral Genomic Address Messenger 2074 (VGAM2074) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[28992] VGAM2074 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2074 was detected is described hereinabove with reference to Figs. 2-8.

[28993] VGAM2074 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Monkeypox virus. VGAM2074 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[28994] VGAM2074 gene, herein designated VGAM GENE, encodes a VGAM2074 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2074 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2074 precursor RNA is designated SEQ ID:2060, and is provided hereinbelow with reference to the sequence listing part. Nu-

cleotide sequence SEQ ID:2060 is located at position 25479 relative to the genome of Monkeypox virus.

[28995] VGAM2074 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2074 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[28996] An enzyme complex designated DICER COMPLEX, dices the VGAM2074 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2074 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2074 RNA is designated SEQ ID:4785, and is provided hereinbelow with reference to the sequence

listing part.

[28997] VGAM2074 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2074 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2074 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[28998] VGAM2074 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2074 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2074 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not

meant to be limiting VGAM2074 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2074 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[28999] The complementary binding of VGAM2074 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2074 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2074 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2074 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[29000] It is appreciated that VGAM2074 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2074 host target genes. The mRNA of each one of this plurality of VGAM2074 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2074 RNA, herein designated VGAM RNA, and which when bound by VGAM2074 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2074 host target proteins.

[29001] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2074 gene, herein designated VGAM GENE, on one or more VGAM2074 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[29002] It is yet further appreciated that a function of VGAM2074

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2074 include diagnosis, prevention and treatment of viral infection by Monkeypox virus. Specific functions, and accordingly utilities, of VGAM2074 correlate with, and may be deduced from, the identity of the host target genes which VGAM2074 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[29003] Nucleotide sequences of the VGAM2074 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2074 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2074 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2074 are further described hereinbelow with reference to Table 1.

[29004] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2074 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[29005] Fig. 1 further provides a conceptual description of another

novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2075 (VGAM2075) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[29006] VGAM2075 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2075 was detected is described hereinabove with reference to Figs. 2-8.

[29007] VGAM2075 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Variola virus. VGAM2075 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[29008] VGAM2075 gene, herein designated VGAM GENE, encodes a VGAM2075 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2075 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2075 precursor RNA is designated SEQ ID:2061, and is provided hereinbelow with reference to the sequence listing part. Nu-

cleotide sequence SEQ ID:2061 is located at position 177494 relative to the genome of Variola virus.

[29009] VGAM2075 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2075 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[29010] An enzyme complex designated DICER COMPLEX, dices the VGAM2075 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2075 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 55%) nucleotide sequence of VGAM2075 RNA is designated SEQ ID:4786, and is provided hereinbelow with reference to the sequence

listing part.

[29011] VGAM2075 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2075 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2075 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[29012] VGAM2075 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2075 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2075 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not

meant to be limiting VGAM2075 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2075 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[29013] The complementary binding of VGAM2075 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2075 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2075 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2075 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[29014] It is appreciated that VGAM2075 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2075 host target genes. The mRNA of each one of this plurality of VGAM2075 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2075 RNA, herein designated VGAM RNA, and which when bound by VGAM2075 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2075 host target proteins.

[29015] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2075 gene, herein designated VGAM GENE, on one or more VGAM2075 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[29016] It is yet further appreciated that a function of VGAM2075

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2075 include diagnosis, prevention and treatment of viral infection by Variola virus. Specific functions, and accordingly utilities, of VGAM2075 correlate with, and may be deduced from, the identity of the host target genes which VGAM2075 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[29017] Nucleotide sequences of the VGAM2075 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2075 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2075 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2075 are further described hereinbelow with reference to Table 1.

[29018] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2075 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[29019] Fig. 1 further provides a conceptual description of another

novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2076 (VGAM2076) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[29020] VGAM2076 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2076 was detected is described hereinabove with reference to Figs. 2-8.

[29021] VGAM2076 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Variola virus. VGAM2076 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[29022] VGAM2076 gene, herein designated VGAM GENE, encodes a VGAM2076 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2076 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2076 precursor RNA is designated SEQ ID:2062, and is provided hereinbelow with reference to the sequence listing part. Nu-

cleotide sequence SEQ ID:2062 is located at position 175023 relative to the genome of Variola virus.

[29023] VGAM2076 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2076 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[29024] An enzyme complex designated DICER COMPLEX, dices the VGAM2076 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2076 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2076 RNA is designated SEQ ID:4787, and is provided hereinbelow with reference to the sequence

listing part.

[29025] VGAM2076 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2076 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2076 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[29026] VGAM2076 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2076 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2076 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not

meant to be limiting VGAM2076 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2076 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[29027] The complementary binding of VGAM2076 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2076 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2076 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2076 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[29028] It is appreciated that VGAM2076 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2076 host target genes. The mRNA of each one of this plurality of VGAM2076 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2076 RNA, herein designated VGAM RNA, and which when bound by VGAM2076 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2076 host target proteins.

[29029] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2076 gene, herein designated VGAM GENE, on one or more VGAM2076 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[29030] It is yet further appreciated that a function of VGAM2076

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2076 include diagnosis, prevention and treatment of viral infection by Variola virus. Specific functions, and accordingly utilities, of VGAM2076 correlate with, and may be deduced from, the identity of the host target genes which VGAM2076 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[29031] Nucleotide sequences of the VGAM2076 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2076 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2076 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2076 are further described hereinbelow with reference to Table 1.

[29032] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2076 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[29033] Fig. 1 further provides a conceptual description of another

novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2077 (VGAM2077) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[29034] VGAM2077 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2077 was detected is described hereinabove with reference to Figs. 2-8.

[29035] VGAM2077 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Variola virus. VGAM2077 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[29036] VGAM2077 gene, herein designated VGAM GENE, encodes a VGAM2077 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2077 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2077 precursor RNA is designated SEQ ID:2063, and is provided hereinbelow with reference to the sequence listing part. Nu-

cleotide sequence SEQ ID:2063 is located at position 178760 relative to the genome of Variola virus.

[29037] VGAM2077 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2077 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[29038] An enzyme complex designated DICER COMPLEX, dices the VGAM2077 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2077 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2077 RNA is designated SEQ ID:4788, and is provided hereinbelow with reference to the sequence

listing part.

[29039] VGAM2077 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2077 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2077 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[29040] VGAM2077 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2077 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2077 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not

meant to be limiting VGAM2077 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2077 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[29041] The complementary binding of VGAM2077 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2077 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2077 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2077 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[29042] It is appreciated that VGAM2077 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2077 host target genes. The mRNA of each one of this plurality of VGAM2077 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2077 RNA, herein designated VGAM RNA, and which when bound by VGAM2077 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2077 host target proteins.

[29043] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2077 gene, herein designated VGAM GENE, on one or more VGAM2077 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[29044] It is yet further appreciated that a function of VGAM2077

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2077 include diagnosis, prevention and treatment of viral infection by Variola virus. Specific functions, and accordingly utilities, of VGAM2077 correlate with, and may be deduced from, the identity of the host target genes which VGAM2077 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[29045] Nucleotide sequences of the VGAM2077 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2077 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2077 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2077 are further described hereinbelow with reference to Table 1.

[29046] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2077 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[29047] Fig. 1 further provides a conceptual description of another

novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2078 (VGAM2078) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[29048] VGAM2078 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2078 was detected is described hereinabove with reference to Figs. 2-8.

[29049] VGAM2078 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Variola virus. VGAM2078 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[29050] VGAM2078 gene, herein designated VGAM GENE, encodes a VGAM2078 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2078 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2078 precursor RNA is designated SEQ ID:2064, and is provided hereinbelow with reference to the sequence listing part. Nu-

cleotide sequence SEQ ID:2064 is located at position 168720 relative to the genome of Variola virus.

[29051] VGAM2078 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2078 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[29052] An enzyme complex designated DICER COMPLEX, dices the VGAM2078 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2078 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 66%) nucleotide sequence of VGAM2078 RNA is designated SEQ ID:4789, and is provided hereinbelow with reference to the sequence

listing part.

[29053] VGAM2078 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2078 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2078 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[29054] VGAM2078 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2078 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2078 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not

meant to be limiting VGAM2078 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2078 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[29055] The complementary binding of VGAM2078 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2078 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2078 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2078 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[29056] It is appreciated that VGAM2078 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2078 host target genes. The mRNA of each one of this plurality of VGAM2078 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2078 RNA, herein designated VGAM RNA, and which when bound by VGAM2078 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2078 host target proteins.

[29057] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2078 gene, herein designated VGAM GENE, on one or more VGAM2078 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[29058] It is yet further appreciated that a function of VGAM2078

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2078 include diagnosis, prevention and treatment of viral infection by Variola virus. Specific functions, and accordingly utilities, of VGAM2078 correlate with, and may be deduced from, the identity of the host target genes which VGAM2078 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[29059] Nucleotide sequences of the VGAM2078 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2078 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2078 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2078 are further described hereinbelow with reference to Table 1.

[29060] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2078 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[29061] Fig. 1 further provides a conceptual description of another

novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2079 (VGAM2079) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[29062] VGAM2079 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2079 was detected is described hereinabove with reference to Figs. 2-8.

[29063] VGAM2079 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Variola virus. VGAM2079 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[29064] VGAM2079 gene, herein designated VGAM GENE, encodes a VGAM2079 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2079 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2079 precursor RNA is designated SEQ ID:2065, and is provided hereinbelow with reference to the sequence listing part. Nu-

cleotide sequence SEQ ID:2065 is located at position 171525 relative to the genome of Variola virus.

[29065] VGAM2079 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2079 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[29066] An enzyme complex designated DICER COMPLEX, dices the VGAM2079 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2079 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 48%) nucleotide sequence of VGAM2079 RNA is designated SEQ ID:4790, and is provided hereinbelow with reference to the sequence

listing part.

[29067] VGAM2079 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2079 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2079 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[29068] VGAM2079 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2079 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2079 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not

meant to be limiting VGAM2079 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2079 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[29069] The complementary binding of VGAM2079 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2079 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2079 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2079 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[29070] It is appreciated that VGAM2079 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2079 host target genes. The mRNA of each one of this plurality of VGAM2079 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2079 RNA, herein designated VGAM RNA, and which when bound by VGAM2079 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2079 host target proteins.

[29071] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2079 gene, herein designated VGAM GENE, on one or more VGAM2079 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[29072] It is yet further appreciated that a function of VGAM2079

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2079 include diagnosis, prevention and treatment of viral infection by Variola virus. Specific functions, and accordingly utilities, of VGAM2079 correlate with, and may be deduced from, the identity of the host target genes which VGAM2079 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[29073] Nucleotide sequences of the VGAM2079 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2079 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2079 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2079 are further described hereinbelow with reference to Table 1.

[29074] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2079 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[29075] Fig. 1 further provides a conceptual description of another

novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2080 (VGAM2080) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[29076] VGAM2080 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2080 was detected is described hereinabove with reference to Figs. 2-8.

[29077] VGAM2080 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Variola virus. VGAM2080 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[29078] VGAM2080 gene, herein designated VGAM GENE, encodes a VGAM2080 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2080 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2080 precursor RNA is designated SEQ ID:2066, and is provided hereinbelow with reference to the sequence listing part. Nu-

cleotide sequence SEQ ID:2066 is located at position 176691 relative to the genome of Variola virus.

[29079] VGAM2080 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2080 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[29080] An enzyme complex designated DICER COMPLEX, dices the VGAM2080 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2080 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 82%) nucleotide sequence of VGAM2080 RNA is designated SEQ ID:4791, and is provided hereinbelow with reference to the sequence

listing part.

[29081] VGAM2080 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2080 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2080 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[29082] VGAM2080 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2080 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2080 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not

meant to be limiting VGAM2080 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2080 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[29083] The complementary binding of VGAM2080 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2080 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2080 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2080 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[29084] It is appreciated that VGAM2080 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2080 host target genes. The mRNA of each one of this plurality of VGAM2080 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2080 RNA, herein designated VGAM RNA, and which when bound by VGAM2080 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2080 host target proteins.

[29085] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2080 gene, herein designated VGAM GENE, on one or more VGAM2080 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[29086] It is yet further appreciated that a function of VGAM2080

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2080 include diagnosis, prevention and treatment of viral infection by Variola virus. Specific functions, and accordingly utilities, of VGAM2080 correlate with, and may be deduced from, the identity of the host target genes which VGAM2080 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[29087] Nucleotide sequences of the VGAM2080 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2080 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2080 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2080 are further described hereinbelow with reference to Table 1.

[29088] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2080 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[29089] Fig. 1 further provides a conceptual description of another

novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2081 (VGAM2081) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[29090] VGAM2081 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2081 was detected is described hereinabove with reference to Figs. 2-8.

[29091] VGAM2081 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Variola virus. VGAM2081 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[29092] VGAM2081 gene, herein designated VGAM GENE, encodes a VGAM2081 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2081 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2081 precursor RNA is designated SEQ ID:2067, and is provided hereinbelow with reference to the sequence listing part. Nu-

cleotide sequence SEQ ID:2067 is located at position 180298 relative to the genome of Variola virus.

[29093] VGAM2081 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2081 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[29094] An enzyme complex designated DICER COMPLEX, dices the VGAM2081 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2081 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2081 RNA is designated SEQ ID:4792, and is provided hereinbelow with reference to the sequence

listing part.

[29095] VGAM2081 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2081 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2081 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[29096] VGAM2081 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2081 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2081 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not

meant to be limiting VGAM2081 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2081 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[29097] The complementary binding of VGAM2081 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2081 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2081 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2081 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[29098] It is appreciated that VGAM2081 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2081 host target genes. The mRNA of each one of this plurality of VGAM2081 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2081 RNA, herein designated VGAM RNA, and which when bound by VGAM2081 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2081 host target proteins.

[29099] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2081 gene, herein designated VGAM GENE, on one or more VGAM2081 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[29100] It is yet further appreciated that a function of VGAM2081

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2081 include diagnosis, prevention and treatment of viral infection by Variola virus. Specific functions, and accordingly utilities, of VGAM2081 correlate with, and may be deduced from, the identity of the host target genes which VGAM2081 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[29101] Nucleotide sequences of the VGAM2081 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2081 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2081 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2081 are further described hereinbelow with reference to Table 1.

[29102] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2081 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[29103] Fig. 1 further provides a conceptual description of another

novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2082 (VGAM2082) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[29104] VGAM2082 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2082 was detected is described hereinabove with reference to Figs. 2-8.

[29105] VGAM2082 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Variola virus. VGAM2082 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[29106] VGAM2082 gene, herein designated VGAM GENE, encodes a VGAM2082 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2082 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2082 precursor RNA is designated SEQ ID:2068, and is provided hereinbelow with reference to the sequence listing part. Nu-

cleotide sequence SEQ ID:2068 is located at position 174739 relative to the genome of Variola virus.

[29107] VGAM2082 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2082 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[29108] An enzyme complex designated DICER COMPLEX, dices the VGAM2082 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2082 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2082 RNA is designated SEQ ID:4793, and is provided hereinbelow with reference to the sequence

listing part.

[29109] VGAM2082 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2082 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2082 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[29110] VGAM2082 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2082 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2082 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not

meant to be limiting VGAM2082 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2082 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[29111] The complementary binding of VGAM2082 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2082 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2082 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2082 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[29112] It is appreciated that VGAM2082 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2082 host target genes. The mRNA of each one of this plurality of VGAM2082 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2082 RNA, herein designated VGAM RNA, and which when bound by VGAM2082 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2082 host target proteins.

[29113] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2082 gene, herein designated VGAM GENE, on one or more VGAM2082 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[29114] It is yet further appreciated that a function of VGAM2082

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2082 include diagnosis, prevention and treatment of viral infection by Variola virus. Specific functions, and accordingly utilities, of VGAM2082 correlate with, and may be deduced from, the identity of the host target genes which VGAM2082 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[29115] Nucleotide sequences of the VGAM2082 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2082 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2082 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2082 are further described hereinbelow with reference to Table 1.

[29116] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2082 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[29117] Fig. 1 further provides a conceptual description of another

novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2083 (VGAM2083) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[29118] VGAM2083 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2083 was detected is described hereinabove with reference to Figs. 2-8.

[29119] VGAM2083 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Camelpox virus. VGAM2083 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[29120] VGAM2083 gene, herein designated VGAM GENE, encodes a VGAM2083 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2083 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2083 precursor RNA is designated SEQ ID:2069, and is provided here-

inbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2069 is located at position 190806 relative to the genome of Camelpox virus.

[29121] VGAM2083 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2083 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[29122] An enzyme complex designated DICER COMPLEX, dices the VGAM2083 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2083 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2083 RNA is designated SEQ ID:4794, and

is provided hereinbelow with reference to the sequence listing part.

[29123] VGAM2083 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2083 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2083 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[29124] VGAM2083 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2083 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2083 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites

shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2083 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2083 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[29125] The complementary binding of VGAM2083 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2083 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2083 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2083 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[29126] It is appreciated that VGAM2083 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2083 host target genes. The mRNA of each one of this plurality of VGAM2083 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2083 RNA, herein designated VGAM RNA, and which when bound by VGAM2083 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2083 host target proteins.

[29127] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2083 gene, herein designated VGAM GENE, on one or more VGAM2083 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[29128] It is yet further appreciated that a function of VGAM2083 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2083 include diagnosis, prevention and treatment of viral infection by Camelpox virus. Specific functions, and accordingly utilities, of VGAM2083 correlate with, and may be deduced from, the identity of the host target genes which VGAM2083 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[29129] Nucleotide sequences of the VGAM2083 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2083 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2083 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2083 are further described hereinbelow with reference to Table 1.

[29130] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2083 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[29131] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2084 (VGAM2084) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[29132] VGAM2084 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2084 was detected is described hereinabove with reference to Figs. 2-8.

[29133] VGAM2084 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Variola virus. VGAM2084 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[29134] VGAM2084 gene, herein designated VGAM GENE, encodes a VGAM2084 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2084 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2084 precursor RNA is designated SEQ ID:2070, and is provided here-

inbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2070 is located at position 170712 relative to the genome of Variola virus.

[29135] VGAM2084 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2084 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[29136] An enzyme complex designated DICER COMPLEX, dices the VGAM2084 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2084 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 48%) nucleotide sequence of VGAM2084 RNA is designated SEQ ID:4795, and

is provided hereinbelow with reference to the sequence listing part.

[29137] VGAM2084 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2084 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2084 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[29138] VGAM2084 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2084 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2084 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites

shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2084 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2084 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[29139] The complementary binding of VGAM2084 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2084 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2084 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2084 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[29140] It is appreciated that VGAM2084 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2084 host target genes. The mRNA of each one of this plurality of VGAM2084 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2084 RNA, herein designated VGAM RNA, and which when bound by VGAM2084 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2084 host target proteins.

[29141] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2084 gene, herein designated VGAM GENE, on one or more VGAM2084 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[29142] It is yet further appreciated that a function of VGAM2084 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2084 include diagnosis, prevention and treatment of viral infection by Variola virus. Specific functions, and accordingly utilities, of VGAM2084 correlate with, and may be deduced from, the identity of the host target genes which VGAM2084 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[29143] Nucleotide sequences of the VGAM2084 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2084 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2084 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2084 are further described hereinbelow with reference to Table 1.

[29144] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2084 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[29145] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2085 (VGAM2085) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[29146] VGAM2085 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2085 was detected is described hereinabove with reference to Figs. 2-8.

[29147] VGAM2085 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Fowlpox virus.
VGAM2085 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[29148] VGAM2085 gene, herein designated VGAM GENE, encodes a VGAM2085 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2085 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2085 precur-

sor RNA is designated SEQ ID:2071, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2071 is located at position 96465 relative to the genome of Fowlpox virus.

[29149] VGAM2085 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2085 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[29150] An enzyme complex designated DICER COMPLEX, dices the VGAM2085 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2085 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 50%) nucleotide se-

quence of VGAM2085 RNA is designated SEQ ID:4796, and is provided hereinbelow with reference to the sequence listing part.

[29151] VGAM2085 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2085 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2085 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[29152] VGAM2085 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2085 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2085 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is ap-

preciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2085 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2085 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[29153] The complementary binding of VGAM2085 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2085 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2085 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2085 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[29154] It is appreciated that VGAM2085 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2085 host target genes. The mRNA of

each one of this plurality of VGAM2085 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2085 RNA, herein designated VGAM RNA, and which when bound by VGAM2085 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2085 host target proteins.

[29155] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2085 gene, herein designated VGAM GENE, on one or more VGAM2085 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science

294,779 (2001)).

[29156] It is yet further appreciated that a function of VGAM2085 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2085 include diagnosis, prevention and treatment of viral infection by Fowlpox virus. Specific functions, and accordingly utilities, of VGAM2085 correlate with, and may be deduced from, the identity of the host target genes which VGAM2085 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[29157] Nucleotide sequences of the VGAM2085 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2085 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2085 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2085 are further described hereinbelow with reference to Table 1.

[29158] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2085 RNA, herein designated VGAM RNA, are de-

scribed hereinbelow with reference to Table 2.

[29159] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2086 (VGAM2086) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[29160] VGAM2086 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2086 was detected is described hereinabove with reference to Figs. 2-8.

[29161] VGAM2086 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Fowlpox virus. VGAM2086 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[29162] VGAM2086 gene, herein designated VGAM GENE, encodes a VGAM2086 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2086 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly

similar to the nucleotide sequence of VGAM2086 precursor RNA is designated SEQ ID:2072, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2072 is located at position 106213 relative to the genome of Fowlpox virus.

[29163] VGAM2086 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2086 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[29164] An enzyme complex designated DICER COMPLEX, dices the VGAM2086 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2086 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 79%) nucleotide sequence of VGAM2086 RNA is designated SEQ ID:4797, and is provided hereinbelow with reference to the sequence listing part.

[29165] VGAM2086 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2086 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2086 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[29166] VGAM2086 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2086 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2086 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I,

BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2086 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2086 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[29167] The complementary binding of VGAM2086 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2086 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2086 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2086 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[29168] It is appreciated that VGAM2086 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM2086 host target genes. The mRNA of each one of this plurality of VGAM2086 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2086 RNA, herein designated VGAM RNA, and which when bound by VGAM2086 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2086 host target proteins.

[29169] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2086 gene, herein designated VGAM GENE, on one or more VGAM2086 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[29170] It is yet further appreciated that a function of VGAM2086 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2086 include diagnosis, prevention and treatment of viral infection by Fowlpox virus. Specific functions, and accordingly utilities, of VGAM2086 correlate with, and may be deduced from, the identity of the host target genes which VGAM2086 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[29171] Nucleotide sequences of the VGAM2086 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2086 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2086 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2086 are further described hereinbelow with reference to Table 1.

[29172] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites

to VGAM2086 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[29173] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2087 (VGAM2087) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[29174] VGAM2087 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2087 was detected is described hereinabove with reference to Figs. 2-8.

[29175] VGAM2087 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Fowlpox virus. VGAM2087 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[29176] VGAM2087 gene, herein designated VGAM GENE, encodes a VGAM2087 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2087 precursor RNA, herein designated VGAM PRECURSOR RNA, does not en-

code a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2087 precursor RNA is designated SEQ ID:2073, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2073 is located at position 115039 relative to the genome of Fowlpox virus.

[29177] VGAM2087 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2087 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[29178] An enzyme complex designated DICER COMPLEX, dices the VGAM2087 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2087 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 59%) nucleotide sequence of VGAM2087 RNA is designated SEQ ID:4798, and is provided hereinbelow with reference to the sequence listing part.

[29179] VGAM2087 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2087 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2087 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[29180] VGAM2087 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2087 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2087 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3

such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2087 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2087 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[29181] The complementary binding of VGAM2087 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2087 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2087 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2087 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[29182] It is appreciated that VGAM2087 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2087 host target genes. The mRNA of each one of this plurality of VGAM2087 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2087 RNA, herein designated VGAM RNA, and which when bound by VGAM2087 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2087 host target proteins.

[29183] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2087 gene, herein designated VGAM GENE, on one or more VGAM2087 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[29184] It is yet further appreciated that a function of VGAM2087 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2087 include diagnosis, prevention and treatment of viral infection by Fowlpox virus. Specific functions, and accordingly utilities, of VGAM2087 correlate with, and may be deduced from, the identity of the host target genes which VGAM2087 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[29185] Nucleotide sequences of the VGAM2087 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2087 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2087 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2087 are further described hereinbelow with reference to Table 1.

[29186] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the

complementarity of each of these host target binding sites to VGAM2087 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[29187] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2088 (VGAM2088) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[29188] VGAM2088 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2088 was detected is described hereinabove with reference to Figs. 2-8.

[29189] VGAM2088 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Fowlpox virus. VGAM2088 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[29190] VGAM2088 gene, herein designated VGAM GENE, encodes a VGAM2088 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2088 precursor RNA,

herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2088 precursor RNA is designated SEQ ID:2074, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2074 is located at position 97767 relative to the genome of Fowlpox virus.

[29191] VGAM2088 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2088 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[29192] An enzyme complex designated DICER COMPLEX, dices the VGAM2088 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2088 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2088 RNA is designated SEQ ID:4799, and is provided hereinbelow with reference to the sequence listing part.

[29193] VGAM2088 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2088 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2088 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[29194] VGAM2088 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2088 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2088 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host

target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2088 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2088 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[29195] The complementary binding of VGAM2088 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2088 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2088 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2088 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[29196] It is appreciated that VGAM2088 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2088 host target genes. The mRNA of each one of this plurality of VGAM2088 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2088 RNA, herein designated VGAM RNA, and which when bound by VGAM2088 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2088 host target proteins.

[29197] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2088 gene, herein designated VGAM GENE, on one or more VGAM2088 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[29198] It is yet further appreciated that a function of VGAM2088 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2088 include diagnosis, prevention and treatment of viral infection by Fowlpox virus. Specific functions, and accordingly utilities, of VGAM2088 correlate with, and may be deduced from, the identity of the host target genes which VGAM2088 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[29199] Nucleotide sequences of the VGAM2088 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2088 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2088 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2088 are further described hereinbelow with reference to Table 1.

[29200] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2088 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[29201] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2089 (VGAM2089) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[29202] VGAM2089 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2089 was detected is described hereinabove with reference to Figs. 2-8.

[29203] VGAM2089 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Fowlpox virus. VGAM2089 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[29204] VGAM2089 gene, herein designated VGAM GENE, encodes a VGAM2089 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and un-

like most ordinary genes, VGAM2089 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2089 precursor RNA is designated SEQ ID:2075, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2075 is located at position 103219 relative to the genome of Fowlpox virus.

[29205] VGAM2089 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2089 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[29206] An enzyme complex designated DICER COMPLEX, dices the VGAM2089 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2089 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2089 RNA is designated SEQ ID:4800, and is provided hereinbelow with reference to the sequence listing part.

[29207] VGAM2089 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2089 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2089 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[29208] VGAM2089 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2089 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2089 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed

sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2089 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2089 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[29209] The complementary binding of VGAM2089 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2089 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2089 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2089 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target

protein is therefore outlined by a broken line.

[29210] It is appreciated that VGAM2089 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2089 host target genes. The mRNA of each one of this plurality of VGAM2089 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2089 RNA, herein designated VGAM RNA, and which when bound by VGAM2089 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2089 host target proteins.

[29211] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2089 gene, herein designated VGAM GENE, on one or more VGAM2089 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[29212] It is yet further appreciated that a function of VGAM2089 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2089 include diagnosis, prevention and treatment of viral infection by Fowlpox virus. Specific functions, and accordingly utilities, of VGAM2089 correlate with, and may be deduced from, the identity of the host target genes which VGAM2089 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[29213] Nucleotide sequences of the VGAM2089 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2089 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2089 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2089 are further described hereinbelow with reference to Table 1.

[29214] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2089 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[29215] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2090 (VGAM2090) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[29216] VGAM2090 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2090 was detected is described hereinabove with reference to Figs. 2-8.

[29217] VGAM2090 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Fowlpox virus.
VGAM2090 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[29218] VGAM2090 gene, herein designated VGAM GENE, encodes a VGAM2090 precursor RNA, herein designated VGAM

PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2090 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2090 precursor RNA is designated SEQ ID:2076, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2076 is located at position 110457 relative to the genome of Fowlpox virus.

[29219] VGAM2090 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2090 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[29220] An enzyme complex designated DICER COMPLEX, dices the VGAM2090 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2090 RNA, herein designated VGAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 49%) nucleotide sequence of VGAM2090 RNA is designated SEQ ID:4801, and is provided hereinbelow with reference to the sequence listing part.

[29221] VGAM2090 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2090 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2090 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[29222] VGAM2090 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2090 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2090 RNA, herein designated

VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2090 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2090 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[29223] The complementary binding of VGAM2090 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2090 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2090 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2090 host target protein, herein desig-

nated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[29224] It is appreciated that VGAM2090 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2090 host target genes. The mRNA of each one of this plurality of VGAM2090 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2090 RNA, herein designated VGAM RNA, and which when bound by VGAM2090 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2090 host target proteins.

[29225] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2090 gene, herein designated VGAM GENE, on one or more VGAM2090 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[29226] It is yet further appreciated that a function of VGAM2090 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2090 include diagnosis, prevention and treatment of viral infection by Fowlpox virus. Specific functions, and accordingly utilities, of VGAM2090 correlate with, and may be deduced from, the identity of the host target genes which VGAM2090 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[29227] Nucleotide sequences of the VGAM2090 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2090 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2090 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2090 are further described hereinbelow with reference to Table 1.

[29228] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2090 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[29229] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2091 (VGAM2091) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[29230] VGAM2091 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2091 was detected is described hereinabove with reference to Figs. 2-8.

[29231] VGAM2091 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Fowlpox virus.
VGAM2091 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[29232] VGAM2091 gene, herein designated VGAM GENE, encodes

a VGAM2091 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2091 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2091 precursor RNA is designated SEQ ID:2077, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2077 is located at position 108768 relative to the genome of Fowlpox virus.

[29233] VGAM2091 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2091 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[29234] An enzyme complex designated DICER COMPLEX, dices the VGAM2091 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2091 RNA,

herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2091 RNA is designated SEQ ID:4802, and is provided hereinbelow with reference to the sequence listing part.

[29235] VGAM2091 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2091 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2091 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[29236] VGAM2091 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2091 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM2091 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2091 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2091 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[29237] The complementary binding of VGAM2091 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2091 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2091 host target RNA, herein designated VGAM HOST TARGET

RNA, into VGAM2091 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[29238] It is appreciated that VGAM2091 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2091 host target genes. The mRNA of each one of this plurality of VGAM2091 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2091 RNA, herein designated VGAM RNA, and which when bound by VGAM2091 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2091 host target proteins.

[29239] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2091 gene, herein designated VGAM GENE, on one or more VGAM2091 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[29240] It is yet further appreciated that a function of VGAM2091 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2091 include diagnosis, prevention and treatment of viral infection by Fowlpox virus. Specific functions, and accordingly utilities, of VGAM2091 correlate with, and may be deduced from, the identity of the host target genes which VGAM2091 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[29241] Nucleotide sequences of the VGAM2091 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2091 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2091 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2091 are further

described hereinbelow with reference to Table 1.

[29242] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2091 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[29243] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2092 (VGAM2092) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[29244] VGAM2092 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2092 was detected is described hereinabove with reference to Figs. 2-8.

[29245] VGAM2092 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Fowlpox virus.
VGAM2092 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[29246] VGAM2092 gene, herein designated VGAM GENE, encodes a VGAM2092 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2092 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2092 precursor RNA is designated SEQ ID:2078, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2078 is located at position 102276 relative to the genome of Fowlpox virus.

[29247] VGAM2092 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2092 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[29248] An enzyme complex designated DICER COMPLEX, dices the VGAM2092 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, into VGAM2092 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 54%) nucleotide sequence of VGAM2092 RNA is designated SEQ ID:4803, and is provided hereinbelow with reference to the sequence listing part.

[29249] VGAM2092 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2092 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2092 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[29250] VGAM2092 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2092 host target RNA, herein designated VGAM HOST TARGET RNA. This

complementary binding is due to the fact that the nucleotide sequence of VGAM2092 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2092 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2092 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[29251] The complementary binding of VGAM2092 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2092 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2092

host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2092 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[29252] It is appreciated that VGAM2092 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2092 host target genes. The mRNA of each one of this plurality of VGAM2092 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2092 RNA, herein designated VGAM RNA, and which when bound by VGAM2092 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2092 host target proteins.

[29253] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2092 gene, herein designated VGAM GENE, on one or more VGAM2092 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[29254] It is yet further appreciated that a function of VGAM2092 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2092 include diagnosis, prevention and treatment of viral infection by Fowlpox virus. Specific functions, and accordingly utilities, of VGAM2092 correlate with, and may be deduced from, the identity of the host target genes which VGAM2092 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[29255] Nucleotide sequences of the VGAM2092 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2092 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2092 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM2092 are further described hereinbelow with reference to Table 1.

[29256] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2092 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[29257] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2093 (VGAM2093) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[29258] VGAM2093 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2093 was detected is described hereinabove with reference to Figs. 2-8.

[29259] VGAM2093 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Camelpox virus. VGAM2093 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the

human genome.

[29260] VGAM2093 gene, herein designated VGAM GENE, encodes a VGAM2093 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2093 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2093 precursor RNA is designated SEQ ID:2079, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2079 is located at position 164255 relative to the genome of Camelpox virus.

[29261] VGAM2093 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2093 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[29262] An enzyme complex designated DICER COMPLEX, dices

the VGAM2093 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2093 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2093 RNA is designated SEQ ID:4804, and is provided hereinbelow with reference to the sequence listing part.

[29263] VGAM2093 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2093 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2093 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[29264] VGAM2093 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2093 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2093 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2093 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2093 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[29265] The complementary binding of VGAM2093 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2093 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM2093 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2093 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[29266] It is appreciated that VGAM2093 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2093 host target genes. The mRNA of each one of this plurality of VGAM2093 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2093 RNA, herein designated VGAM RNA, and which when bound by VGAM2093 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2093 host target proteins.

[29267] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2093 gene, herein designated VGAM GENE, on one or more VGAM2093 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[29268] It is yet further appreciated that a function of VGAM2093 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2093 include diagnosis, prevention and treatment of viral infection by Camelpox virus. Specific functions, and accordingly utilities, of VGAM2093 correlate with, and may be deduced from, the identity of the host target genes which VGAM2093 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[29269] Nucleotide sequences of the VGAM2093 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2093 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of

VGAM2093 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2093 are further described hereinbelow with reference to Table 1.

[29270] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2093 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[29271] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2094 (VGAM2094) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[29272] VGAM2094 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2094 was detected is described hereinabove with reference to Figs. 2-8.

[29273] VGAM2094 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Camelpox virus. VGAM2094 host target gene, herein designated VGAM

HOST TARGET GENE, is a human gene contained in the human genome.

[29274] VGAM2094 gene, herein designated VGAM GENE, encodes a VGAM2094 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2094 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2094 precursor RNA is designated SEQ ID:2080, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2080 is located at position 169679 relative to the genome of Camelpox virus.

[29275] VGAM2094 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2094 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[29276] An enzyme complex designated DICER COMPLEX, dices the VGAM2094 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2094 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of VGAM2094 RNA is designated SEQ ID:4805, and is provided hereinbelow with reference to the sequence listing part.

[29277] VGAM2094 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2094 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2094 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[29278] VGAM2094 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites

located in untranslated regions of VGAM2094 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2094 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2094 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2094 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[29279] The complementary binding of VGAM2094 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2094 host target RNA, herein designated VGAM

HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2094 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2094 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[29280] It is appreciated that VGAM2094 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2094 host target genes. The mRNA of each one of this plurality of VGAM2094 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2094 RNA, herein designated VGAM RNA, and which when bound by VGAM2094 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2094 host target proteins.

[29281] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2094 gene, herein designated VGAM GENE, on one or more VGAM2094 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove

with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[29282] It is yet further appreciated that a function of VGAM2094 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2094 include diagnosis, prevention and treatment of viral infection by Camelpox virus. Specific functions, and accordingly utilities, of VGAM2094 correlate with, and may be deduced from, the identity of the host target genes which VGAM2094 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[29283] Nucleotide sequences of the VGAM2094 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2094 RNA, herein designated VGAM RNA, and

a schematic representation of the secondary folding of VGAM2094 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2094 are further described hereinbelow with reference to Table 1.

[29284] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2094 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[29285] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2095 (VGAM2095) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[29286] VGAM2095 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2095 was detected is described hereinabove with reference to Figs. 2-8.

[29287] VGAM2095 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Camelpox virus.

VGAM2095 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[29288] VGAM2095 gene, herein designated VGAM GENE, encodes a VGAM2095 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2095 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2095 precursor RNA is designated SEQ ID:2081, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2081 is located at position 174432 relative to the genome of Camelpox virus.

[29289] VGAM2095 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2095 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[29290] An enzyme complex designated DICER COMPLEX, dices the VGAM2095 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2095 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2095 RNA is designated SEQ ID:4806, and is provided hereinbelow with reference to the sequence listing part.

[29291] VGAM2095 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2095 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2095 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[29292] VGAM2095 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM2095 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2095 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2095 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2095 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[29293] The complementary binding of VGAM2095 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM2095 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2095 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2095 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[29294] It is appreciated that VGAM2095 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2095 host target genes. The mRNA of each one of this plurality of VGAM2095 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2095 RNA, herein designated VGAM RNA, and which when bound by VGAM2095 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2095 host target proteins.

[29295] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2095 gene, herein designated VGAM GENE, on one or more VGAM2095 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[29296] It is yet further appreciated that a function of VGAM2095 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2095 include diagnosis, prevention and treatment of viral infection by Camelpox virus. Specific functions, and accordingly utilities, of VGAM2095 correlate with, and may be deduced from, the identity of the host target genes which VGAM2095 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[29297] Nucleotide sequences of the VGAM2095 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

diced VGAM2095 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2095 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2095 are further described hereinbelow with reference to Table 1.

[29298] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2095 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[29299] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2096 (VGAM2096) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[29300] VGAM2096 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2096 was detected is described hereinabove with reference to Figs. 2-8.

[29301] VGAM2096 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of Camelpox virus. VGAM2096 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[29302] VGAM2096 gene, herein designated VGAM GENE, encodes a VGAM2096 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2096 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2096 precursor RNA is designated SEQ ID:2082, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2082 is located at position 170764 relative to the genome of Camelpox virus.

[29303] VGAM2096 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2096 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[29304] An enzyme complex designated DICER COMPLEX, dices the VGAM2096 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2096 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 65%) nucleotide sequence of VGAM2096 RNA is designated SEQ ID:4807, and is provided hereinbelow with reference to the sequence listing part.

[29305] VGAM2096 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2096 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2096 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[29306] VGAM2096 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2096 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2096 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2096 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2096 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[29307] The complementary binding of VGAM2096 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM2096 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2096 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2096 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[29308] It is appreciated that VGAM2096 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2096 host target genes. The mRNA of each one of this plurality of VGAM2096 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2096 RNA, herein designated VGAM RNA, and which when bound by VGAM2096 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2096 host target proteins.

[29309] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2096 gene, herein designated VGAM GENE, on one or more VGAM2096 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[29310] It is yet further appreciated that a function of VGAM2096 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2096 include diagnosis, prevention and treatment of viral infection by Camelpox virus. Specific functions, and accordingly utilities, of VGAM2096 correlate with, and may be deduced from, the identity of the host target genes which VGAM2096 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[29311] Nucleotide sequences of the VGAM2096 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the diced VGAM2096 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2096 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2096 are further described hereinbelow with reference to Table 1.

[29312] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2096 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[29313] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2097 (VGAM2097) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[29314] VGAM2097 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2097 was detected is described hereinabove with reference to Figs. 2-8.

[29315] VGAM2097 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Camelpox virus. VGAM2097 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[29316] VGAM2097 gene, herein designated VGAM GENE, encodes a VGAM2097 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2097 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2097 precursor RNA is designated SEQ ID:2083, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2083 is located at position 176879 relative to the genome of Camelpox virus.

[29317] VGAM2097 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2097 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[29318] An enzyme complex designated DICER COMPLEX, dices the VGAM2097 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2097 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 68%) nucleotide sequence of VGAM2097 RNA is designated SEQ ID:4808, and is provided hereinbelow with reference to the sequence listing part.

[29319] VGAM2097 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2097 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2097 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN COD-

ING and 3UTR respectively.

[29320] VGAM2097 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2097 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2097 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2097 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2097 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[29321] The complementary binding of VGAM2097 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2097 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2097 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2097 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[29322] It is appreciated that VGAM2097 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2097 host target genes. The mRNA of each one of this plurality of VGAM2097 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2097 RNA, herein designated VGAM RNA, and which when bound by VGAM2097 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2097 host target proteins.

[29323] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2097 gene, herein designated VGAM GENE, on one

or more VGAM2097 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[29324] It is yet further appreciated that a function of VGAM2097 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2097 include diagnosis, prevention and treatment of viral infection by Camelpox virus. Specific functions, and accordingly utilities, of VGAM2097 correlate with, and may be deduced from, the identity of the host target genes which VGAM2097 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[29325] Nucleotide sequences of the VGAM2097 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2097 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2097 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2097 are further described hereinbelow with reference to Table 1.

[29326] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2097 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[29327] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2098 (VGAM2098) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[29328] VGAM2098 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2098 was detected is de-

scribed hereinabove with reference to Figs. 2-8.

[29329] VGAM2098 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Camelpox virus. VGAM2098 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[29330] VGAM2098 gene, herein designated VGAM GENE, encodes a VGAM2098 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2098 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2098 precursor RNA is designated SEQ ID:2084, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2084 is located at position 174573 relative to the genome of Camelpox virus.

[29331] VGAM2098 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2098 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[29332] An enzyme complex designated DICER COMPLEX, dices the VGAM2098 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2098 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2098 RNA is designated SEQ ID:4809, and is provided hereinbelow with reference to the sequence listing part.

[29333] VGAM2098 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2098 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2098 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and

a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[29334] VGAM2098 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2098 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2098 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2098 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2098 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both

3UTR and 5UTR regions.

[29335] The complementary binding of VGAM2098 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2098 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2098 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2098 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[29336] It is appreciated that VGAM2098 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2098 host target genes. The mRNA of each one of this plurality of VGAM2098 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2098 RNA, herein designated VGAM RNA, and which when bound by VGAM2098 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2098 host target proteins.

[29337] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM2098 gene, herein designated VGAM GENE, on one or more VGAM2098 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[29338] It is yet further appreciated that a function of VGAM2098 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2098 include diagnosis, prevention and treatment of viral infection by Camelpox virus. Specific functions, and accordingly utilities, of VGAM2098 correlate with, and may be deduced from, the identity of the host target genes which VGAM2098 binds and inhibits, and the function of these host target genes, as elaborated

hereinbelow.

[29339] Nucleotide sequences of the VGAM2098 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2098 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2098 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2098 are further described hereinbelow with reference to Table 1.

[29340] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2098 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[29341] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2099 (VGAM2099) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[29342] VGAM2099 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene.

The method by which VGAM2099 was detected is described hereinabove with reference to Figs. 2-8.

[29343] VGAM2099 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Camelpox virus. VGAM2099 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[29344] VGAM2099 gene, herein designated VGAM GENE, encodes a VGAM2099 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2099 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2099 precursor RNA is designated SEQ ID:2085, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2085 is located at position 174840 relative to the genome of Camelpox virus.

[29345] VGAM2099 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2099 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[29346] An enzyme complex designated DICER COMPLEX, dices the VGAM2099 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2099 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2099 RNA is designated SEQ ID:4810, and is provided hereinbelow with reference to the sequence listing part.

[29347] VGAM2099 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2099 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2099 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding

gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[29348] VGAM2099 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2099 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2099 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2099 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2099 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be lo-

cated in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[29349] The complementary binding of VGAM2099 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2099 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2099 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2099 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[29350] It is appreciated that VGAM2099 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2099 host target genes. The mRNA of each one of this plurality of VGAM2099 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2099 RNA, herein designated VGAM RNA, and which when bound by VGAM2099 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2099 host target proteins.

[29351] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM2099 gene, herein designated VGAM GENE, on one or more VGAM2099 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[29352] It is yet further appreciated that a function of VGAM2099 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2099 include diagnosis, prevention and treatment of viral infection by Camelpox virus. Specific functions, and accordingly utilities, of VGAM2099 correlate with, and may be deduced from, the identity of the host target genes which VGAM2099 binds and inhibits,

and the function of these host target genes, as elaborated hereinbelow.

[29353] Nucleotide sequences of the VGAM2099 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2099 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2099 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2099 are further described hereinbelow with reference to Table 1.

[29354] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2099 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[29355] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2100 (VGAM2100) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[29356] VGAM2100 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2100 was detected is described hereinabove with reference to Figs. 2-8.

[29357] VGAM2100 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Camelpox virus. VGAM2100 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[29358] VGAM2100 gene, herein designated VGAM GENE, encodes a VGAM2100 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2100 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2100 precursor RNA is designated SEQ ID:2086, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2086 is located at position 176689 relative to the genome of Camelpox virus.

[29359] VGAM2100 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2100 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[29360] An enzyme complex designated DICER COMPLEX, dices the VGAM2100 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2100 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2100 RNA is designated SEQ ID:4811, and is provided hereinbelow with reference to the sequence listing part.

[29361] VGAM2100 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2100 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2100 host target RNA, herein designated VGAM HOST TARGET RNA, comprises

three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[29362] VGAM2100 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2100 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2100 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2100 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2100 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an

example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[29363] The complementary binding of VGAM2100 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2100 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2100 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2100 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[29364] It is appreciated that VGAM2100 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2100 host target genes. The mRNA of each one of this plurality of VGAM2100 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2100 RNA, herein designated VGAM RNA, and which when bound by VGAM2100 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2100 host target proteins.

[29365] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2100 gene, herein designated VGAM GENE, on one or more VGAM2100 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[29366] It is yet further appreciated that a function of VGAM2100 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2100 include diagnosis, prevention and treatment of viral infection by Camelpox virus. Specific functions, and accordingly utilities, of VGAM2100 correlate with, and may be deduced from, the identity of the

host target genes which VGAM2100 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[29367] Nucleotide sequences of the VGAM2100 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2100 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2100 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2100 are further described hereinbelow with reference to Table 1.

[29368] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2100 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[29369] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2101 (VGAM2101) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[29370] VGAM2101 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2101 was detected is described hereinabove with reference to Figs. 2-8.

[29371] VGAM2101 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Camelpox virus. VGAM2101 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[29372] VGAM2101 gene, herein designated VGAM GENE, encodes a VGAM2101 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2101 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2101 precursor RNA is designated SEQ ID:2087, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2087 is located at position 171927 relative to the genome of Camelpox virus.

[29373] VGAM2101 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2101 folded precursor RNA, herein designated VGAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[29374] An enzyme complex designated DICER COMPLEX, dices the VGAM2101 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2101 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2101 RNA is designated SEQ ID:4812, and is provided hereinbelow with reference to the sequence listing part.

[29375] VGAM2101 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2101 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2101 host target RNA,

herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[29376] VGAM2101 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2101 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2101 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2101 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2101 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host tar-

get binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[29377] The complementary binding of VGAM2101 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2101 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2101 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2101 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[29378] It is appreciated that VGAM2101 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2101 host target genes. The mRNA of each one of this plurality of VGAM2101 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2101 RNA, herein designated VGAM RNA, and which when bound by VGAM2101 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2101 host target proteins.

[29379] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2101 gene, herein designated VGAM GENE, on one or more VGAM2101 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[29380] It is yet further appreciated that a function of VGAM2101 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2101 include diagnosis, prevention and treatment of viral infection by Camelpox virus. Specific functions, and accordingly utilities, of VGAM2101 corre-

late with, and may be deduced from, the identity of the host target genes which VGAM2101 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[29381] Nucleotide sequences of the VGAM2101 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2101 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2101 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2101 are further described hereinbelow with reference to Table 1.

[29382] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2101 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[29383] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2102 (VGAM2102) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the

art.

[29384] VGAM2102 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2102 was detected is described hereinabove with reference to Figs. 2-8.

[29385] VGAM2102 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Camelpox virus. VGAM2102 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[29386] VGAM2102 gene, herein designated VGAM GENE, encodes a VGAM2102 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2102 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2102 precursor RNA is designated SEQ ID:2088, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2088 is located at position 168981 relative to the genome of Camelpox virus.

[29387] VGAM2102 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2102 folded

precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[29388] An enzyme complex designated DICER COMPLEX, dices the VGAM2102 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2102 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 53%) nucleotide sequence of VGAM2102 RNA is designated SEQ ID:4813, and is provided hereinbelow with reference to the sequence listing part.

[29389] VGAM2102 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2102 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM2102 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[29390] VGAM2102 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2102 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2102 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2102 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2102 host target RNA, herein designated VGAM HOST TARGET RNA.

It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[29391] The complementary binding of VGAM2102 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2102 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2102 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2102 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[29392] It is appreciated that VGAM2102 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2102 host target genes. The mRNA of each one of this plurality of VGAM2102 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2102 RNA, herein designated VGAM RNA, and which when bound by VGAM2102 RNA, herein designated VGAM RNA, causes inhibition of translation of

respective one or more VGAM2102 host target proteins.

[29393] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2102 gene, herein designated VGAM GENE, on one or more VGAM2102 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[29394] It is yet further appreciated that a function of VGAM2102 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2102 include diagnosis, prevention and treatment of viral infection by Camelpox virus. Specific

functions, and accordingly utilities, of VGAM2102 correlate with, and may be deduced from, the identity of the host target genes which VGAM2102 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[29395] Nucleotide sequences of the VGAM2102 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2102 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2102 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2102 are further described hereinbelow with reference to Table 1.

[29396] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2102 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[29397] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2103 (VGAM2103) viral gene, which modulates expression of respective host target genes thereof, the func-

tion and utility of which host target genes is known in the art.

[29398] VGAM2103 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2103 was detected is described hereinabove with reference to Figs. 2-8.

[29399] VGAM2103 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Camelpox virus. VGAM2103 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[29400] VGAM2103 gene, herein designated VGAM GENE, encodes a VGAM2103 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2103 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2103 precursor RNA is designated SEQ ID:2089, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2089 is located at position 177859 relative to the genome of Camelpox virus.

[29401] VGAM2103 precursor RNA, herein designated VGAM PRE-

CURSOR RNA, folds onto itself, forming VGAM2103 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[29402] An enzyme complex designated DICER COMPLEX, dices the VGAM2103 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2103 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2103 RNA is designated SEQ ID:4814, and is provided hereinbelow with reference to the sequence listing part.

[29403] VGAM2103 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM2103 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2103 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[29404] VGAM2103 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2103 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2103 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2103 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2103 host

target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[29405] The complementary binding of VGAM2103 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2103 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2103 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2103 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[29406] It is appreciated that VGAM2103 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2103 host target genes. The mRNA of each one of this plurality of VGAM2103 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2103 RNA, herein designated VGAM RNA, and which when bound by VGAM2103 RNA, herein

designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2103 host target proteins.

[29407] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2103 gene, herein designated VGAM GENE, on one or more VGAM2103 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[29408] It is yet further appreciated that a function of VGAM2103 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2103 include diagnosis, prevention and

treatment of viral infection by Camelpox virus. Specific functions, and accordingly utilities, of VGAM2103 correlate with, and may be deduced from, the identity of the host target genes which VGAM2103 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[29409] Nucleotide sequences of the VGAM2103 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2103 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2103 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2103 are further described hereinbelow with reference to Table 1.

[29410] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2103 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[29411] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2104 (VGAM2104) viral gene, which modulates ex-

pression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[29412] VGAM2104 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2104 was detected is described hereinabove with reference to Figs. 2-8.

[29413] VGAM2104 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Camelpox virus. VGAM2104 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[29414] VGAM2104 gene, herein designated VGAM GENE, encodes a VGAM2104 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2104 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2104 precursor RNA is designated SEQ ID:2090, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2090 is located at position 161818 relative to the genome of Camelpox virus.

[29415] VGAM2104 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2104 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[29416] An enzyme complex designated DICER COMPLEX, dices the VGAM2104 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2104 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2104 RNA is designated SEQ ID:4815, and is provided hereinbelow with reference to the sequence listing part.

[29417] VGAM2104 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2104 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2104 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[29418] VGAM2104 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2104 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2104 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2104 RNA, herein designated VGAM RNA, may have a different number of host target

binding sites in untranslated regions of a VGAM2104 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[29419] The complementary binding of VGAM2104 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2104 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2104 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2104 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[29420] It is appreciated that VGAM2104 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2104 host target genes. The mRNA of each one of this plurality of VGAM2104 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2104 RNA, herein designated VGAM

RNA, and which when bound by VGAM2104 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2104 host target proteins.

[29421] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2104 gene, herein designated VGAM GENE, on one or more VGAM2104 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[29422] It is yet further appreciated that a function of VGAM2104 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM2104 include diagnosis, prevention and treatment of viral infection by Camelpox virus. Specific functions, and accordingly utilities, of VGAM2104 correlate with, and may be deduced from, the identity of the host target genes which VGAM2104 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[29423] Nucleotide sequences of the VGAM2104 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2104 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2104 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2104 are further described hereinbelow with reference to Table 1.

[29424] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2104 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[29425] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Mes-

senger 2105 (VGAM2105) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[29426] VGAM2105 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2105 was detected is described hereinabove with reference to Figs. 2-8.

[29427] VGAM2105 gene, herein designated VGAM GENE, is a viral gene contained in the genome of grapevine chrome mosaic virus. VGAM2105 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[29428] VGAM2105 gene, herein designated VGAM GENE, encodes a VGAM2105 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2105 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2105 precursor RNA is designated SEQ ID:2091, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2091 is located at position 3783

relative to the genome of grapevine chrome mosaic virus.

[29429] VGAM2105 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2105 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[29430] An enzyme complex designated DICER COMPLEX, dices the VGAM2105 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2105 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 81%) nucleotide sequence of VGAM2105 RNA is designated SEQ ID:4816, and is provided hereinbelow with reference to the sequence listing part.

[29431] VGAM2105 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2105 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2105 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[29432] VGAM2105 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2105 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2105 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2105 RNA, herein designated

VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2105 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[29433] The complementary binding of VGAM2105 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2105 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2105 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2105 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[29434] It is appreciated that VGAM2105 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2105 host target genes. The mRNA of each one of this plurality of VGAM2105 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM2105 RNA, herein designated VGAM RNA, and which when bound by VGAM2105 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2105 host target proteins.

[29435] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2105 gene, herein designated VGAM GENE, on one or more VGAM2105 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[29436] It is yet further appreciated that a function of VGAM2105 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2105 include diagnosis, prevention and treatment of viral infection by grapevine chrome mosaic virus. Specific functions, and accordingly utilities, of VGAM2105 correlate with, and may be deduced from, the identity of the host target genes which VGAM2105 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[29437] Nucleotide sequences of the VGAM2105 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2105 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2105 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2105 are further described hereinbelow with reference to Table 1.

[29438] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2105 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[29439] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present

invention, referred to here as Viral Genomic Address Messenger 2106 (VGAM2106) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[29440] VGAM2106 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2106 was detected is described hereinabove with reference to Figs. 2-8.

[29441] VGAM2106 gene, herein designated VGAM GENE, is a viral gene contained in the genome of grapevine chrome mosaic virus. VGAM2106 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[29442] VGAM2106 gene, herein designated VGAM GENE, encodes a VGAM2106 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2106 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2106 precursor RNA is designated SEQ ID:2092, and is provided hereinbelow with reference to the sequence listing part. Nu-

cleotide sequence SEQ ID:2092 is located at position 4094 relative to the genome of grapevine chrome mosaic virus.

[29443] VGAM2106 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2106 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[29444] An enzyme complex designated DICER COMPLEX, dices the VGAM2106 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2106 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 59%) nucleotide sequence of VGAM2106 RNA is designated SEQ ID:4817, and is provided hereinbelow with reference to the sequence

listing part.

[29445] VGAM2106 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2106 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2106 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[29446] VGAM2106 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2106 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2106 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not

meant to be limiting VGAM2106 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2106 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[29447] The complementary binding of VGAM2106 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2106 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2106 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2106 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[29448] It is appreciated that VGAM2106 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2106 host target genes. The mRNA of each one of this plurality of VGAM2106 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2106 RNA, herein designated VGAM RNA, and which when bound by VGAM2106 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2106 host target proteins.

[29449] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2106 gene, herein designated VGAM GENE, on one or more VGAM2106 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[29450] It is yet further appreciated that a function of VGAM2106

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2106 include diagnosis, prevention and treatment of viral infection by grapevine chrome mosaic virus. Specific functions, and accordingly utilities, of VGAM2106 correlate with, and may be deduced from, the identity of the host target genes which VGAM2106 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[29451] Nucleotide sequences of the VGAM2106 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2106 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2106 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2106 are further described hereinbelow with reference to Table 1.

[29452] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2106 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[29453] Fig. 1 further provides a conceptual description of another

novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2107 (VGAM2107) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[29454] VGAM2107 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2107 was detected is described hereinabove with reference to Figs. 2-8.

[29455] VGAM2107 gene, herein designated VGAM GENE, is a viral gene contained in the genome of grapevine chrome mosaic virus. VGAM2107 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[29456] VGAM2107 gene, herein designated VGAM GENE, encodes a VGAM2107 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2107 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2107 precursor RNA is designated SEQ ID:2093, and is provided here-

inbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2093 is located at position 2929 relative to the genome of grapevine chrome mosaic virus.

[29457] VGAM2107 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2107 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[29458] An enzyme complex designated DICER COMPLEX, dices the VGAM2107 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2107 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2107 RNA is designated SEQ ID:4818, and

is provided hereinbelow with reference to the sequence listing part.

[29459] VGAM2107 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2107 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2107 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[29460] VGAM2107 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2107 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2107 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites

shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2107 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2107 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[29461] The complementary binding of VGAM2107 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2107 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2107 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2107 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[29462] It is appreciated that VGAM2107 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2107 host target genes. The mRNA of each one of this plurality of VGAM2107 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2107 RNA, herein designated VGAM RNA, and which when bound by VGAM2107 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2107 host target proteins.

[29463] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2107 gene, herein designated VGAM GENE, on one or more VGAM2107 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[29464] It is yet further appreciated that a function of VGAM2107 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2107 include diagnosis, prevention and treatment of viral infection by grapevine chrome mosaic virus. Specific functions, and accordingly utilities, of VGAM2107 correlate with, and may be deduced from, the identity of the host target genes which VGAM2107 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[29465] Nucleotide sequences of the VGAM2107 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2107 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2107 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2107 are further described hereinbelow with reference to Table 1.

[29466] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2107 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[29467] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2108 (VGAM2108) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[29468] VGAM2108 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2108 was detected is described hereinabove with reference to Figs. 2-8.

[29469] VGAM2108 gene, herein designated VGAM GENE, is a viral gene contained in the genome of grapevine chrome mosaic virus. VGAM2108 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[29470] VGAM2108 gene, herein designated VGAM GENE, encodes a VGAM2108 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2108 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2108 precur-

sor RNA is designated SEQ ID:2094, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2094 is located at position 3193 relative to the genome of grapevine chrome mosaic virus.

[29471] VGAM2108 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2108 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[29472] An enzyme complex designated DICER COMPLEX, dices the VGAM2108 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2108 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 51%) nucleotide se-

quence of VGAM2108 RNA is designated SEQ ID:4819, and is provided hereinbelow with reference to the sequence listing part.

[29473] VGAM2108 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2108 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2108 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[29474] VGAM2108 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2108 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2108 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is ap-

preciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2108 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2108 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[29475] The complementary binding of VGAM2108 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2108 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2108 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2108 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[29476] It is appreciated that VGAM2108 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2108 host target genes. The mRNA of

each one of this plurality of VGAM2108 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2108 RNA, herein designated VGAM RNA, and which when bound by VGAM2108 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2108 host target proteins.

[29477] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2108 gene, herein designated VGAM GENE, on one or more VGAM2108 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science

294,779 (2001)).

[29478] It is yet further appreciated that a function of VGAM2108 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2108 include diagnosis, prevention and treatment of viral infection by grapevine chrome mosaic virus. Specific functions, and accordingly utilities, of VGAM2108 correlate with, and may be deduced from, the identity of the host target genes which VGAM2108 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[29479] Nucleotide sequences of the VGAM2108 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2108 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2108 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2108 are further described hereinbelow with reference to Table 1.

[29480] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2108 RNA, herein designated VGAM RNA, are de-

scribed hereinbelow with reference to Table 2.

[29481] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2109 (VGAM2109) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[29482] VGAM2109 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2109 was detected is described hereinabove with reference to Figs. 2-8.

[29483] VGAM2109 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox virus. VGAM2109 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[29484] VGAM2109 gene, herein designated VGAM GENE, encodes a VGAM2109 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2109 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly

similar to the nucleotide sequence of VGAM2109 precursor RNA is designated SEQ ID:2095, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2095 is located at position 22662 relative to the genome of Goatpox virus.

[29485] VGAM2109 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2109 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[29486] An enzyme complex designated DICER COMPLEX, dices the VGAM2109 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2109 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 71%) nucleotide sequence of VGAM2109 RNA is designated SEQ ID:4820, and is provided hereinbelow with reference to the sequence listing part.

[29487] VGAM2109 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2109 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2109 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[29488] VGAM2109 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2109 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2109 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I,

BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2109 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2109 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[29489] The complementary binding of VGAM2109 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2109 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2109 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2109 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[29490] It is appreciated that VGAM2109 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM2109 host target genes. The mRNA of each one of this plurality of VGAM2109 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2109 RNA, herein designated VGAM RNA, and which when bound by VGAM2109 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2109 host target proteins.

[29491] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2109 gene, herein designated VGAM GENE, on one or more VGAM2109 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[29492] It is yet further appreciated that a function of VGAM2109 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2109 include diagnosis, prevention and treatment of viral infection by Goatpox virus. Specific functions, and accordingly utilities, of VGAM2109 correlate with, and may be deduced from, the identity of the host target genes which VGAM2109 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[29493] Nucleotide sequences of the VGAM2109 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2109 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2109 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2109 are further described hereinbelow with reference to Table 1.

[29494] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites

to VGAM2109 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[29495] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2110 (VGAM2110) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[29496] VGAM2110 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2110 was detected is described hereinabove with reference to Figs. 2-8.

[29497] VGAM2110 gene, herein designated VGAM GENE, is a viral gene contained in the genome of grapevine chrome mosaic virus. VGAM2110 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[29498] VGAM2110 gene, herein designated VGAM GENE, encodes a VGAM2110 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2110 precursor RNA, herein designated VGAM PRECURSOR RNA, does not en-

code a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2110 precursor RNA is designated SEQ ID:2096, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2096 is located at position 1090 relative to the genome of grapevine chrome mosaic virus.

[29499] VGAM2110 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2110 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[29500] An enzyme complex designated DICER COMPLEX, dices the VGAM2110 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2110 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2110 RNA is designated SEQ ID:4821, and is provided hereinbelow with reference to the sequence listing part.

[29501] VGAM2110 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2110 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2110 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[29502] VGAM2110 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2110 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2110 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3

such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2110 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2110 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[29503] The complementary binding of VGAM2110 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2110 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2110 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2110 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[29504] It is appreciated that VGAM2110 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2110 host target genes. The mRNA of each one of this plurality of VGAM2110 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2110 RNA, herein designated VGAM RNA, and which when bound by VGAM2110 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2110 host target proteins.

[29505] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2110 gene, herein designated VGAM GENE, on one or more VGAM2110 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[29506] It is yet further appreciated that a function of VGAM2110 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2110 include diagnosis, prevention and treatment of viral infection by grapevine chrome mosaic virus. Specific functions, and accordingly utilities, of VGAM2110 correlate with, and may be deduced from, the identity of the host target genes which VGAM2110 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[29507] Nucleotide sequences of the VGAM2110 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2110 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2110 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2110 are further described hereinbelow with reference to Table 1.

[29508] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the

complementarity of each of these host target binding sites to VGAM2110 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[29509] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2111 (VGAM2111) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[29510] VGAM2111 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2111 was detected is described hereinabove with reference to Figs. 2-8.

[29511] VGAM2111 gene, herein designated VGAM GENE, is a viral gene contained in the genome of sheeppox virus. VGAM2111 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[29512] VGAM2111 gene, herein designated VGAM GENE, encodes a VGAM2111 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2111 precursor RNA,

herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2111 precursor RNA is designated SEQ ID:2097, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2097 is located at position 6922 relative to the genome of sheeppox virus.

[29513] VGAM2111 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2111 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[29514] An enzyme complex designated DICER COMPLEX, dices the VGAM2111 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2111 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2111 RNA is designated SEQ ID:4822, and is provided hereinbelow with reference to the sequence listing part.

[29515] VGAM2111 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2111 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2111 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[29516] VGAM2111 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2111 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2111 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host

target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2111 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2111 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[29517] The complementary binding of VGAM2111 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2111 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2111 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2111 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[29518] It is appreciated that VGAM2111 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2111 host target genes. The mRNA of each one of this plurality of VGAM2111 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2111 RNA, herein designated VGAM RNA, and which when bound by VGAM2111 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2111 host target proteins.

[29519] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2111 gene, herein designated VGAM GENE, on one or more VGAM2111 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[29520] It is yet further appreciated that a function of VGAM2111 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2111 include diagnosis, prevention and treatment of viral infection by sheeppox virus. Specific functions, and accordingly utilities, of VGAM2111 correlate with, and may be deduced from, the identity of the host target genes which VGAM2111 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[29521] Nucleotide sequences of the VGAM2111 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2111 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2111 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2111 are further described hereinbelow with reference to Table 1.

[29522] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2111 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[29523] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2112 (VGAM2112) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[29524] VGAM2112 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2112 was detected is described hereinabove with reference to Figs. 2-8.

[29525] VGAM2112 gene, herein designated VGAM GENE, is a viral gene contained in the genome of grapevine chrome mosaic virus. VGAM2112 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[29526] VGAM2112 gene, herein designated VGAM GENE, encodes a VGAM2112 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and un-

like most ordinary genes, VGAM2112 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2112 precursor RNA is designated SEQ ID:2098, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2098 is located at position 1230 relative to the genome of grapevine chrome mosaic virus.

[29527] VGAM2112 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2112 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[29528] An enzyme complex designated DICER COMPLEX, dices the VGAM2112 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2112 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 81%) nucleotide sequence of VGAM2112 RNA is designated SEQ ID:4823, and is provided hereinbelow with reference to the sequence listing part.

[29529] VGAM2112 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2112 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2112 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[29530] VGAM2112 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2112 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2112 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed

sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2112 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2112 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[29531] The complementary binding of VGAM2112 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2112 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2112 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2112 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target

protein is therefore outlined by a broken line.

[29532] It is appreciated that VGAM2112 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2112 host target genes. The mRNA of each one of this plurality of VGAM2112 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2112 RNA, herein designated VGAM RNA, and which when bound by VGAM2112 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2112 host target proteins.

[29533] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2112 gene, herein designated VGAM GENE, on one or more VGAM2112 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[29534] It is yet further appreciated that a function of VGAM2112 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2112 include diagnosis, prevention and treatment of viral infection by grapevine chrome mosaic virus. Specific functions, and accordingly utilities, of VGAM2112 correlate with, and may be deduced from, the identity of the host target genes which VGAM2112 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[29535] Nucleotide sequences of the VGAM2112 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2112 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2112 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2112 are further described hereinbelow with reference to Table 1.

[29536] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2112 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[29537] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2113 (VGAM2113) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[29538] VGAM2113 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2113 was detected is described hereinabove with reference to Figs. 2-8.

[29539] VGAM2113 gene, herein designated VGAM GENE, is a viral gene contained in the genome of sheeppox virus. VGAM2113 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[29540] VGAM2113 gene, herein designated VGAM GENE, encodes a VGAM2113 precursor RNA, herein designated VGAM

PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2113 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2113 precursor RNA is designated SEQ ID:2099, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2099 is located at position 7750 relative to the genome of sheeppox virus.

[29541] VGAM2113 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2113 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[29542] An enzyme complex designated DICER COMPLEX, dices the VGAM2113 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2113 RNA, herein designated VGAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2113 RNA is designated SEQ ID:4824, and is provided hereinbelow with reference to the sequence listing part.

[29543] VGAM2113 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2113 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2113 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[29544] VGAM2113 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2113 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2113 RNA, herein designated

VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2113 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2113 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[29545] The complementary binding of VGAM2113 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2113 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2113 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2113 host target protein, herein desig-

nated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[29546] It is appreciated that VGAM2113 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2113 host target genes. The mRNA of each one of this plurality of VGAM2113 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2113 RNA, herein designated VGAM RNA, and which when bound by VGAM2113 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2113 host target proteins.

[29547] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2113 gene, herein designated VGAM GENE, on one or more VGAM2113 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[29548] It is yet further appreciated that a function of VGAM2113 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2113 include diagnosis, prevention and treatment of viral infection by sheeppox virus. Specific functions, and accordingly utilities, of VGAM2113 correlate with, and may be deduced from, the identity of the host target genes which VGAM2113 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[29549] Nucleotide sequences of the VGAM2113 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2113 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2113 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2113 are further described hereinbelow with reference to Table 1.

[29550] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2113 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[29551] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2114 (VGAM2114) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[29552] VGAM2114 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2114 was detected is described hereinabove with reference to Figs. 2-8.

[29553] VGAM2114 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cowpox virus.
VGAM2114 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[29554] VGAM2114 gene, herein designated VGAM GENE, encodes

a VGAM2114 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2114 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2114 precursor RNA is designated SEQ ID:2100, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2100 is located at position 9163 relative to the genome of Cowpox virus.

[29555] VGAM2114 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2114 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[29556] An enzyme complex designated DICER COMPLEX, dices the VGAM2114 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2114 RNA,

herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 50%) nucleotide sequence of VGAM2114 RNA is designated SEQ ID:4825, and is provided hereinbelow with reference to the sequence listing part.

[29557] VGAM2114 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2114 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2114 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[29558] VGAM2114 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2114 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM2114 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2114 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2114 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[29559] The complementary binding of VGAM2114 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2114 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2114 host target RNA, herein designated VGAM HOST TARGET

RNA, into VGAM2114 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[29560] It is appreciated that VGAM2114 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2114 host target genes. The mRNA of each one of this plurality of VGAM2114 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2114 RNA, herein designated VGAM RNA, and which when bound by VGAM2114 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2114 host target proteins.

[29561] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2114 gene, herein designated VGAM GENE, on one or more VGAM2114 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[29562] It is yet further appreciated that a function of VGAM2114 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2114 include diagnosis, prevention and treatment of viral infection by Cowpox virus. Specific functions, and accordingly utilities, of VGAM2114 correlate with, and may be deduced from, the identity of the host target genes which VGAM2114 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[29563] Nucleotide sequences of the VGAM2114 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2114 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2114 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2114 are further

described hereinbelow with reference to Table 1.

[29564] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2114 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[29565] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2115 (VGAM2115) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[29566] VGAM2115 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2115 was detected is described hereinabove with reference to Figs. 2-8.

[29567] VGAM2115 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cowpox virus.
VGAM2115 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[29568] VGAM2115 gene, herein designated VGAM GENE, encodes a VGAM2115 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2115 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2115 precursor RNA is designated SEQ ID:2101, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2101 is located at position 211598 relative to the genome of Cowpox virus.

[29569] VGAM2115 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2115 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[29570] An enzyme complex designated DICER COMPLEX, dices the VGAM2115 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2115 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2115 RNA is designated SEQ ID:4826, and is provided hereinbelow with reference to the sequence listing part.

[29571] VGAM2115 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2115 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2115 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[29572] VGAM2115 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites

located in untranslated regions of VGAM2115 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2115 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2115 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2115 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[29573] The complementary binding of VGAM2115 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2115 host target RNA, herein designated VGAM

HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2115 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2115 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[29574] It is appreciated that VGAM2115 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2115 host target genes. The mRNA of each one of this plurality of VGAM2115 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2115 RNA, herein designated VGAM RNA, and which when bound by VGAM2115 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2115 host target proteins.

[29575] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2115 gene, herein designated VGAM GENE, on one or more VGAM2115 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove

with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[29576] It is yet further appreciated that a function of VGAM2115 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2115 include diagnosis, prevention and treatment of viral infection by Cowpox virus. Specific functions, and accordingly utilities, of VGAM2115 correlate with, and may be deduced from, the identity of the host target genes which VGAM2115 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[29577] Nucleotide sequences of the VGAM2115 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2115 RNA, herein designated VGAM RNA, and

a schematic representation of the secondary folding of VGAM2115 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2115 are further described hereinbelow with reference to Table 1.

[29578] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2115 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[29579] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2116 (VGAM2116) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[29580] VGAM2116 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2116 was detected is described hereinabove with reference to Figs. 2-8.

[29581] VGAM2116 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cowpox virus.

VGAM2116 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[29582] VGAM2116 gene, herein designated VGAM GENE, encodes a VGAM2116 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2116 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2116 precursor RNA is designated SEQ ID:2102, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2102 is located at position 208834 relative to the genome of Cowpox virus.

[29583] VGAM2116 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2116 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[29584] An enzyme complex designated DICER COMPLEX, dices the VGAM2116 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2116 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 52%) nucleotide sequence of VGAM2116 RNA is designated SEQ ID:4827, and is provided hereinbelow with reference to the sequence listing part.

[29585] VGAM2116 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2116 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2116 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[29586] VGAM2116 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM2116 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2116 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2116 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2116 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[29587] The complementary binding of VGAM2116 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM2116 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2116 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2116 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[29588] It is appreciated that VGAM2116 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2116 host target genes. The mRNA of each one of this plurality of VGAM2116 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2116 RNA, herein designated VGAM RNA, and which when bound by VGAM2116 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2116 host target proteins.

[29589] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2116 gene, herein designated VGAM GENE, on one or more VGAM2116 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[29590] It is yet further appreciated that a function of VGAM2116 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2116 include diagnosis, prevention and treatment of viral infection by Cowpox virus. Specific functions, and accordingly utilities, of VGAM2116 correlate with, and may be deduced from, the identity of the host target genes which VGAM2116 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[29591] Nucleotide sequences of the VGAM2116 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

diced VGAM2116 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2116 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2116 are further described hereinbelow with reference to Table 1.

[29592] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2116 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[29593] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2117 (VGAM2117) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[29594] VGAM2117 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2117 was detected is described hereinabove with reference to Figs. 2-8.

[29595] VGAM2117 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of Cowpox virus. VGAM2117 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[29596] VGAM2117 gene, herein designated VGAM GENE, encodes a VGAM2117 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2117 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2117 precursor RNA is designated SEQ ID:2103, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2103 is located at position 206477 relative to the genome of Cowpox virus.

[29597] VGAM2117 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2117 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[29598] An enzyme complex designated DICER COMPLEX, dices the VGAM2117 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2117 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2117 RNA is designated SEQ ID:4828, and is provided hereinbelow with reference to the sequence listing part.

[29599] VGAM2117 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2117 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2117 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[29600] VGAM2117 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2117 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2117 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2117 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2117 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[29601] The complementary binding of VGAM2117 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM2117 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2117 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2117 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[29602] It is appreciated that VGAM2117 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2117 host target genes. The mRNA of each one of this plurality of VGAM2117 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2117 RNA, herein designated VGAM RNA, and which when bound by VGAM2117 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2117 host target proteins.

[29603] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2117 gene, herein designated VGAM GENE, on one or more VGAM2117 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[29604] It is yet further appreciated that a function of VGAM2117 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2117 include diagnosis, prevention and treatment of viral infection by Cowpox virus. Specific functions, and accordingly utilities, of VGAM2117 correlate with, and may be deduced from, the identity of the host target genes which VGAM2117 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[29605] Nucleotide sequences of the VGAM2117 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the diced VGAM2117 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2117 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2117 are further described hereinbelow with reference to Table 1.

[29606] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2117 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[29607] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2118 (VGAM2118) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[29608] VGAM2118 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2118 was detected is described hereinabove with reference to Figs. 2-8.

[29609] VGAM2118 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cowpox virus. VGAM2118 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[29610] VGAM2118 gene, herein designated VGAM GENE, encodes a VGAM2118 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2118 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2118 precursor RNA is designated SEQ ID:2104, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2104 is located at position 6717 relative to the genome of Cowpox virus.

[29611] VGAM2118 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2118 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[29612] An enzyme complex designated DICER COMPLEX, dices the VGAM2118 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2118 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2118 RNA is designated SEQ ID:4829, and is provided hereinbelow with reference to the sequence listing part.

[29613] VGAM2118 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2118 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2118 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN COD-

ING and 3UTR respectively.

[29614] VGAM2118 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2118 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2118 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2118 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2118 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[29615] The complementary binding of VGAM2118 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2118 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2118 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2118 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[29616] It is appreciated that VGAM2118 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2118 host target genes. The mRNA of each one of this plurality of VGAM2118 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2118 RNA, herein designated VGAM RNA, and which when bound by VGAM2118 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2118 host target proteins.

[29617] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2118 gene, herein designated VGAM GENE, on one

or more VGAM2118 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[29618] It is yet further appreciated that a function of VGAM2118 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2118 include diagnosis, prevention and treatment of viral infection by Cowpox virus. Specific functions, and accordingly utilities, of VGAM2118 correlate with, and may be deduced from, the identity of the host target genes which VGAM2118 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[29619] Nucleotide sequences of the VGAM2118 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2118 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2118 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2118 are further described hereinbelow with reference to Table 1.

[29620] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2118 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[29621] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2119 (VGAM2119) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[29622] VGAM2119 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2119 was detected is de-

scribed hereinabove with reference to Figs. 2-8.

[29623] VGAM2119 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cowpox virus. VGAM2119 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[29624] VGAM2119 gene, herein designated VGAM GENE, encodes a VGAM2119 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2119 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2119 precursor RNA is designated SEQ ID:2105, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2105 is located at position 206331 relative to the genome of Cowpox virus.

[29625] VGAM2119 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2119 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[29626] An enzyme complex designated DICER COMPLEX, dices the VGAM2119 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2119 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2119 RNA is designated SEQ ID:4830, and is provided hereinbelow with reference to the sequence listing part.

[29627] VGAM2119 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2119 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2119 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and

a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[29628] VGAM2119 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2119 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2119 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2119 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2119 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both

3UTR and 5UTR regions.

[29629] The complementary binding of VGAM2119 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2119 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2119 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2119 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[29630] It is appreciated that VGAM2119 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2119 host target genes. The mRNA of each one of this plurality of VGAM2119 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2119 RNA, herein designated VGAM RNA, and which when bound by VGAM2119 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2119 host target proteins.

[29631] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM2119 gene, herein designated VGAM GENE, on one or more VGAM2119 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[29632] It is yet further appreciated that a function of VGAM2119 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2119 include diagnosis, prevention and treatment of viral infection by Cowpox virus. Specific functions, and accordingly utilities, of VGAM2119 correlate with, and may be deduced from, the identity of the host target genes which VGAM2119 binds and inhibits, and the function of these host target genes, as elaborated

hereinbelow.

[29633] Nucleotide sequences of the VGAM2119 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2119 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2119 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2119 are further described hereinbelow with reference to Table 1.

[29634] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2119 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[29635] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2120 (VGAM2120) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[29636] VGAM2120 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene.

The method by which VGAM2120 was detected is described hereinabove with reference to Figs. 2-8.

[29637] VGAM2120 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cowpox virus. VGAM2120 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[29638] VGAM2120 gene, herein designated VGAM GENE, encodes a VGAM2120 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2120 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2120 precursor RNA is designated SEQ ID:2106, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2106 is located at position 214751 relative to the genome of Cowpox virus.

[29639] VGAM2120 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2120 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[29640] An enzyme complex designated DICER COMPLEX, dices the VGAM2120 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2120 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2120 RNA is designated SEQ ID:4831, and is provided hereinbelow with reference to the sequence listing part.

[29641] VGAM2120 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2120 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2120 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding

gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[29642] VGAM2120 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2120 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2120 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2120 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2120 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be lo-

cated in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[29643] The complementary binding of VGAM2120 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2120 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2120 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2120 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[29644] It is appreciated that VGAM2120 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2120 host target genes. The mRNA of each one of this plurality of VGAM2120 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2120 RNA, herein designated VGAM RNA, and which when bound by VGAM2120 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2120 host target proteins.

[29645] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM2120 gene, herein designated VGAM GENE, on one or more VGAM2120 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[29646] It is yet further appreciated that a function of VGAM2120 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2120 include diagnosis, prevention and treatment of viral infection by Cowpox virus. Specific functions, and accordingly utilities, of VGAM2120 correlate with, and may be deduced from, the identity of the host target genes which VGAM2120 binds and inhibits,

and the function of these host target genes, as elaborated hereinbelow.

[29647] Nucleotide sequences of the VGAM2120 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2120 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2120 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2120 are further described hereinbelow with reference to Table 1.

[29648] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2120 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[29649] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2121 (VGAM2121) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[29650] VGAM2121 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2121 was detected is described hereinabove with reference to Figs. 2-8.

[29651] VGAM2121 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cowpox virus. VGAM2121 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[29652] VGAM2121 gene, herein designated VGAM GENE, encodes a VGAM2121 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2121 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2121 precursor RNA is designated SEQ ID:2107, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2107 is located at position 6122 relative to the genome of Cowpox virus.

[29653] VGAM2121 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2121 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[29654] An enzyme complex designated DICER COMPLEX, dices the VGAM2121 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2121 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide sequence of VGAM2121 RNA is designated SEQ ID:4832, and is provided hereinbelow with reference to the sequence listing part.

[29655] VGAM2121 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2121 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2121 host target RNA, herein designated VGAM HOST TARGET RNA, comprises

three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[29656] VGAM2121 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2121 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2121 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2121 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2121 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an

example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[29657] The complementary binding of VGAM2121 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2121 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2121 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2121 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[29658] It is appreciated that VGAM2121 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2121 host target genes. The mRNA of each one of this plurality of VGAM2121 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2121 RNA, herein designated VGAM RNA, and which when bound by VGAM2121 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2121 host target proteins.

[29659] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2121 gene, herein designated VGAM GENE, on one or more VGAM2121 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[29660] It is yet further appreciated that a function of VGAM2121 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2121 include diagnosis, prevention and treatment of viral infection by Cowpox virus. Specific functions, and accordingly utilities, of VGAM2121 correlate with, and may be deduced from, the identity of the

host target genes which VGAM2121 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[29661] Nucleotide sequences of the VGAM2121 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2121 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2121 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2121 are further described hereinbelow with reference to Table 1.

[29662] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2121 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[29663] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2122 (VGAM2122) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[29664] VGAM2122 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2122 was detected is described hereinabove with reference to Figs. 2-8.

[29665] VGAM2122 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cowpox virus. VGAM2122 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[29666] VGAM2122 gene, herein designated VGAM GENE, encodes a VGAM2122 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2122 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2122 precursor RNA is designated SEQ ID:2108, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2108 is located at position 5631 relative to the genome of Cowpox virus.

[29667] VGAM2122 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2122 folded precursor RNA, herein designated VGAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[29668] An enzyme complex designated DICER COMPLEX, dices the VGAM2122 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2122 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 74%) nucleotide sequence of VGAM2122 RNA is designated SEQ ID:4833, and is provided hereinbelow with reference to the sequence listing part.

[29669] VGAM2122 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2122 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2122 host target RNA,

herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[29670] VGAM2122 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2122 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2122 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2122 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2122 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host tar-

get binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[29671] The complementary binding of VGAM2122 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2122 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2122 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2122 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[29672] It is appreciated that VGAM2122 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2122 host target genes. The mRNA of each one of this plurality of VGAM2122 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2122 RNA, herein designated VGAM RNA, and which when bound by VGAM2122 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2122 host target proteins.

[29673] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2122 gene, herein designated VGAM GENE, on one or more VGAM2122 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[29674] It is yet further appreciated that a function of VGAM2122 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2122 include diagnosis, prevention and treatment of viral infection by Cowpox virus. Specific functions, and accordingly utilities, of VGAM2122 corre-

late with, and may be deduced from, the identity of the host target genes which VGAM2122 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[29675] Nucleotide sequences of the VGAM2122 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2122 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2122 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2122 are further described hereinbelow with reference to Table 1.

[29676] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2122 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[29677] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2123 (VGAM2123) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the

art.

[29678] VGAM2123 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2123 was detected is described hereinabove with reference to Figs. 2-8.

[29679] VGAM2123 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cowpox virus. VGAM2123 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[29680] VGAM2123 gene, herein designated VGAM GENE, encodes a VGAM2123 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2123 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2123 precursor RNA is designated SEQ ID:2109, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2109 is located at position 208014 relative to the genome of Cowpox virus.

[29681] VGAM2123 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2123 folded

precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[29682] An enzyme complex designated DICER COMPLEX, dices the VGAM2123 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2123 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2123 RNA is designated SEQ ID:4834, and is provided hereinbelow with reference to the sequence listing part.

[29683] VGAM2123 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2123 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM2123 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[29684] VGAM2123 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2123 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2123 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2123 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2123 host target RNA, herein designated VGAM HOST TARGET RNA.

It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[29685] The complementary binding of VGAM2123 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2123 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2123 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2123 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[29686] It is appreciated that VGAM2123 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2123 host target genes. The mRNA of each one of this plurality of VGAM2123 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2123 RNA, herein designated VGAM RNA, and which when bound by VGAM2123 RNA, herein designated VGAM RNA, causes inhibition of translation of

respective one or more VGAM2123 host target proteins.

[29687] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2123 gene, herein designated VGAM GENE, on one or more VGAM2123 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[29688] It is yet further appreciated that a function of VGAM2123 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2123 include diagnosis, prevention and treatment of viral infection by Cowpox virus. Specific

functions, and accordingly utilities, of VGAM2123 correlate with, and may be deduced from, the identity of the host target genes which VGAM2123 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[29689] Nucleotide sequences of the VGAM2123 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2123 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2123 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2123 are further described hereinbelow with reference to Table 1.

[29690] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2123 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[29691] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2124 (VGAM2124) viral gene, which modulates expression of respective host target genes thereof, the func-

tion and utility of which host target genes is known in the art.

[29692] VGAM2124 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2124 was detected is described hereinabove with reference to Figs. 2-8.

[29693] VGAM2124 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cowpox virus. VGAM2124 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[29694] VGAM2124 gene, herein designated VGAM GENE, encodes a VGAM2124 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2124 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2124 precursor RNA is designated SEQ ID:2110, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2110 is located at position 205910 relative to the genome of Cowpox virus.

[29695] VGAM2124 precursor RNA, herein designated VGAM PRE-

CURSOR RNA, folds onto itself, forming VGAM2124 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[29696] An enzyme complex designated DICER COMPLEX, dices the VGAM2124 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2124 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 53%) nucleotide sequence of VGAM2124 RNA is designated SEQ ID:4835, and is provided hereinbelow with reference to the sequence listing part.

[29697] VGAM2124 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM2124 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2124 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[29698] VGAM2124 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2124 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2124 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2124 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2124 host

target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[29699] The complementary binding of VGAM2124 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2124 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2124 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2124 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[29700] It is appreciated that VGAM2124 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2124 host target genes. The mRNA of each one of this plurality of VGAM2124 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2124 RNA, herein designated VGAM RNA, and which when bound by VGAM2124 RNA, herein

designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2124 host target proteins.

[29701] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2124 gene, herein designated VGAM GENE, on one or more VGAM2124 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[29702] It is yet further appreciated that a function of VGAM2124 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2124 include diagnosis, prevention and

treatment of viral infection by Cowpox virus. Specific functions, and accordingly utilities, of VGAM2124 correlate with, and may be deduced from, the identity of the host target genes which VGAM2124 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[29703] Nucleotide sequences of the VGAM2124 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2124 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2124 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2124 are further described hereinbelow with reference to Table 1.

[29704] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2124 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[29705] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2125 (VGAM2125) viral gene, which modulates ex-

pression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[29706] VGAM2125 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2125 was detected is described hereinabove with reference to Figs. 2-8.

[29707] VGAM2125 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ateline herpesvirus 3. VGAM2125 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[29708] VGAM2125 gene, herein designated VGAM GENE, encodes a VGAM2125 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2125 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2125 precursor RNA is designated SEQ ID:2111, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2111 is located at position 18618 relative to the genome of Ateline herpesvirus 3.

[29709] VGAM2125 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2125 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[29710] An enzyme complex designated DICER COMPLEX, dices the VGAM2125 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2125 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2125 RNA is designated SEQ ID:4836, and is provided hereinbelow with reference to the sequence listing part.

[29711] VGAM2125 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2125 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2125 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[29712] VGAM2125 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2125 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2125 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2125 RNA, herein designated VGAM RNA, may have a different number of host target

binding sites in untranslated regions of a VGAM2125 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[29713] The complementary binding of VGAM2125 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2125 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2125 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2125 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[29714] It is appreciated that VGAM2125 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2125 host target genes. The mRNA of each one of this plurality of VGAM2125 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2125 RNA, herein designated VGAM

RNA, and which when bound by VGAM2125 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2125 host target proteins.

[29715] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2125 gene, herein designated VGAM GENE, on one or more VGAM2125 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[29716] It is yet further appreciated that a function of VGAM2125 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM2125 include diagnosis, prevention and treatment of viral infection by Ateline herpesvirus 3. Specific functions, and accordingly utilities, of VGAM2125 correlate with, and may be deduced from, the identity of the host target genes which VGAM2125 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[29717] Nucleotide sequences of the VGAM2125 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2125 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2125 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2125 are further described hereinbelow with reference to Table 1.

[29718] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2125 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[29719] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Mes-

senger 2126 (VGAM2126) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[29720] VGAM2126 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2126 was detected is described hereinabove with reference to Figs. 2-8.

[29721] VGAM2126 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ateline herpesvirus 3. VGAM2126 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[29722] VGAM2126 gene, herein designated VGAM GENE, encodes a VGAM2126 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2126 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2126 precursor RNA is designated SEQ ID:2112, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2112 is located at position 6412

relative to the genome of Ateline herpesvirus 3.

[29723] VGAM2126 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2126 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[29724] An enzyme complex designated DICER COMPLEX, dices the VGAM2126 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2126 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2126 RNA is designated SEQ ID:4837, and is provided hereinbelow with reference to the sequence listing part.

[29725] VGAM2126 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2126 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2126 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[29726] VGAM2126 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2126 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2126 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2126 RNA, herein designated

VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2126 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[29727] The complementary binding of VGAM2126 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2126 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2126 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2126 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[29728] It is appreciated that VGAM2126 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2126 host target genes. The mRNA of each one of this plurality of VGAM2126 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM2126 RNA, herein designated VGAM RNA, and which when bound by VGAM2126 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2126 host target proteins.

[29729] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2126 gene, herein designated VGAM GENE, on one or more VGAM2126 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[29730] It is yet further appreciated that a function of VGAM2126 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2126 include diagnosis, prevention and treatment of viral infection by Ateline herpesvirus 3. Specific functions, and accordingly utilities, of VGAM2126 correlate with, and may be deduced from, the identity of the host target genes which VGAM2126 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[29731] Nucleotide sequences of the VGAM2126 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2126 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2126 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2126 are further described hereinbelow with reference to Table 1.

[29732] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2126 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[29733] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present

invention, referred to here as Viral Genomic Address Messenger 2127 (VGAM2127) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[29734] VGAM2127 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2127 was detected is described hereinabove with reference to Figs. 2-8.

[29735] VGAM2127 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ateline herpesvirus 3. VGAM2127 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[29736] VGAM2127 gene, herein designated VGAM GENE, encodes a VGAM2127 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2127 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2127 precursor RNA is designated SEQ ID:2113, and is provided hereinbelow with reference to the sequence listing part. Nu-

cleotide sequence SEQ ID:2113 is located at position 22317 relative to the genome of Ateline herpesvirus 3.

[29737] VGAM2127 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2127 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[29738] An enzyme complex designated DICER COMPLEX, dices the VGAM2127 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2127 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 86%) nucleotide sequence of VGAM2127 RNA is designated SEQ ID:4838, and is provided hereinbelow with reference to the sequence

listing part.

[29739] VGAM2127 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2127 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2127 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[29740] VGAM2127 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2127 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2127 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not

meant to be limiting VGAM2127 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2127 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[29741] The complementary binding of VGAM2127 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2127 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2127 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2127 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[29742] It is appreciated that VGAM2127 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2127 host target genes. The mRNA of each one of this plurality of VGAM2127 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2127 RNA, herein designated VGAM RNA, and which when bound by VGAM2127 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2127 host target proteins.

[29743] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2127 gene, herein designated VGAM GENE, on one or more VGAM2127 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[29744] It is yet further appreciated that a function of VGAM2127

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2127 include diagnosis, prevention and treatment of viral infection by Ateline herpesvirus 3. Specific functions, and accordingly utilities, of VGAM2127 correlate with, and may be deduced from, the identity of the host target genes which VGAM2127 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[29745] Nucleotide sequences of the VGAM2127 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2127 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2127 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2127 are further described hereinbelow with reference to Table 1.

[29746] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2127 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[29747] Fig. 1 further provides a conceptual description of another

novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2128 (VGAM2128) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[29748] VGAM2128 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2128 was detected is described hereinabove with reference to Figs. 2-8.

[29749] VGAM2128 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ateline herpesvirus 3. VGAM2128 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[29750] VGAM2128 gene, herein designated VGAM GENE, encodes a VGAM2128 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2128 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2128 precursor RNA is designated SEQ ID:2114, and is provided here-

inbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2114 is located at position 22124 relative to the genome of Ateline herpesvirus 3.

[29751] VGAM2128 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2128 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[29752] An enzyme complex designated DICER COMPLEX, dices the VGAM2128 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2128 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2128 RNA is designated SEQ ID:4839, and

is provided hereinbelow with reference to the sequence listing part.

[29753] VGAM2128 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2128 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2128 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[29754] VGAM2128 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2128 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2128 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites

shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2128 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2128 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[29755] The complementary binding of VGAM2128 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2128 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2128 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2128 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[29756] It is appreciated that VGAM2128 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2128 host target genes. The mRNA of each one of this plurality of VGAM2128 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2128 RNA, herein designated VGAM RNA, and which when bound by VGAM2128 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2128 host target proteins.

[29757] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2128 gene, herein designated VGAM GENE, on one or more VGAM2128 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[29758] It is yet further appreciated that a function of VGAM2128 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2128 include diagnosis, prevention and treatment of viral infection by Ateline herpesvirus 3. Specific functions, and accordingly utilities, of VGAM2128 correlate with, and may be deduced from, the identity of the host target genes which VGAM2128 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[29759] Nucleotide sequences of the VGAM2128 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2128 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2128 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2128 are further described hereinbelow with reference to Table 1.

[29760] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2128 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[29761] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2129 (VGAM2129) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[29762] VGAM2129 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2129 was detected is described hereinabove with reference to Figs. 2-8.

[29763] VGAM2129 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ateline herpesvirus 3. VGAM2129 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[29764] VGAM2129 gene, herein designated VGAM GENE, encodes a VGAM2129 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2129 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2129 precur-

sor RNA is designated SEQ ID:2115, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2115 is located at position 9401 relative to the genome of Ateline herpesvirus 3.

[29765] VGAM2129 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2129 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[29766] An enzyme complex designated DICER COMPLEX, dices the VGAM2129 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2129 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 81%) nucleotide se-

quence of VGAM2129 RNA is designated SEQ ID:4840, and is provided hereinbelow with reference to the sequence listing part.

[29767] VGAM2129 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2129 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2129 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[29768] VGAM2129 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2129 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2129 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is ap-

preciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2129 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2129 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[29769] The complementary binding of VGAM2129 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2129 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2129 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2129 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[29770] It is appreciated that VGAM2129 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2129 host target genes. The mRNA of

each one of this plurality of VGAM2129 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2129 RNA, herein designated VGAM RNA, and which when bound by VGAM2129 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2129 host target proteins.

[29771] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2129 gene, herein designated VGAM GENE, on one or more VGAM2129 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science

294,779 (2001)).

[29772] It is yet further appreciated that a function of VGAM2129 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2129 include diagnosis, prevention and treatment of viral infection by Ateline herpesvirus 3. Specific functions, and accordingly utilities, of VGAM2129 correlate with, and may be deduced from, the identity of the host target genes which VGAM2129 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[29773] Nucleotide sequences of the VGAM2129 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2129 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2129 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2129 are further described hereinbelow with reference to Table 1.

[29774] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2129 RNA, herein designated VGAM RNA, are de-

scribed hereinbelow with reference to Table 2.

[29775] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2130 (VGAM2130) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[29776] VGAM2130 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2130 was detected is described hereinabove with reference to Figs. 2-8.

[29777] VGAM2130 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ateline herpesvirus 3. VGAM2130 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[29778] VGAM2130 gene, herein designated VGAM GENE, encodes a VGAM2130 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2130 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly

similar to the nucleotide sequence of VGAM2130 precursor RNA is designated SEQ ID:2116, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2116 is located at position 23005 relative to the genome of Ateline herpesvirus 3.

[29779] VGAM2130 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2130 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[29780] An enzyme complex designated DICER COMPLEX, dices the VGAM2130 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2130 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2130 RNA is designated SEQ ID:4841, and is provided hereinbelow with reference to the sequence listing part.

[29781] VGAM2130 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2130 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2130 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[29782] VGAM2130 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2130 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2130 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I,

BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2130 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2130 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[29783] The complementary binding of VGAM2130 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2130 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2130 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2130 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[29784] It is appreciated that VGAM2130 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM2130 host target genes. The mRNA of each one of this plurality of VGAM2130 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2130 RNA, herein designated VGAM RNA, and which when bound by VGAM2130 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2130 host target proteins.

[29785] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2130 gene, herein designated VGAM GENE, on one or more VGAM2130 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[29786] It is yet further appreciated that a function of VGAM2130 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2130 include diagnosis, prevention and treatment of viral infection by Ateline herpesvirus 3. Specific functions, and accordingly utilities, of VGAM2130 correlate with, and may be deduced from, the identity of the host target genes which VGAM2130 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[29787] Nucleotide sequences of the VGAM2130 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2130 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2130 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2130 are further described hereinbelow with reference to Table 1.

[29788] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites

to VGAM2130 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[29789] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2131 (VGAM2131) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[29790] VGAM2131 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2131 was detected is described hereinabove with reference to Figs. 2-8.

[29791] VGAM2131 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ateline herpesvirus 3. VGAM2131 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[29792] VGAM2131 gene, herein designated VGAM GENE, encodes a VGAM2131 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2131 precursor RNA, herein designated VGAM PRECURSOR RNA, does not en-

code a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2131 precursor RNA is designated SEQ ID:2117, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2117 is located at position 9609 relative to the genome of Ateline herpesvirus 3.

[29793] VGAM2131 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2131 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[29794] An enzyme complex designated DICER COMPLEX, dices the VGAM2131 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2131 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2131 RNA is designated SEQ ID:4842, and is provided hereinbelow with reference to the sequence listing part.

[29795] VGAM2131 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2131 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2131 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[29796] VGAM2131 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2131 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2131 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3

such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2131 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2131 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[29797] The complementary binding of VGAM2131 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2131 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2131 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2131 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[29798] It is appreciated that VGAM2131 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2131 host target genes. The mRNA of each one of this plurality of VGAM2131 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2131 RNA, herein designated VGAM RNA, and which when bound by VGAM2131 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2131 host target proteins.

[29799] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2131 gene, herein designated VGAM GENE, on one or more VGAM2131 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[29800] It is yet further appreciated that a function of VGAM2131 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2131 include diagnosis, prevention and treatment of viral infection by Ateline herpesvirus 3. Specific functions, and accordingly utilities, of VGAM2131 correlate with, and may be deduced from, the identity of the host target genes which VGAM2131 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[29801] Nucleotide sequences of the VGAM2131 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2131 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2131 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2131 are further described hereinbelow with reference to Table 1.

[29802] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the

complementarity of each of these host target binding sites to VGAM2131 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[29803] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2132 (VGAM2132) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[29804] VGAM2132 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2132 was detected is described hereinabove with reference to Figs. 2-8.

[29805] VGAM2132 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ateline herpesvirus 3. VGAM2132 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[29806] VGAM2132 gene, herein designated VGAM GENE, encodes a VGAM2132 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2132 precursor RNA,

herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2132 precursor RNA is designated SEQ ID:2118, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2118 is located at position 17602 relative to the genome of Ateline herpesvirus 3.

[29807] VGAM2132 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2132 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[29808] An enzyme complex designated DICER COMPLEX, dices the VGAM2132 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2132 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 57%) nucleotide sequence of VGAM2132 RNA is designated SEQ ID:4843, and is provided hereinbelow with reference to the sequence listing part.

[29809] VGAM2132 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2132 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2132 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[29810] VGAM2132 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2132 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2132 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host

target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2132 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2132 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[29811] The complementary binding of VGAM2132 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2132 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2132 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2132 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[29812] It is appreciated that VGAM2132 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2132 host target genes. The mRNA of each one of this plurality of VGAM2132 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2132 RNA, herein designated VGAM RNA, and which when bound by VGAM2132 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2132 host target proteins.

[29813] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2132 gene, herein designated VGAM GENE, on one or more VGAM2132 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[29814] It is yet further appreciated that a function of VGAM2132 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2132 include diagnosis, prevention and treatment of viral infection by Ateline herpesvirus 3. Specific functions, and accordingly utilities, of VGAM2132 correlate with, and may be deduced from, the identity of the host target genes which VGAM2132 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[29815] Nucleotide sequences of the VGAM2132 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2132 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2132 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2132 are further described hereinbelow with reference to Table 1.

[29816] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2132 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[29817] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2133 (VGAM2133) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[29818] VGAM2133 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2133 was detected is described hereinabove with reference to Figs. 2-8.

[29819] VGAM2133 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ateline herpesvirus 3. VGAM2133 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[29820] VGAM2133 gene, herein designated VGAM GENE, encodes a VGAM2133 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and un-

like most ordinary genes, VGAM2133 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2133 precursor RNA is designated SEQ ID:2119, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2119 is located at position 4296 relative to the genome of Ateline herpesvirus 3.

[29821] VGAM2133 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2133 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[29822] An enzyme complex designated DICER COMPLEX, dices the VGAM2133 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2133 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2133 RNA is designated SEQ ID:4844, and is provided hereinbelow with reference to the sequence listing part.

[29823] VGAM2133 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2133 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2133 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[29824] VGAM2133 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2133 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2133 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed

sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2133 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2133 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[29825] The complementary binding of VGAM2133 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2133 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2133 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2133 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target

protein is therefore outlined by a broken line.

[29826] It is appreciated that VGAM2133 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2133 host target genes. The mRNA of each one of this plurality of VGAM2133 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2133 RNA, herein designated VGAM RNA, and which when bound by VGAM2133 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2133 host target proteins.

[29827] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2133 gene, herein designated VGAM GENE, on one or more VGAM2133 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[29828] It is yet further appreciated that a function of VGAM2133 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2133 include diagnosis, prevention and treatment of viral infection by Ateline herpesvirus 3. Specific functions, and accordingly utilities, of VGAM2133 correlate with, and may be deduced from, the identity of the host target genes which VGAM2133 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[29829] Nucleotide sequences of the VGAM2133 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2133 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2133 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2133 are further described hereinbelow with reference to Table 1.

[29830] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2133 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[29831] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2134 (VGAM2134) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[29832] VGAM2134 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2134 was detected is described hereinabove with reference to Figs. 2-8.

[29833] VGAM2134 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ateline herpesvirus 3. VGAM2134 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[29834] VGAM2134 gene, herein designated VGAM GENE, encodes a VGAM2134 precursor RNA, herein designated VGAM

PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2134 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2134 precursor RNA is designated SEQ ID:2120, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2120 is located at position 20245 relative to the genome of Ateline herpesvirus 3.

[29835] VGAM2134 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2134 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[29836] An enzyme complex designated DICER COMPLEX, dices the VGAM2134 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2134 RNA, herein designated VGAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 65%) nucleotide sequence of VGAM2134 RNA is designated SEQ ID:4845, and is provided hereinbelow with reference to the sequence listing part.

[29837] VGAM2134 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2134 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2134 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[29838] VGAM2134 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2134 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2134 RNA, herein designated

VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2134 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2134 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[29839] The complementary binding of VGAM2134 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2134 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2134 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2134 host target protein, herein desig-

nated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[29840] It is appreciated that VGAM2134 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2134 host target genes. The mRNA of each one of this plurality of VGAM2134 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2134 RNA, herein designated VGAM RNA, and which when bound by VGAM2134 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2134 host target proteins.

[29841] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2134 gene, herein designated VGAM GENE, on one or more VGAM2134 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[29842] It is yet further appreciated that a function of VGAM2134 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2134 include diagnosis, prevention and treatment of viral infection by Ateline herpesvirus 3. Specific functions, and accordingly utilities, of VGAM2134 correlate with, and may be deduced from, the identity of the host target genes which VGAM2134 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[29843] Nucleotide sequences of the VGAM2134 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2134 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2134 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2134 are further described hereinbelow with reference to Table 1.

[29844] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2134 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[29845] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2135 (VGAM2135) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[29846] VGAM2135 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2135 was detected is described hereinabove with reference to Figs. 2-8.

[29847] VGAM2135 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ateline herpesvirus 3. VGAM2135 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[29848] VGAM2135 gene, herein designated VGAM GENE, encodes

a VGAM2135 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2135 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2135 precursor RNA is designated SEQ ID:2121, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2121 is located at position 17990 relative to the genome of Ateline herpesvirus 3.

[29849] VGAM2135 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2135 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[29850] An enzyme complex designated DICER COMPLEX, dices the VGAM2135 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2135 RNA,

herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2135 RNA is designated SEQ ID:4846, and is provided hereinbelow with reference to the sequence listing part.

[29851] VGAM2135 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2135 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2135 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[29852] VGAM2135 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2135 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM2135 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2135 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2135 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[29853] The complementary binding of VGAM2135 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2135 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2135 host target RNA, herein designated VGAM HOST TARGET

RNA, into VGAM2135 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[29854] It is appreciated that VGAM2135 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2135 host target genes. The mRNA of each one of this plurality of VGAM2135 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2135 RNA, herein designated VGAM RNA, and which when bound by VGAM2135 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2135 host target proteins.

[29855] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2135 gene, herein designated VGAM GENE, on one or more VGAM2135 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[29856] It is yet further appreciated that a function of VGAM2135 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2135 include diagnosis, prevention and treatment of viral infection by Ateline herpesvirus 3. Specific functions, and accordingly utilities, of VGAM2135 correlate with, and may be deduced from, the identity of the host target genes which VGAM2135 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[29857] Nucleotide sequences of the VGAM2135 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2135 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2135 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2135 are further

described hereinbelow with reference to Table 1.

[29858] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2135 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[29859] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2136 (VGAM2136) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[29860] VGAM2136 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2136 was detected is described hereinabove with reference to Figs. 2-8.

[29861] VGAM2136 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia virus. VGAM2136 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[29862] VGAM2136 gene, herein designated VGAM GENE, encodes a VGAM2136 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2136 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2136 precursor RNA is designated SEQ ID:2122, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2122 is located at position 176642 relative to the genome of Ectromelia virus.

[29863] VGAM2136 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2136 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[29864] An enzyme complex designated DICER COMPLEX, dices the VGAM2136 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, into VGAM2136 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 92%) nucleotide sequence of VGAM2136 RNA is designated SEQ ID:4847, and is provided hereinbelow with reference to the sequence listing part.

[29865] VGAM2136 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2136 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2136 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[29866] VGAM2136 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2136 host target RNA, herein designated VGAM HOST TARGET RNA. This

complementary binding is due to the fact that the nucleotide sequence of VGAM2136 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2136 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2136 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[29867] The complementary binding of VGAM2136 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2136 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2136

host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2136 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[29868] It is appreciated that VGAM2136 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2136 host target genes. The mRNA of each one of this plurality of VGAM2136 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2136 RNA, herein designated VGAM RNA, and which when bound by VGAM2136 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2136 host target proteins.

[29869] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2136 gene, herein designated VGAM GENE, on one or more VGAM2136 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[29870] It is yet further appreciated that a function of VGAM2136 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2136 include diagnosis, prevention and treatment of viral infection by Ectromelia virus. Specific functions, and accordingly utilities, of VGAM2136 correlate with, and may be deduced from, the identity of the host target genes which VGAM2136 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[29871] Nucleotide sequences of the VGAM2136 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2136 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2136 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM2136 are further described hereinbelow with reference to Table 1.

[29872] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2136 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[29873] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2137 (VGAM2137) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[29874] VGAM2137 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2137 was detected is described hereinabove with reference to Figs. 2-8.

[29875] VGAM2137 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia virus. VGAM2137 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the

human genome.

[29876] VGAM2137 gene, herein designated VGAM GENE, encodes a VGAM2137 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2137 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2137 precursor RNA is designated SEQ ID:2123, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2123 is located at position 174026 relative to the genome of Ectromelia virus.

[29877] VGAM2137 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2137 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[29878] An enzyme complex designated DICER COMPLEX, dices

the VGAM2137 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2137 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2137 RNA is designated SEQ ID:4848, and is provided hereinbelow with reference to the sequence listing part.

[29879] VGAM2137 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2137 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2137 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[29880] VGAM2137 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2137 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2137 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2137 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2137 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[29881] The complementary binding of VGAM2137 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2137 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM2137 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2137 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[29882] It is appreciated that VGAM2137 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2137 host target genes. The mRNA of each one of this plurality of VGAM2137 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2137 RNA, herein designated VGAM RNA, and which when bound by VGAM2137 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2137 host target proteins.

[29883] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2137 gene, herein designated VGAM GENE, on one or more VGAM2137 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[29884] It is yet further appreciated that a function of VGAM2137 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2137 include diagnosis, prevention and treatment of viral infection by Ectromelia virus. Specific functions, and accordingly utilities, of VGAM2137 correlate with, and may be deduced from, the identity of the host target genes which VGAM2137 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[29885] Nucleotide sequences of the VGAM2137 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2137 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of

VGAM2137 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2137 are further described hereinbelow with reference to Table 1.

[29886] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2137 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[29887] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2138 (VGAM2138) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[29888] VGAM2138 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2138 was detected is described hereinabove with reference to Figs. 2-8.

[29889] VGAM2138 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia virus. VGAM2138 host target gene, herein designated VGAM

HOST TARGET GENE, is a human gene contained in the human genome.

[29890] VGAM2138 gene, herein designated VGAM GENE, encodes a VGAM2138 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2138 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2138 precursor RNA is designated SEQ ID:2124, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2124 is located at position 168635 relative to the genome of Ectromelia virus.

[29891] VGAM2138 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2138 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[29892] An enzyme complex designated DICER COMPLEX, dices the VGAM2138 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2138 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2138 RNA is designated SEQ ID:4849, and is provided hereinbelow with reference to the sequence listing part.

[29893] VGAM2138 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2138 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2138 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[29894] VGAM2138 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites

located in untranslated regions of VGAM2138 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2138 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2138 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2138 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[29895] The complementary binding of VGAM2138 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2138 host target RNA, herein designated VGAM

HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2138 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2138 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[29896] It is appreciated that VGAM2138 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2138 host target genes. The mRNA of each one of this plurality of VGAM2138 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2138 RNA, herein designated VGAM RNA, and which when bound by VGAM2138 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2138 host target proteins.

[29897] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2138 gene, herein designated VGAM GENE, on one or more VGAM2138 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove

with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[29898] It is yet further appreciated that a function of VGAM2138 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2138 include diagnosis, prevention and treatment of viral infection by Ectromelia virus. Specific functions, and accordingly utilities, of VGAM2138 correlate with, and may be deduced from, the identity of the host target genes which VGAM2138 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[29899] Nucleotide sequences of the VGAM2138 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2138 RNA, herein designated VGAM RNA, and

a schematic representation of the secondary folding of VGAM2138 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2138 are further described hereinbelow with reference to Table 1.

[29900] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2138 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[29901] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2139 (VGAM2139) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[29902] VGAM2139 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2139 was detected is described hereinabove with reference to Figs. 2-8.

[29903] VGAM2139 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia virus.

VGAM2139 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[29904] VGAM2139 gene, herein designated VGAM GENE, encodes a VGAM2139 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2139 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2139 precursor RNA is designated SEQ ID:2125, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2125 is located at position 179020 relative to the genome of Ectromelia virus.

[29905] VGAM2139 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2139 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[29906] An enzyme complex designated DICER COMPLEX, dices the VGAM2139 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2139 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2139 RNA is designated SEQ ID:4850, and is provided hereinbelow with reference to the sequence listing part.

[29907] VGAM2139 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2139 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2139 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[29908] VGAM2139 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM2139 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2139 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2139 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2139 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[29909] The complementary binding of VGAM2139 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM2139 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2139 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2139 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[29910] It is appreciated that VGAM2139 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2139 host target genes. The mRNA of each one of this plurality of VGAM2139 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2139 RNA, herein designated VGAM RNA, and which when bound by VGAM2139 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2139 host target proteins.

[29911] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2139 gene, herein designated VGAM GENE, on one or more VGAM2139 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[29912] It is yet further appreciated that a function of VGAM2139 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2139 include diagnosis, prevention and treatment of viral infection by Ectromelia virus. Specific functions, and accordingly utilities, of VGAM2139 correlate with, and may be deduced from, the identity of the host target genes which VGAM2139 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[29913] Nucleotide sequences of the VGAM2139 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

diced VGAM2139 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2139 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2139 are further described hereinbelow with reference to Table 1.

[29914] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2139 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[29915] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2140 (VGAM2140) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[29916] VGAM2140 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2140 was detected is described hereinabove with reference to Figs. 2-8.

[29917] VGAM2140 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of Ectromelia virus. VGAM2140 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[29918] VGAM2140 gene, herein designated VGAM GENE, encodes a VGAM2140 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2140 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2140 precursor RNA is designated SEQ ID:2126, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2126 is located at position 172080 relative to the genome of Ectromelia virus.

[29919] VGAM2140 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2140 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[29920] An enzyme complex designated DICER COMPLEX, dices the VGAM2140 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2140 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 70%) nucleotide sequence of VGAM2140 RNA is designated SEQ ID:4851, and is provided hereinbelow with reference to the sequence listing part.

[29921] VGAM2140 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2140 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2140 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[29922] VGAM2140 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2140 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2140 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2140 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2140 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[29923] The complementary binding of VGAM2140 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM2140 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2140 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2140 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[29924] It is appreciated that VGAM2140 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2140 host target genes. The mRNA of each one of this plurality of VGAM2140 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2140 RNA, herein designated VGAM RNA, and which when bound by VGAM2140 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2140 host target proteins.

[29925] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2140 gene, herein designated VGAM GENE, on one or more VGAM2140 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[29926] It is yet further appreciated that a function of VGAM2140 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2140 include diagnosis, prevention and treatment of viral infection by Ectromelia virus. Specific functions, and accordingly utilities, of VGAM2140 correlate with, and may be deduced from, the identity of the host target genes which VGAM2140 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[29927] Nucleotide sequences of the VGAM2140 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the diced VGAM2140 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2140 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2140 are further described hereinbelow with reference to Table 1.

[29928] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2140 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[29929] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2141 (VGAM2141) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[29930] VGAM2141 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2141 was detected is described hereinabove with reference to Figs. 2-8.

[29931] VGAM2141 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia virus. VGAM2141 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[29932] VGAM2141 gene, herein designated VGAM GENE, encodes a VGAM2141 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2141 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2141 precursor RNA is designated SEQ ID:2127, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2127 is located at position 169712 relative to the genome of Ectromelia virus.

[29933] VGAM2141 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2141 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[29934] An enzyme complex designated DICER COMPLEX, dices the VGAM2141 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2141 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2141 RNA is designated SEQ ID:4852, and is provided hereinbelow with reference to the sequence listing part.

[29935] VGAM2141 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2141 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2141 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN COD-

ING and 3UTR respectively.

[29936] VGAM2141 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2141 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2141 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2141 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2141 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[29937] The complementary binding of VGAM2141 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2141 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2141 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2141 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[29938] It is appreciated that VGAM2141 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2141 host target genes. The mRNA of each one of this plurality of VGAM2141 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2141 RNA, herein designated VGAM RNA, and which when bound by VGAM2141 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2141 host target proteins.

[29939] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2141 gene, herein designated VGAM GENE, on one

or more VGAM2141 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[29940] It is yet further appreciated that a function of VGAM2141 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2141 include diagnosis, prevention and treatment of viral infection by Ectromelia virus. Specific functions, and accordingly utilities, of VGAM2141 correlate with, and may be deduced from, the identity of the host target genes which VGAM2141 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[29941] Nucleotide sequences of the VGAM2141 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2141 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2141 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2141 are further described hereinbelow with reference to Table 1.

[29942] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2141 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[29943] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2142 (VGAM2142) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[29944] VGAM2142 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2142 was detected is de-

scribed hereinabove with reference to Figs. 2-8.

[29945] VGAM2142 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia virus. VGAM2142 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[29946] VGAM2142 gene, herein designated VGAM GENE, encodes a VGAM2142 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2142 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2142 precursor RNA is designated SEQ ID:2128, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2128 is located at position 168447 relative to the genome of Ectromelia virus.

[29947] VGAM2142 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2142 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[29948] An enzyme complex designated DICER COMPLEX, dices the VGAM2142 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2142 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2142 RNA is designated SEQ ID:4853, and is provided hereinbelow with reference to the sequence listing part.

[29949] VGAM2142 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2142 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2142 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and

a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[29950] VGAM2142 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2142 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2142 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2142 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2142 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both

3UTR and 5UTR regions.

[29951] The complementary binding of VGAM2142 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2142 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2142 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2142 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[29952] It is appreciated that VGAM2142 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2142 host target genes. The mRNA of each one of this plurality of VGAM2142 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2142 RNA, herein designated VGAM RNA, and which when bound by VGAM2142 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2142 host target proteins.

[29953] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM2142 gene, herein designated VGAM GENE, on one or more VGAM2142 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[29954] It is yet further appreciated that a function of VGAM2142 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2142 include diagnosis, prevention and treatment of viral infection by Ectromelia virus. Specific functions, and accordingly utilities, of VGAM2142 correlate with, and may be deduced from, the identity of the host target genes which VGAM2142 binds and inhibits, and the function of these host target genes, as elaborated

hereinbelow.

[29955] Nucleotide sequences of the VGAM2142 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2142 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2142 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2142 are further described hereinbelow with reference to Table 1.

[29956] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2142 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[29957] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2143 (VGAM2143) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[29958] VGAM2143 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene.

The method by which VGAM2143 was detected is described hereinabove with reference to Figs. 2-8.

[29959] VGAM2143 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia virus. VGAM2143 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[29960] VGAM2143 gene, herein designated VGAM GENE, encodes a VGAM2143 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2143 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2143 precursor RNA is designated SEQ ID:2129, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2129 is located at position 165143 relative to the genome of Ectromelia virus.

[29961] VGAM2143 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2143 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[29962] An enzyme complex designated DICER COMPLEX, dices the VGAM2143 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2143 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2143 RNA is designated SEQ ID:4854, and is provided hereinbelow with reference to the sequence listing part.

[29963] VGAM2143 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2143 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2143 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding

gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[29964] VGAM2143 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2143 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2143 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2143 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2143 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be lo-

cated in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[29965] The complementary binding of VGAM2143 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2143 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2143 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2143 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[29966] It is appreciated that VGAM2143 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2143 host target genes. The mRNA of each one of this plurality of VGAM2143 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2143 RNA, herein designated VGAM RNA, and which when bound by VGAM2143 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2143 host target proteins.

[29967] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM2143 gene, herein designated VGAM GENE, on one or more VGAM2143 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[29968] It is yet further appreciated that a function of VGAM2143 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2143 include diagnosis, prevention and treatment of viral infection by Ectromelia virus. Specific functions, and accordingly utilities, of VGAM2143 correlate with, and may be deduced from, the identity of the host target genes which VGAM2143 binds and inhibits,

and the function of these host target genes, as elaborated hereinbelow.

[29969] Nucleotide sequences of the VGAM2143 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2143 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2143 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2143 are further described hereinbelow with reference to Table 1.

[29970] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2143 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[29971] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2144 (VGAM2144) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[29972] VGAM2144 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2144 was detected is described hereinabove with reference to Figs. 2-8.

[29973] VGAM2144 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia virus. VGAM2144 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[29974] VGAM2144 gene, herein designated VGAM GENE, encodes a VGAM2144 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2144 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2144 precursor RNA is designated SEQ ID:2130, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2130 is located at position 168263 relative to the genome of Ectromelia virus.

[29975] VGAM2144 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2144 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[29976] An enzyme complex designated DICER COMPLEX, dices the VGAM2144 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2144 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2144 RNA is designated SEQ ID:4855, and is provided hereinbelow with reference to the sequence listing part.

[29977] VGAM2144 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2144 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2144 host target RNA, herein designated VGAM HOST TARGET RNA, comprises

three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[29978] VGAM2144 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2144 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2144 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2144 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2144 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an

example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[29979] The complementary binding of VGAM2144 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2144 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2144 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2144 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[29980] It is appreciated that VGAM2144 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2144 host target genes. The mRNA of each one of this plurality of VGAM2144 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2144 RNA, herein designated VGAM RNA, and which when bound by VGAM2144 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2144 host target proteins.

[29981] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2144 gene, herein designated VGAM GENE, on one or more VGAM2144 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[29982] It is yet further appreciated that a function of VGAM2144 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2144 include diagnosis, prevention and treatment of viral infection by Ectromelia virus. Specific functions, and accordingly utilities, of VGAM2144 correlate with, and may be deduced from, the identity of the

host target genes which VGAM2144 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[29983] Nucleotide sequences of the VGAM2144 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2144 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2144 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2144 are further described hereinbelow with reference to Table 1.

[29984] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2144 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[29985] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2145 (VGAM2145) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[29986] VGAM2145 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2145 was detected is described hereinabove with reference to Figs. 2-8.

[29987] VGAM2145 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia virus. VGAM2145 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[29988] VGAM2145 gene, herein designated VGAM GENE, encodes a VGAM2145 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2145 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2145 precursor RNA is designated SEQ ID:2131, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2131 is located at position 182220 relative to the genome of Ectromelia virus.

[29989] VGAM2145 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2145 folded precursor RNA, herein designated VGAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[29990] An enzyme complex designated DICER COMPLEX, dices the VGAM2145 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2145 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2145 RNA is designated SEQ ID:4856, and is provided hereinbelow with reference to the sequence listing part.

[29991] VGAM2145 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2145 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2145 host target RNA,

herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[29992] VGAM2145 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2145 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2145 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2145 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2145 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host tar-

get binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[29993] The complementary binding of VGAM2145 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2145 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2145 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2145 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[29994] It is appreciated that VGAM2145 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2145 host target genes. The mRNA of each one of this plurality of VGAM2145 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2145 RNA, herein designated VGAM RNA, and which when bound by VGAM2145 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2145 host target proteins.

[29995] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2145 gene, herein designated VGAM GENE, on one or more VGAM2145 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[29996] It is yet further appreciated that a function of VGAM2145 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2145 include diagnosis, prevention and treatment of viral infection by Ectromelia virus. Specific functions, and accordingly utilities, of VGAM2145 corre-

late with, and may be deduced from, the identity of the host target genes which VGAM2145 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[29997] Nucleotide sequences of the VGAM2145 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2145 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2145 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2145 are further described hereinbelow with reference to Table 1.

[29998] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2145 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[29999] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2146 (VGAM2146) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the

art.

[30000] VGAM2146 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2146 was detected is described hereinabove with reference to Figs. 2-8.

[30001] VGAM2146 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rana tigrina ranavirus. VGAM2146 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[30002] VGAM2146 gene, herein designated VGAM GENE, encodes a VGAM2146 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2146 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2146 precursor RNA is designated SEQ ID:2132, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2132 is located at position 55138 relative to the genome of Rana tigrina ranavirus.

[30003] VGAM2146 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2146 folded

precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30004] An enzyme complex designated DICER COMPLEX, dices the VGAM2146 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2146 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2146 RNA is designated SEQ ID:4857, and is provided hereinbelow with reference to the sequence listing part.

[30005] VGAM2146 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2146 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM2146 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30006] VGAM2146 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2146 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2146 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2146 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2146 host target RNA, herein designated VGAM HOST TARGET RNA.

It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30007] The complementary binding of VGAM2146 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2146 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2146 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2146 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[30008] It is appreciated that VGAM2146 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2146 host target genes. The mRNA of each one of this plurality of VGAM2146 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2146 RNA, herein designated VGAM RNA, and which when bound by VGAM2146 RNA, herein designated VGAM RNA, causes inhibition of translation of

respective one or more VGAM2146 host target proteins.

[30009] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2146 gene, herein designated VGAM GENE, on one or more VGAM2146 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30010] It is yet further appreciated that a function of VGAM2146 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2146 include diagnosis, prevention and treatment of viral infection by Rana tigrina ranavirus. Spe-

cific functions, and accordingly utilities, of VGAM2146 correlate with, and may be deduced from, the identity of the host target genes which VGAM2146 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[30011] Nucleotide sequences of the VGAM2146 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2146 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2146 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2146 are further described hereinbelow with reference to Table 1.

[30012] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2146 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[30013] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2147 (VGAM2147) viral gene, which modulates expression of respective host target genes thereof, the func-

tion and utility of which host target genes is known in the art.

[30014] VGAM2147 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2147 was detected is described hereinabove with reference to Figs. 2-8.

[30015] VGAM2147 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rana tigrina ranavirus. VGAM2147 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[30016] VGAM2147 gene, herein designated VGAM GENE, encodes a VGAM2147 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2147 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2147 precursor RNA is designated SEQ ID:2133, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2133 is located at position 47097 relative to the genome of Rana tigrina ranavirus.

[30017] VGAM2147 precursor RNA, herein designated VGAM PRE-

CURSOR RNA, folds onto itself, forming VGAM2147 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30018] An enzyme complex designated DICER COMPLEX, dices the VGAM2147 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2147 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 49%) nucleotide sequence of VGAM2147 RNA is designated SEQ ID:4858, and is provided hereinbelow with reference to the sequence listing part.

[30019] VGAM2147 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM2147 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2147 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30020] VGAM2147 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2147 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2147 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2147 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2147 host

target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30021] The complementary binding of VGAM2147 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2147 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2147 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2147 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[30022] It is appreciated that VGAM2147 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2147 host target genes. The mRNA of each one of this plurality of VGAM2147 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2147 RNA, herein designated VGAM RNA, and which when bound by VGAM2147 RNA, herein

designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2147 host target proteins.

[30023] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2147 gene, herein designated VGAM GENE, on one or more VGAM2147 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30024] It is yet further appreciated that a function of VGAM2147 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2147 include diagnosis, prevention and

treatment of viral infection by Rana tigrina ranavirus. Specific functions, and accordingly utilities, of VGAM2147 correlate with, and may be deduced from, the identity of the host target genes which VGAM2147 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[30025] Nucleotide sequences of the VGAM2147 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2147 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2147 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2147 are further described hereinbelow with reference to Table 1.

[30026] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2147 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[30027] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2148 (VGAM2148) viral gene, which modulates ex-

pression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[30028] VGAM2148 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2148 was detected is described hereinabove with reference to Figs. 2-8.

[30029] VGAM2148 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rana tigrina ranavirus. VGAM2148 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[30030] VGAM2148 gene, herein designated VGAM GENE, encodes a VGAM2148 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2148 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2148 precursor RNA is designated SEQ ID:2134, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2134 is located at position 62911 relative to the genome of Rana tigrina ranavirus.

[30031] VGAM2148 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2148 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30032] An enzyme complex designated DICER COMPLEX, dices the VGAM2148 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2148 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 73%) nucleotide sequence of VGAM2148 RNA is designated SEQ ID:4859, and is provided hereinbelow with reference to the sequence listing part.

[30033] VGAM2148 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2148 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2148 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30034] VGAM2148 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2148 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2148 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2148 RNA, herein designated VGAM RNA, may have a different number of host target

binding sites in untranslated regions of a VGAM2148 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30035] The complementary binding of VGAM2148 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2148 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2148 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2148 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[30036] It is appreciated that VGAM2148 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2148 host target genes. The mRNA of each one of this plurality of VGAM2148 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2148 RNA, herein designated VGAM

RNA, and which when bound by VGAM2148 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2148 host target proteins.

[30037] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2148 gene, herein designated VGAM GENE, on one or more VGAM2148 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30038] It is yet further appreciated that a function of VGAM2148 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM2148 include diagnosis, prevention and treatment of viral infection by Rana tigrina ranavirus. Specific functions, and accordingly utilities, of VGAM2148 correlate with, and may be deduced from, the identity of the host target genes which VGAM2148 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[30039] Nucleotide sequences of the VGAM2148 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2148 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2148 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2148 are further described hereinbelow with reference to Table 1.

[30040] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2148 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[30041] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Mes-

senger 2149 (VGAM2149) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[30042] VGAM2149 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2149 was detected is described hereinabove with reference to Figs. 2-8.

[30043] VGAM2149 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rana tigrina ranavirus. VGAM2149 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[30044] VGAM2149 gene, herein designated VGAM GENE, encodes a VGAM2149 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2149 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2149 precursor RNA is designated SEQ ID:2135, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2135 is located at position

50593 relative to the genome of Rana tigrina ranavirus.

[30045] VGAM2149 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2149 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30046] An enzyme complex designated DICER COMPLEX, dices the VGAM2149 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2149 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2149 RNA is designated SEQ ID:4860, and is provided hereinbelow with reference to the sequence listing part.

[30047] VGAM2149 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2149 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2149 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30048] VGAM2149 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2149 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2149 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2149 RNA, herein designated

VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2149 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30049] The complementary binding of VGAM2149 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2149 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2149 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2149 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[30050] It is appreciated that VGAM2149 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2149 host target genes. The mRNA of each one of this plurality of VGAM2149 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM2149 RNA, herein designated VGAM RNA, and which when bound by VGAM2149 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2149 host target proteins.

[30051] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2149 gene, herein designated VGAM GENE, on one or more VGAM2149 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30052] It is yet further appreciated that a function of VGAM2149 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2149 include diagnosis, prevention and treatment of viral infection by Rana tigrina ranavirus. Specific functions, and accordingly utilities, of VGAM2149 correlate with, and may be deduced from, the identity of the host target genes which VGAM2149 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[30053] Nucleotide sequences of the VGAM2149 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2149 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2149 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2149 are further described hereinbelow with reference to Table 1.

[30054] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2149 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[30055] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present

invention, referred to here as Viral Genomic Address Messenger 2150 (VGAM2150) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[30056] VGAM2150 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2150 was detected is described hereinabove with reference to Figs. 2-8.

[30057] VGAM2150 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rana tigrina ranavirus. VGAM2150 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[30058] VGAM2150 gene, herein designated VGAM GENE, encodes a VGAM2150 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2150 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2150 precursor RNA is designated SEQ ID:2136, and is provided hereinbelow with reference to the sequence listing part. Nu-

cleotide sequence SEQ ID:2136 is located at position 52091 relative to the genome of Rana tigrina ranavirus.

[30059] VGAM2150 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2150 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30060] An enzyme complex designated DICER COMPLEX, dices the VGAM2150 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2150 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 52%) nucleotide sequence of VGAM2150 RNA is designated SEQ ID:4861, and is provided hereinbelow with reference to the sequence

listing part.

[30061] VGAM2150 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2150 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2150 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30062] VGAM2150 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2150 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2150 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not

meant to be limiting VGAM2150 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2150 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30063] The complementary binding of VGAM2150 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2150 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2150 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2150 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[30064] It is appreciated that VGAM2150 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2150 host target genes. The mRNA of each one of this plurality of VGAM2150 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2150 RNA, herein designated VGAM RNA, and which when bound by VGAM2150 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2150 host target proteins.

[30065] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2150 gene, herein designated VGAM GENE, on one or more VGAM2150 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30066] It is yet further appreciated that a function of VGAM2150

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2150 include diagnosis, prevention and treatment of viral infection by Rana tigrina ranavirus. Specific functions, and accordingly utilities, of VGAM2150 correlate with, and may be deduced from, the identity of the host target genes which VGAM2150 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[30067] Nucleotide sequences of the VGAM2150 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2150 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2150 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2150 are further described hereinbelow with reference to Table 1.

[30068] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2150 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[30069] Fig. 1 further provides a conceptual description of another

novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2151 (VGAM2151) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[30070] VGAM2151 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2151 was detected is described hereinabove with reference to Figs. 2-8.

[30071] VGAM2151 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rana tigrina ranavirus. VGAM2151 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[30072] VGAM2151 gene, herein designated VGAM GENE, encodes a VGAM2151 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2151 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2151 precursor RNA is designated SEQ ID:2137, and is provided here-

inbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2137 is located at position 54437 relative to the genome of Rana tigrina ranavirus.

[30073] VGAM2151 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2151 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30074] An enzyme complex designated DICER COMPLEX, dices the VGAM2151 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2151 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2151 RNA is designated SEQ ID:4862, and

is provided hereinbelow with reference to the sequence listing part.

[30075] VGAM2151 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2151 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2151 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30076] VGAM2151 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2151 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites

shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2151 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2151 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30077] The complementary binding of VGAM2151 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2151 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2151 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2151 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[30078] It is appreciated that VGAM2151 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2151 host target genes. The mRNA of each one of this plurality of VGAM2151 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2151 RNA, herein designated VGAM RNA, and which when bound by VGAM2151 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2151 host target proteins.

[30079] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2151 gene, herein designated VGAM GENE, on one or more VGAM2151 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30080] It is yet further appreciated that a function of VGAM2151 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of viral infection by Rana tigrina ranavirus. Specific functions, and accordingly utilities, of VGAM2151 correlate with, and may be deduced from, the identity of the host target genes which VGAM2151 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[30081] Nucleotide sequences of the VGAM2151 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2151 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2151 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2151 are further described hereinbelow with reference to Table 1.

[30082] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2151 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[30083] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2152 (VGAM2152) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[30084] VGAM2152 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2152 was detected is described hereinabove with reference to Figs. 2-8.

[30085] VGAM2152 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rana tigrina ranavirus. VGAM2152 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[30086] VGAM2152 gene, herein designated VGAM GENE, encodes a VGAM2152 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2152 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2152 precur-

sor RNA is designated SEQ ID:2138, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2138 is located at position 44423 relative to the genome of Rana tigrina ranavirus.

[30087] VGAM2152 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2152 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30088] An enzyme complex designated DICER COMPLEX, dices the VGAM2152 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2152 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide se-

quence of VGAM2152 RNA is designated SEQ ID:4863, and is provided hereinbelow with reference to the sequence listing part.

[30089] VGAM2152 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2152 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2152 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30090] VGAM2152 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2152 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2152 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is ap-

preciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2152 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2152 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30091] The complementary binding of VGAM2152 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2152 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2152 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2152 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[30092] It is appreciated that VGAM2152 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2152 host target genes. The mRNA of

each one of this plurality of VGAM2152 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2152 RNA, herein designated VGAM RNA, and which when bound by VGAM2152 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2152 host target proteins.

[30093] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2152 gene, herein designated VGAM GENE, on one or more VGAM2152 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science

294,779 (2001)).

[30094] It is yet further appreciated that a function of VGAM2152 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2152 include diagnosis, prevention and treatment of viral infection by Rana tigrina ranavirus. Specific functions, and accordingly utilities, of VGAM2152 correlate with, and may be deduced from, the identity of the host target genes which VGAM2152 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[30095] Nucleotide sequences of the VGAM2152 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2152 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2152 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2152 are further described hereinbelow with reference to Table 1.

[30096] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2152 RNA, herein designated VGAM RNA, are de-

scribed hereinbelow with reference to Table 2.

[30097] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2153 (VGAM2153) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[30098] VGAM2153 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2153 was detected is described hereinabove with reference to Figs. 2-8.

[30099] VGAM2153 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rana tigrina ranavirus. VGAM2153 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[30100] VGAM2153 gene, herein designated VGAM GENE, encodes a VGAM2153 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2153 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly

similar to the nucleotide sequence of VGAM2153 precursor RNA is designated SEQ ID:2139, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2139 is located at position 59440 relative to the genome of Rana tigrina ranavirus.

[30101] VGAM2153 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2153 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30102] An enzyme complex designated DICER COMPLEX, dices the VGAM2153 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2153 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2153 RNA is designated SEQ ID:4864, and is provided hereinbelow with reference to the sequence listing part.

[30103] VGAM2153 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2153 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2153 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30104] VGAM2153 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2153 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2153 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I,

BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2153 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2153 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30105] The complementary binding of VGAM2153 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2153 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2153 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2153 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[30106] It is appreciated that VGAM2153 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM2153 host target genes. The mRNA of each one of this plurality of VGAM2153 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2153 RNA, herein designated VGAM RNA, and which when bound by VGAM2153 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2153 host target proteins.

[30107] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2153 gene, herein designated VGAM GENE, on one or more VGAM2153 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30108] It is yet further appreciated that a function of VGAM2153 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2153 include diagnosis, prevention and treatment of viral infection by Rana tigrina ranavirus. Specific functions, and accordingly utilities, of VGAM2153 correlate with, and may be deduced from, the identity of the host target genes which VGAM2153 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[30109] Nucleotide sequences of the VGAM2153 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2153 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2153 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2153 are further described hereinbelow with reference to Table 1.

[30110] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites

to VGAM2153 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[30111] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2154 (VGAM2154) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[30112] VGAM2154 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2154 was detected is described hereinabove with reference to Figs. 2-8.

[30113] VGAM2154 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rana tigrina ranavirus. VGAM2154 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[30114] VGAM2154 gene, herein designated VGAM GENE, encodes a VGAM2154 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2154 precursor RNA, herein designated VGAM PRECURSOR RNA, does not en-

code a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2154 precursor RNA is designated SEQ ID:2140, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2140 is located at position 48817 relative to the genome of Rana tigrina ranavirus.

[30115] VGAM2154 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2154 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30116] An enzyme complex designated DICER COMPLEX, dices the VGAM2154 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2154 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 70%) nucleotide sequence of VGAM2154 RNA is designated SEQ ID:4865, and is provided hereinbelow with reference to the sequence listing part.

[30117] VGAM2154 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2154 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2154 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30118] VGAM2154 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2154 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2154 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3

such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2154 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2154 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30119] The complementary binding of VGAM2154 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2154 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2154 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2154 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[30120] It is appreciated that VGAM2154 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2154 host target genes. The mRNA of each one of this plurality of VGAM2154 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2154 RNA, herein designated VGAM RNA, and which when bound by VGAM2154 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2154 host target proteins.

[30121] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2154 gene, herein designated VGAM GENE, on one or more VGAM2154 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30122] It is yet further appreciated that a function of VGAM2154 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2154 include diagnosis, prevention and treatment of viral infection by Rana tigrina ranavirus. Specific functions, and accordingly utilities, of VGAM2154 correlate with, and may be deduced from, the identity of the host target genes which VGAM2154 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[30123] Nucleotide sequences of the VGAM2154 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2154 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2154 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2154 are further described hereinbelow with reference to Table 1.

[30124] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the

complementarity of each of these host target binding sites to VGAM2154 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[30125] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2155 (VGAM2155) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[30126] VGAM2155 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2155 was detected is described hereinabove with reference to Figs. 2-8.

[30127] VGAM2155 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Monkeypox virus. VGAM2155 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[30128] VGAM2155 gene, herein designated VGAM GENE, encodes a VGAM2155 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2155 precursor RNA,

herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2155 precursor RNA is designated SEQ ID:2141, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2141 is located at position 168488 relative to the genome of Monkeypox virus.

[30129] VGAM2155 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2155 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30130] An enzyme complex designated DICER COMPLEX, dices the VGAM2155 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2155 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2155 RNA is designated SEQ ID:4866, and is provided hereinbelow with reference to the sequence listing part.

[30131] VGAM2155 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2155 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2155 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30132] VGAM2155 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2155 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2155 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host

target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2155 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2155 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30133] The complementary binding of VGAM2155 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2155 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2155 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2155 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[30134] It is appreciated that VGAM2155 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2155 host target genes. The mRNA of each one of this plurality of VGAM2155 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2155 RNA, herein designated VGAM RNA, and which when bound by VGAM2155 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2155 host target proteins.

[30135] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2155 gene, herein designated VGAM GENE, on one or more VGAM2155 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30136] It is yet further appreciated that a function of VGAM2155 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2155 include diagnosis, prevention and treatment of viral infection by Monkeypox virus. Specific functions, and accordingly utilities, of VGAM2155 correlate with, and may be deduced from, the identity of the host target genes which VGAM2155 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[30137] Nucleotide sequences of the VGAM2155 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2155 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2155 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2155 are further described hereinbelow with reference to Table 1.

[30138] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2155 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[30139] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2156 (VGAM2156) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[30140] VGAM2156 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2156 was detected is described hereinabove with reference to Figs. 2-8.

[30141] VGAM2156 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Monkeypox virus. VGAM2156 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[30142] VGAM2156 gene, herein designated VGAM GENE, encodes a VGAM2156 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and un-

like most ordinary genes, VGAM2156 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2156 precursor RNA is designated SEQ ID:2142, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2142 is located at position 170622 relative to the genome of Monkeypox virus.

[30143] VGAM2156 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2156 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30144] An enzyme complex designated DICER COMPLEX, dices the VGAM2156 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2156 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 59%) nucleotide sequence of VGAM2156 RNA is designated SEQ ID:4867, and is provided hereinbelow with reference to the sequence listing part.

[30145] VGAM2156 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2156 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2156 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30146] VGAM2156 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2156 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2156 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed

sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2156 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2156 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30147] The complementary binding of VGAM2156 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2156 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2156 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2156 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target

protein is therefore outlined by a broken line.

[30148] It is appreciated that VGAM2156 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2156 host target genes. The mRNA of each one of this plurality of VGAM2156 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2156 RNA, herein designated VGAM RNA, and which when bound by VGAM2156 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2156 host target proteins.

[30149] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2156 gene, herein designated VGAM GENE, on one or more VGAM2156 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30150] It is yet further appreciated that a function of VGAM2156 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2156 include diagnosis, prevention and treatment of viral infection by Monkeypox virus. Specific functions, and accordingly utilities, of VGAM2156 correlate with, and may be deduced from, the identity of the host target genes which VGAM2156 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[30151] Nucleotide sequences of the VGAM2156 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2156 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2156 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2156 are further described hereinbelow with reference to Table 1.

[30152] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2156 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[30153] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2157 (VGAM2157) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[30154] VGAM2157 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2157 was detected is described hereinabove with reference to Figs. 2-8.

[30155] VGAM2157 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Monkeypox virus. VGAM2157 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[30156] VGAM2157 gene, herein designated VGAM GENE, encodes a VGAM2157 precursor RNA, herein designated VGAM

PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2157 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2157 precursor RNA is designated SEQ ID:2143, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2143 is located at position 162621 relative to the genome of Monkeypox virus.

[30157] VGAM2157 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2157 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30158] An enzyme complex designated DICER COMPLEX, dices the VGAM2157 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2157 RNA, herein designated VGAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2157 RNA is designated SEQ ID:4868, and is provided hereinbelow with reference to the sequence listing part.

[30159] VGAM2157 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2157 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2157 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30160] VGAM2157 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2157 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2157 RNA, herein designated

VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2157 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2157 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30161] The complementary binding of VGAM2157 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2157 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2157 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2157 host target protein, herein desig-

nated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[30162] It is appreciated that VGAM2157 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2157 host target genes. The mRNA of each one of this plurality of VGAM2157 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2157 RNA, herein designated VGAM RNA, and which when bound by VGAM2157 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2157 host target proteins.

[30163] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2157 gene, herein designated VGAM GENE, on one or more VGAM2157 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30164] It is yet further appreciated that a function of VGAM2157 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2157 include diagnosis, prevention and treatment of viral infection by Monkeypox virus. Specific functions, and accordingly utilities, of VGAM2157 correlate with, and may be deduced from, the identity of the host target genes which VGAM2157 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[30165] Nucleotide sequences of the VGAM2157 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2157 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2157 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2157 are further described hereinbelow with reference to Table 1.

[30166] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2157 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[30167] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2158 (VGAM2158) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[30168] VGAM2158 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2158 was detected is described hereinabove with reference to Figs. 2-8.

[30169] VGAM2158 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Monkeypox virus. VGAM2158 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[30170] VGAM2158 gene, herein designated VGAM GENE, encodes

a VGAM2158 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2158 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2158 precursor RNA is designated SEQ ID:2144, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2144 is located at position 165985 relative to the genome of Monkeypox virus.

[30171] VGAM2158 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2158 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30172] An enzyme complex designated DICER COMPLEX, dices the VGAM2158 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2158 RNA,

herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2158 RNA is designated SEQ ID:4869, and is provided hereinbelow with reference to the sequence listing part.

[30173] VGAM2158 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2158 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2158 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30174] VGAM2158 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2158 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM2158 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2158 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2158 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30175] The complementary binding of VGAM2158 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2158 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2158 host target RNA, herein designated VGAM HOST TARGET

RNA, into VGAM2158 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[30176] It is appreciated that VGAM2158 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2158 host target genes. The mRNA of each one of this plurality of VGAM2158 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2158 RNA, herein designated VGAM RNA, and which when bound by VGAM2158 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2158 host target proteins.

[30177] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2158 gene, herein designated VGAM GENE, on one or more VGAM2158 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30178] It is yet further appreciated that a function of VGAM2158 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2158 include diagnosis, prevention and treatment of viral infection by Monkeypox virus. Specific functions, and accordingly utilities, of VGAM2158 correlate with, and may be deduced from, the identity of the host target genes which VGAM2158 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[30179] Nucleotide sequences of the VGAM2158 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2158 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2158 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2158 are further

described hereinbelow with reference to Table 1.

[30180] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2158 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[30181] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2159 (VGAM2159) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[30182] VGAM2159 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2159 was detected is described hereinabove with reference to Figs. 2-8.

[30183] VGAM2159 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Monkeypox virus. VGAM2159 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[30184] VGAM2159 gene, herein designated VGAM GENE, encodes a VGAM2159 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2159 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2159 precursor RNA is designated SEQ ID:2145, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2145 is located at position 155355 relative to the genome of Monkeypox virus.

[30185] VGAM2159 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2159 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30186] An enzyme complex designated DICER COMPLEX, dices the VGAM2159 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, into VGAM2159 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2159 RNA is designated SEQ ID:4870, and is provided hereinbelow with reference to the sequence listing part.

[30187] VGAM2159 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2159 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2159 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30188] VGAM2159 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2159 host target RNA, herein designated VGAM HOST TARGET RNA. This

complementary binding is due to the fact that the nucleotide sequence of VGAM2159 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2159 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2159 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30189] The complementary binding of VGAM2159 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2159 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2159

host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2159 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[30190] It is appreciated that VGAM2159 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2159 host target genes. The mRNA of each one of this plurality of VGAM2159 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2159 RNA, herein designated VGAM RNA, and which when bound by VGAM2159 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2159 host target proteins.

[30191] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2159 gene, herein designated VGAM GENE, on one or more VGAM2159 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30192] It is yet further appreciated that a function of VGAM2159 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2159 include diagnosis, prevention and treatment of viral infection by Monkeypox virus. Specific functions, and accordingly utilities, of VGAM2159 correlate with, and may be deduced from, the identity of the host target genes which VGAM2159 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[30193] Nucleotide sequences of the VGAM2159 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2159 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2159 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM2159 are further described hereinbelow with reference to Table 1.

[30194] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2159 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[30195] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2160 (VGAM2160) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[30196] VGAM2160 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2160 was detected is described hereinabove with reference to Figs. 2-8.

[30197] VGAM2160 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Monkeypox virus. VGAM2160 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the

human genome.

[30198] VGAM2160 gene, herein designated VGAM GENE, encodes a VGAM2160 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2160 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2160 precursor RNA is designated SEQ ID:2146, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2146 is located at position 168205 relative to the genome of Monkeypox virus.

[30199] VGAM2160 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2160 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30200] An enzyme complex designated DICER COMPLEX, dices

the VGAM2160 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2160 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 49%) nucleotide sequence of VGAM2160 RNA is designated SEQ ID:4871, and is provided hereinbelow with reference to the sequence listing part.

[30201] VGAM2160 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2160 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2160 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30202] VGAM2160 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2160 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2160 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2160 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2160 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30203] The complementary binding of VGAM2160 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2160 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM2160 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2160 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[30204] It is appreciated that VGAM2160 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2160 host target genes. The mRNA of each one of this plurality of VGAM2160 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2160 RNA, herein designated VGAM RNA, and which when bound by VGAM2160 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2160 host target proteins.

[30205] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2160 gene, herein designated VGAM GENE, on one or more VGAM2160 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30206] It is yet further appreciated that a function of VGAM2160 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2160 include diagnosis, prevention and treatment of viral infection by Monkeypox virus. Specific functions, and accordingly utilities, of VGAM2160 correlate with, and may be deduced from, the identity of the host target genes which VGAM2160 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[30207] Nucleotide sequences of the VGAM2160 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2160 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of

VGAM2160 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2160 are further described hereinbelow with reference to Table 1.

[30208] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2160 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[30209] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2161 (VGAM2161) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[30210] VGAM2161 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2161 was detected is described hereinabove with reference to Figs. 2-8.

[30211] VGAM2161 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Camelpox virus. VGAM2161 host target gene, herein designated VGAM

HOST TARGET GENE, is a human gene contained in the human genome.

[30212] VGAM2161 gene, herein designated VGAM GENE, encodes a VGAM2161 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2161 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2161 precursor RNA is designated SEQ ID:2147, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2147 is located at position 194827 relative to the genome of Camelpox virus.

[30213] VGAM2161 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2161 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30214] An enzyme complex designated DICER COMPLEX, dices the VGAM2161 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2161 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2161 RNA is designated SEQ ID:4872, and is provided hereinbelow with reference to the sequence listing part.

[30215] VGAM2161 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2161 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2161 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30216] VGAM2161 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites

located in untranslated regions of VGAM2161 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2161 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2161 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2161 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30217] The complementary binding of VGAM2161 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2161 host target RNA, herein designated VGAM

HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2161 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2161 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[30218] It is appreciated that VGAM2161 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2161 host target genes. The mRNA of each one of this plurality of VGAM2161 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2161 RNA, herein designated VGAM RNA, and which when bound by VGAM2161 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2161 host target proteins.

[30219] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2161 gene, herein designated VGAM GENE, on one or more VGAM2161 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove

with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30220] It is yet further appreciated that a function of VGAM2161 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2161 include diagnosis, prevention and treatment of viral infection by Camelpox virus. Specific functions, and accordingly utilities, of VGAM2161 correlate with, and may be deduced from, the identity of the host target genes which VGAM2161 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[30221] Nucleotide sequences of the VGAM2161 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2161 RNA, herein designated VGAM RNA, and

a schematic representation of the secondary folding of VGAM2161 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2161 are further described hereinbelow with reference to Table 1.

[30222] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2161 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[30223] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2162 (VGAM2162) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[30224] VGAM2162 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2162 was detected is described hereinabove with reference to Figs. 2-8.

[30225] VGAM2162 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Camelpox virus.

VGAM2162 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[30226] VGAM2162 gene, herein designated VGAM GENE, encodes a VGAM2162 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2162 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2162 precursor RNA is designated SEQ ID:2148, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2148 is located at position 195253 relative to the genome of Camelpox virus.

[30227] VGAM2162 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2162 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[30228] An enzyme complex designated DICER COMPLEX, dices the VGAM2162 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2162 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 52%) nucleotide sequence of VGAM2162 RNA is designated SEQ ID:4873, and is provided hereinbelow with reference to the sequence listing part.

[30229] VGAM2162 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2162 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2162 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30230] VGAM2162 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM2162 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2162 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2162 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2162 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30231] The complementary binding of VGAM2162 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM2162 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2162 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2162 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[30232] It is appreciated that VGAM2162 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2162 host target genes. The mRNA of each one of this plurality of VGAM2162 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2162 RNA, herein designated VGAM RNA, and which when bound by VGAM2162 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2162 host target proteins.

[30233] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2162 gene, herein designated VGAM GENE, on one or more VGAM2162 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30234] It is yet further appreciated that a function of VGAM2162 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2162 include diagnosis, prevention and treatment of viral infection by Camelpox virus. Specific functions, and accordingly utilities, of VGAM2162 correlate with, and may be deduced from, the identity of the host target genes which VGAM2162 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[30235] Nucleotide sequences of the VGAM2162 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

diced VGAM2162 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2162 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2162 are further described hereinbelow with reference to Table 1.

[30236] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2162 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[30237] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2163 (VGAM2163) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[30238] VGAM2163 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2163 was detected is described hereinabove with reference to Figs. 2-8.

[30239] VGAM2163 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of Camelpox virus. VGAM2163 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[30240] VGAM2163 gene, herein designated VGAM GENE, encodes a VGAM2163 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2163 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2163 precursor RNA is designated SEQ ID:2149, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2149 is located at position 184394 relative to the genome of Camelpox virus.

[30241] VGAM2163 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2163 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30242] An enzyme complex designated DICER COMPLEX, dices the VGAM2163 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2163 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2163 RNA is designated SEQ ID:4874, and is provided hereinbelow with reference to the sequence listing part.

[30243] VGAM2163 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2163 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2163 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30244] VGAM2163 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2163 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2163 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2163 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2163 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30245] The complementary binding of VGAM2163 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM2163 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2163 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2163 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[30246] It is appreciated that VGAM2163 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2163 host target genes. The mRNA of each one of this plurality of VGAM2163 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2163 RNA, herein designated VGAM RNA, and which when bound by VGAM2163 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2163 host target proteins.

[30247] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2163 gene, herein designated VGAM GENE, on one or more VGAM2163 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30248] It is yet further appreciated that a function of VGAM2163 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2163 include diagnosis, prevention and treatment of viral infection by Camelpox virus. Specific functions, and accordingly utilities, of VGAM2163 correlate with, and may be deduced from, the identity of the host target genes which VGAM2163 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[30249] Nucleotide sequences of the VGAM2163 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the diced VGAM2163 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2163 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2163 are further described hereinbelow with reference to Table 1.

[30250] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2163 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[30251] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2164 (VGAM2164) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[30252] VGAM2164 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2164 was detected is described hereinabove with reference to Figs. 2-8.

[30253] VGAM2164 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Parsnip yellow fleck virus. VGAM2164 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[30254] VGAM2164 gene, herein designated VGAM GENE, encodes a VGAM2164 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2164 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2164 precursor RNA is designated SEQ ID:2150, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2150 is located at position 4805 relative to the genome of Parsnip yellow fleck virus.

[30255] VGAM2164 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2164 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30256] An enzyme complex designated DICER COMPLEX, dices the VGAM2164 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2164 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2164 RNA is designated SEQ ID:4875, and is provided hereinbelow with reference to the sequence listing part.

[30257] VGAM2164 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2164 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2164 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN COD-

ING and 3UTR respectively.

[30258] VGAM2164 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2164 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2164 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2164 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2164 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30259] The complementary binding of VGAM2164 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2164 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2164 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2164 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[30260] It is appreciated that VGAM2164 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2164 host target genes. The mRNA of each one of this plurality of VGAM2164 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2164 RNA, herein designated VGAM RNA, and which when bound by VGAM2164 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2164 host target proteins.

[30261] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2164 gene, herein designated VGAM GENE, on one

or more VGAM2164 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30262] It is yet further appreciated that a function of VGAM2164 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2164 include diagnosis, prevention and treatment of viral infection by Parsnip yellow fleck virus. Specific functions, and accordingly utilities, of VGAM2164 correlate with, and may be deduced from, the identity of the host target genes which VGAM2164 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[30263] Nucleotide sequences of the VGAM2164 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2164 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2164 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2164 are further described hereinbelow with reference to Table 1.

[30264] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2164 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[30265] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2165 (VGAM2165) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[30266] VGAM2165 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2165 was detected is de-

scribed hereinabove with reference to Figs. 2-8.

[30267] VGAM2165 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Camelpox virus. VGAM2165 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[30268] VGAM2165 gene, herein designated VGAM GENE, encodes a VGAM2165 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2165 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2165 precursor RNA is designated SEQ ID:2151, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2151 is located at position 196786 relative to the genome of Camelpox virus.

[30269] VGAM2165 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2165 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30270] An enzyme complex designated DICER COMPLEX, dices the VGAM2165 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2165 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2165 RNA is designated SEQ ID:4876, and is provided hereinbelow with reference to the sequence listing part.

[30271] VGAM2165 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2165 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2165 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and

a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30272] VGAM2165 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2165 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2165 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2165 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2165 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both

3UTR and 5UTR regions.

[30273] The complementary binding of VGAM2165 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2165 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2165 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2165 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[30274] It is appreciated that VGAM2165 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2165 host target genes. The mRNA of each one of this plurality of VGAM2165 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2165 RNA, herein designated VGAM RNA, and which when bound by VGAM2165 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2165 host target proteins.

[30275] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM2165 gene, herein designated VGAM GENE, on one or more VGAM2165 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30276] It is yet further appreciated that a function of VGAM2165 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2165 include diagnosis, prevention and treatment of viral infection by Camelpox virus. Specific functions, and accordingly utilities, of VGAM2165 correlate with, and may be deduced from, the identity of the host target genes which VGAM2165 binds and inhibits, and the function of these host target genes, as elaborated

hereinbelow.

[30277] Nucleotide sequences of the VGAM2165 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2165 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2165 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2165 are further described hereinbelow with reference to Table 1.

[30278] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2165 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[30279] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2166 (VGAM2166) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[30280] VGAM2166 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene.

The method by which VGAM2166 was detected is described hereinabove with reference to Figs. 2-8.

[30281] VGAM2166 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Camelpox virus. VGAM2166 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[30282] VGAM2166 gene, herein designated VGAM GENE, encodes a VGAM2166 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2166 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2166 precursor RNA is designated SEQ ID:2152, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2152 is located at position 186373 relative to the genome of Camelpox virus.

[30283] VGAM2166 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2166 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30284] An enzyme complex designated DICER COMPLEX, dices the VGAM2166 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2166 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2166 RNA is designated SEQ ID:4877, and is provided hereinbelow with reference to the sequence listing part.

[30285] VGAM2166 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2166 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2166 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding

gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30286] VGAM2166 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2166 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2166 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2166 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2166 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be lo-

cated in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30287] The complementary binding of VGAM2166 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2166 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2166 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2166 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[30288] It is appreciated that VGAM2166 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2166 host target genes. The mRNA of each one of this plurality of VGAM2166 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2166 RNA, herein designated VGAM RNA, and which when bound by VGAM2166 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2166 host target proteins.

[30289] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM2166 gene, herein designated VGAM GENE, on one or more VGAM2166 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30290] It is yet further appreciated that a function of VGAM2166 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2166 include diagnosis, prevention and treatment of viral infection by Camelpox virus. Specific functions, and accordingly utilities, of VGAM2166 correlate with, and may be deduced from, the identity of the host target genes which VGAM2166 binds and inhibits,

and the function of these host target genes, as elaborated hereinbelow.

[30291] Nucleotide sequences of the VGAM2166 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2166 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2166 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2166 are further described hereinbelow with reference to Table 1.

[30292] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2166 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[30293] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2167 (VGAM2167) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[30294] VGAM2167 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2167 was detected is described hereinabove with reference to Figs. 2-8.

[30295] VGAM2167 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Parsnip yellow fleck virus. VGAM2167 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[30296] VGAM2167 gene, herein designated VGAM GENE, encodes a VGAM2167 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2167 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2167 precursor RNA is designated SEQ ID:2153, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2153 is located at position 7389 relative to the genome of Parsnip yellow fleck virus.

[30297] VGAM2167 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2167 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30298] An enzyme complex designated DICER COMPLEX, dices the VGAM2167 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2167 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 81%) nucleotide sequence of VGAM2167 RNA is designated SEQ ID:4878, and is provided hereinbelow with reference to the sequence listing part.

[30299] VGAM2167 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2167 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2167 host target RNA, herein designated VGAM HOST TARGET RNA, comprises

three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30300] VGAM2167 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2167 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2167 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2167 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2167 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an

example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30301] The complementary binding of VGAM2167 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2167 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2167 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2167 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[30302] It is appreciated that VGAM2167 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2167 host target genes. The mRNA of each one of this plurality of VGAM2167 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2167 RNA, herein designated VGAM RNA, and which when bound by VGAM2167 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2167 host target proteins.

[30303] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2167 gene, herein designated VGAM GENE, on one or more VGAM2167 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30304] It is yet further appreciated that a function of VGAM2167 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2167 include diagnosis, prevention and treatment of viral infection by Parsnip yellow fleck virus. Specific functions, and accordingly utilities, of VGAM2167 correlate with, and may be deduced from, the identity of

the host target genes which VGAM2167 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[30305] Nucleotide sequences of the VGAM2167 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2167 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2167 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2167 are further described hereinbelow with reference to Table 1.

[30306] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2167 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[30307] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2168 (VGAM2168) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[30308] VGAM2168 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2168 was detected is described hereinabove with reference to Figs. 2-8.

[30309] VGAM2168 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Parsnip yellow fleck virus. VGAM2168 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[30310] VGAM2168 gene, herein designated VGAM GENE, encodes a VGAM2168 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2168 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2168 precursor RNA is designated SEQ ID:2154, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2154 is located at position 4305 relative to the genome of Parsnip yellow fleck virus.

[30311] VGAM2168 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2168 folded precursor RNA, herein designated VGAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30312] An enzyme complex designated DICER COMPLEX, dices the VGAM2168 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2168 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2168 RNA is designated SEQ ID:4879, and is provided hereinbelow with reference to the sequence listing part.

[30313] VGAM2168 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2168 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2168 host target RNA,

herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30314] VGAM2168 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2168 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2168 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2168 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2168 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host tar-

get binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30315] The complementary binding of VGAM2168 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2168 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2168 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2168 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[30316] It is appreciated that VGAM2168 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2168 host target genes. The mRNA of each one of this plurality of VGAM2168 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2168 RNA, herein designated VGAM RNA, and which when bound by VGAM2168 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2168 host target proteins.

[30317] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2168 gene, herein designated VGAM GENE, on one or more VGAM2168 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30318] It is yet further appreciated that a function of VGAM2168 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2168 include diagnosis, prevention and treatment of viral infection by Parsnip yellow fleck virus. Specific functions, and accordingly utilities, of VGAM2168

correlate with, and may be deduced from, the identity of the host target genes which VGAM2168 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[30319] Nucleotide sequences of the VGAM2168 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2168 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2168 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2168 are further described hereinbelow with reference to Table 1.

[30320] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2168 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[30321] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2169 (VGAM2169) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the

art.

[30322] VGAM2169 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2169 was detected is described hereinabove with reference to Figs. 2-8.

[30323] VGAM2169 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Camelpox virus. VGAM2169 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[30324] VGAM2169 gene, herein designated VGAM GENE, encodes a VGAM2169 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2169 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2169 precursor RNA is designated SEQ ID:2155, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2155 is located at position 183939 relative to the genome of Camelpox virus.

[30325] VGAM2169 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2169 folded

precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30326] An enzyme complex designated DICER COMPLEX, dices the VGAM2169 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2169 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 51%) nucleotide sequence of VGAM2169 RNA is designated SEQ ID:4880, and is provided hereinbelow with reference to the sequence listing part.

[30327] VGAM2169 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2169 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM2169 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30328] VGAM2169 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2169 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2169 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2169 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2169 host target RNA, herein designated VGAM HOST TARGET RNA.

It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30329] The complementary binding of VGAM2169 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2169 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2169 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2169 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[30330] It is appreciated that VGAM2169 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2169 host target genes. The mRNA of each one of this plurality of VGAM2169 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2169 RNA, herein designated VGAM RNA, and which when bound by VGAM2169 RNA, herein designated VGAM RNA, causes inhibition of translation of

respective one or more VGAM2169 host target proteins.

[30331] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2169 gene, herein designated VGAM GENE, on one or more VGAM2169 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30332] It is yet further appreciated that a function of VGAM2169 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2169 include diagnosis, prevention and treatment of viral infection by Camelpox virus. Specific

functions, and accordingly utilities, of VGAM2169 correlate with, and may be deduced from, the identity of the host target genes which VGAM2169 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[30333] Nucleotide sequences of the VGAM2169 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2169 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2169 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2169 are further described hereinbelow with reference to Table 1.

[30334] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2169 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[30335] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2170 (VGAM2170) viral gene, which modulates expression of respective host target genes thereof, the func-

tion and utility of which host target genes is known in the art.

[30336] VGAM2170 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2170 was detected is described hereinabove with reference to Figs. 2-8.

[30337] VGAM2170 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Parsnip yellow fleck virus. VGAM2170 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[30338] VGAM2170 gene, herein designated VGAM GENE, encodes a VGAM2170 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2170 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2170 precursor RNA is designated SEQ ID:2156, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2156 is located at position 8639 relative to the genome of Parsnip yellow fleck virus.

[30339] VGAM2170 precursor RNA, herein designated VGAM PRE-

CURSOR RNA, folds onto itself, forming VGAM2170 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30340] An enzyme complex designated DICER COMPLEX, dices the VGAM2170 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2170 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2170 RNA is designated SEQ ID:4881, and is provided hereinbelow with reference to the sequence listing part.

[30341] VGAM2170 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM2170 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2170 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30342] VGAM2170 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2170 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2170 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2170 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2170 host

target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30343] The complementary binding of VGAM2170 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2170 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2170 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2170 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[30344] It is appreciated that VGAM2170 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2170 host target genes. The mRNA of each one of this plurality of VGAM2170 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2170 RNA, herein designated VGAM RNA, and which when bound by VGAM2170 RNA, herein

designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2170 host target proteins.

[30345] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2170 gene, herein designated VGAM GENE, on one or more VGAM2170 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30346] It is yet further appreciated that a function of VGAM2170 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2170 include diagnosis, prevention and

treatment of viral infection by Parsnip yellow fleck virus. Specific functions, and accordingly utilities, of VGAM2170 correlate with, and may be deduced from, the identity of the host target genes which VGAM2170 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[30347] Nucleotide sequences of the VGAM2170 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2170 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2170 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2170 are further described hereinbelow with reference to Table 1.

[30348] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2170 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[30349] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2171 (VGAM2171) viral gene, which modulates ex-

pression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[30350] VGAM2171 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2171 was detected is described hereinabove with reference to Figs. 2-8.

[30351] VGAM2171 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Parsnip yellow fleck virus. VGAM2171 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[30352] VGAM2171 gene, herein designated VGAM GENE, encodes a VGAM2171 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2171 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2171 precursor RNA is designated SEQ ID:2157, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2157 is located at position 5077 relative to the genome of Parsnip yellow fleck virus.

[30353] VGAM2171 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2171 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30354] An enzyme complex designated DICER COMPLEX, dices the VGAM2171 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2171 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2171 RNA is designated SEQ ID:4882, and is provided hereinbelow with reference to the sequence listing part.

[30355] VGAM2171 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2171 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2171 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30356] VGAM2171 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2171 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2171 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2171 RNA, herein designated VGAM RNA, may have a different number of host target

binding sites in untranslated regions of a VGAM2171 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30357] The complementary binding of VGAM2171 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2171 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2171 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2171 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[30358] It is appreciated that VGAM2171 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2171 host target genes. The mRNA of each one of this plurality of VGAM2171 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2171 RNA, herein designated VGAM

RNA, and which when bound by VGAM2171 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2171 host target proteins.

[30359] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2171 gene, herein designated VGAM GENE, on one or more VGAM2171 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30360] It is yet further appreciated that a function of VGAM2171 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM2171 include diagnosis, prevention and treatment of viral infection by Parsnip yellow fleck virus. Specific functions, and accordingly utilities, of VGAM2171 correlate with, and may be deduced from, the identity of the host target genes which VGAM2171 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[30361] Nucleotide sequences of the VGAM2171 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2171 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2171 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2171 are further described hereinbelow with reference to Table 1.

[30362] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2171 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[30363] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Mes-

senger 2172 (VGAM2172) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[30364] VGAM2172 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2172 was detected is described hereinabove with reference to Figs. 2-8.

[30365] VGAM2172 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Parsnip yellow fleck virus. VGAM2172 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[30366] VGAM2172 gene, herein designated VGAM GENE, encodes a VGAM2172 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2172 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2172 precursor RNA is designated SEQ ID:2158, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2158 is located at position 578

relative to the genome of Parsnip yellow fleck virus.

[30367] VGAM2172 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2172 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30368] An enzyme complex designated DICER COMPLEX, dices the VGAM2172 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2172 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 63%) nucleotide sequence of VGAM2172 RNA is designated SEQ ID:4883, and is provided hereinbelow with reference to the sequence listing part.

[30369] VGAM2172 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2172 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2172 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30370] VGAM2172 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2172 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2172 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2172 RNA, herein designated

VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2172 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30371] The complementary binding of VGAM2172 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2172 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2172 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2172 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[30372] It is appreciated that VGAM2172 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2172 host target genes. The mRNA of each one of this plurality of VGAM2172 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM2172 RNA, herein designated VGAM RNA, and which when bound by VGAM2172 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2172 host target proteins.

[30373] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2172 gene, herein designated VGAM GENE, on one or more VGAM2172 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30374] It is yet further appreciated that a function of VGAM2172 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2172 include diagnosis, prevention and treatment of viral infection by Parsnip yellow fleck virus. Specific functions, and accordingly utilities, of VGAM2172 correlate with, and may be deduced from, the identity of the host target genes which VGAM2172 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[30375] Nucleotide sequences of the VGAM2172 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2172 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2172 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2172 are further described hereinbelow with reference to Table 1.

[30376] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2172 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[30377] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present

invention, referred to here as Viral Genomic Address Messenger 2173 (VGAM2173) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[30378] VGAM2173 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2173 was detected is described hereinabove with reference to Figs. 2-8.

[30379] VGAM2173 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Parsnip yellow fleck virus. VGAM2173 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[30380] VGAM2173 gene, herein designated VGAM GENE, encodes a VGAM2173 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2173 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2173 precursor RNA is designated SEQ ID:2159, and is provided hereinbelow with reference to the sequence listing part. Nu-

cleotide sequence SEQ ID:2159 is located at position 3661 relative to the genome of Parsnip yellow fleck virus.

[30381] VGAM2173 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2173 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30382] An enzyme complex designated DICER COMPLEX, dices the VGAM2173 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2173 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 74%) nucleotide sequence of VGAM2173 RNA is designated SEQ ID:4884, and is provided hereinbelow with reference to the sequence

listing part.

[30383] VGAM2173 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2173 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2173 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30384] VGAM2173 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2173 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2173 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not

meant to be limiting VGAM2173 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2173 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30385] The complementary binding of VGAM2173 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2173 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2173 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2173 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[30386] It is appreciated that VGAM2173 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2173 host target genes. The mRNA of each one of this plurality of VGAM2173 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2173 RNA, herein designated VGAM RNA, and which when bound by VGAM2173 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2173 host target proteins.

[30387] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2173 gene, herein designated VGAM GENE, on one or more VGAM2173 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30388] It is yet further appreciated that a function of VGAM2173

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2173 include diagnosis, prevention and treatment of viral infection by Parsnip yellow fleck virus. Specific functions, and accordingly utilities, of VGAM2173 correlate with, and may be deduced from, the identity of the host target genes which VGAM2173 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[30389] Nucleotide sequences of the VGAM2173 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2173 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2173 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2173 are further described hereinbelow with reference to Table 1.

[30390] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2173 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[30391] Fig. 1 further provides a conceptual description of another

novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2174 (VGAM2174) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[30392] VGAM2174 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2174 was detected is described hereinabove with reference to Figs. 2-8.

[30393] VGAM2174 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rabbit fibroma virus. VGAM2174 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[30394] VGAM2174 gene, herein designated VGAM GENE, encodes a VGAM2174 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2174 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2174 precursor RNA is designated SEQ ID:2160, and is provided here-

inbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2160 is located at position 17511 relative to the genome of Rabbit fibroma virus.

[30395] VGAM2174 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2174 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30396] An enzyme complex designated DICER COMPLEX, dices the VGAM2174 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2174 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 60%) nucleotide sequence of VGAM2174 RNA is designated SEQ ID:4885, and

is provided hereinbelow with reference to the sequence listing part.

[30397] VGAM2174 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2174 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2174 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30398] VGAM2174 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2174 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2174 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites

shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2174 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2174 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30399] The complementary binding of VGAM2174 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2174 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2174 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2174 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[30400] It is appreciated that VGAM2174 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2174 host target genes. The mRNA of each one of this plurality of VGAM2174 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2174 RNA, herein designated VGAM RNA, and which when bound by VGAM2174 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2174 host target proteins.

[30401] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2174 gene, herein designated VGAM GENE, on one or more VGAM2174 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30402] It is yet further appreciated that a function of VGAM2174 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2174 include diagnosis, prevention and treatment of viral infection by Rabbit fibroma virus. Specific functions, and accordingly utilities, of VGAM2174 correlate with, and may be deduced from, the identity of the host target genes which VGAM2174 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[30403] Nucleotide sequences of the VGAM2174 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2174 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2174 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2174 are further described hereinbelow with reference to Table 1.

[30404] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2174 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[30405] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2175 (VGAM2175) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[30406] VGAM2175 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2175 was detected is described hereinabove with reference to Figs. 2-8.

[30407] VGAM2175 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rabbit fibroma virus. VGAM2175 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[30408] VGAM2175 gene, herein designated VGAM GENE, encodes a VGAM2175 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2175 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2175 precur-

sor RNA is designated SEQ ID:2161, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2161 is located at position 10893 relative to the genome of Rabbit fibroma virus.

[30409] VGAM2175 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2175 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30410] An enzyme complex designated DICER COMPLEX, dices the VGAM2175 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2175 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 68%) nucleotide se-

quence of VGAM2175 RNA is designated SEQ ID:4886, and is provided hereinbelow with reference to the sequence listing part.

[30411] VGAM2175 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2175 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2175 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30412] VGAM2175 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2175 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2175 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is ap-

preciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2175 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2175 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30413] The complementary binding of VGAM2175 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2175 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2175 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2175 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[30414] It is appreciated that VGAM2175 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2175 host target genes. The mRNA of

each one of this plurality of VGAM2175 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2175 RNA, herein designated VGAM RNA, and which when bound by VGAM2175 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2175 host target proteins.

[30415] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2175 gene, herein designated VGAM GENE, on one or more VGAM2175 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science

294,779 (2001)).

[30416] It is yet further appreciated that a function of VGAM2175 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2175 include diagnosis, prevention and treatment of viral infection by Rabbit fibroma virus. Specific functions, and accordingly utilities, of VGAM2175 correlate with, and may be deduced from, the identity of the host target genes which VGAM2175 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[30417] Nucleotide sequences of the VGAM2175 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2175 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2175 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2175 are further described hereinbelow with reference to Table 1.

[30418] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2175 RNA, herein designated VGAM RNA, are de-

scribed hereinbelow with reference to Table 2.

[30419] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2176 (VGAM2176) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[30420] VGAM2176 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2176 was detected is described hereinabove with reference to Figs. 2-8.

[30421] VGAM2176 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rabbit fibroma virus. VGAM2176 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[30422] VGAM2176 gene, herein designated VGAM GENE, encodes a VGAM2176 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2176 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly

similar to the nucleotide sequence of VGAM2176 precursor RNA is designated SEQ ID:2162, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2162 is located at position 10073 relative to the genome of Rabbit fibroma virus.

[30423] VGAM2176 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2176 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30424] An enzyme complex designated DICER COMPLEX, dices the VGAM2176 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2176 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 51%) nucleotide sequence of VGAM2176 RNA is designated SEQ ID:4887, and is provided hereinbelow with reference to the sequence listing part.

[30425] VGAM2176 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2176 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2176 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30426] VGAM2176 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2176 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2176 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I,

BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2176 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2176 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30427] The complementary binding of VGAM2176 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2176 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2176 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2176 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[30428] It is appreciated that VGAM2176 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM2176 host target genes. The mRNA of each one of this plurality of VGAM2176 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2176 RNA, herein designated VGAM RNA, and which when bound by VGAM2176 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2176 host target proteins.

[30429] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2176 gene, herein designated VGAM GENE, on one or more VGAM2176 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30430] It is yet further appreciated that a function of VGAM2176 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2176 include diagnosis, prevention and treatment of viral infection by Rabbit fibroma virus. Specific functions, and accordingly utilities, of VGAM2176 correlate with, and may be deduced from, the identity of the host target genes which VGAM2176 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[30431] Nucleotide sequences of the VGAM2176 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2176 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2176 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2176 are further described hereinbelow with reference to Table 1.

[30432] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites

to VGAM2176 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[30433] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2177 (VGAM2177) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[30434] VGAM2177 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2177 was detected is described hereinabove with reference to Figs. 2-8.

[30435] VGAM2177 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rabbit fibroma virus. VGAM2177 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[30436] VGAM2177 gene, herein designated VGAM GENE, encodes a VGAM2177 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2177 precursor RNA, herein designated VGAM PRECURSOR RNA, does not en-

code a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2177 precursor RNA is designated SEQ ID:2163, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2163 is located at position 14151 relative to the genome of Rabbit fibroma virus.

[30437] VGAM2177 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2177 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30438] An enzyme complex designated DICER COMPLEX, dices the VGAM2177 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2177 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 52%) nucleotide sequence of VGAM2177 RNA is designated SEQ ID:4888, and is provided hereinbelow with reference to the sequence listing part.

[30439] VGAM2177 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2177 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2177 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30440] VGAM2177 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2177 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2177 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3

such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2177 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2177 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30441] The complementary binding of VGAM2177 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2177 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2177 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2177 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[30442] It is appreciated that VGAM2177 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2177 host target genes. The mRNA of each one of this plurality of VGAM2177 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2177 RNA, herein designated VGAM RNA, and which when bound by VGAM2177 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2177 host target proteins.

[30443] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2177 gene, herein designated VGAM GENE, on one or more VGAM2177 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30444] It is yet further appreciated that a function of VGAM2177 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2177 include diagnosis, prevention and treatment of viral infection by Rabbit fibroma virus. Specific functions, and accordingly utilities, of VGAM2177 correlate with, and may be deduced from, the identity of the host target genes which VGAM2177 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[30445] Nucleotide sequences of the VGAM2177 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2177 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2177 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2177 are further described hereinbelow with reference to Table 1.

[30446] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the

complementarity of each of these host target binding sites to VGAM2177 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[30447] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2178 (VGAM2178) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[30448] VGAM2178 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2178 was detected is described hereinabove with reference to Figs. 2-8.

[30449] VGAM2178 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rabbit fibroma virus. VGAM2178 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[30450] VGAM2178 gene, herein designated VGAM GENE, encodes a VGAM2178 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2178 precursor RNA,

herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2178 precursor RNA is designated SEQ ID:2164, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2164 is located at position 22881 relative to the genome of Rabbit fibroma virus.

[30451] VGAM2178 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2178 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30452] An enzyme complex designated DICER COMPLEX, dices the VGAM2178 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2178 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2178 RNA is designated SEQ ID:4889, and is provided hereinbelow with reference to the sequence listing part.

[30453] VGAM2178 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2178 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2178 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30454] VGAM2178 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2178 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2178 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host

target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2178 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2178 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30455] The complementary binding of VGAM2178 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2178 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2178 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2178 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[30456] It is appreciated that VGAM2178 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2178 host target genes. The mRNA of each one of this plurality of VGAM2178 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2178 RNA, herein designated VGAM RNA, and which when bound by VGAM2178 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2178 host target proteins.

[30457] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2178 gene, herein designated VGAM GENE, on one or more VGAM2178 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30458] It is yet further appreciated that a function of VGAM2178 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2178 include diagnosis, prevention and treatment of viral infection by Rabbit fibroma virus. Specific functions, and accordingly utilities, of VGAM2178 correlate with, and may be deduced from, the identity of the host target genes which VGAM2178 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[30459] Nucleotide sequences of the VGAM2178 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2178 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2178 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2178 are further described hereinbelow with reference to Table 1.

[30460] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2178 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[30461] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2179 (VGAM2179) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[30462] VGAM2179 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2179 was detected is described hereinabove with reference to Figs. 2-8.

[30463] VGAM2179 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rabbit fibroma virus. VGAM2179 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[30464] VGAM2179 gene, herein designated VGAM GENE, encodes a VGAM2179 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and un-

like most ordinary genes, VGAM2179 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2179 precursor RNA is designated SEQ ID:2165, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2165 is located at position 15205 relative to the genome of Rabbit fibroma virus.

[30465] VGAM2179 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2179 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30466] An enzyme complex designated DICER COMPLEX, dices the VGAM2179 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2179 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2179 RNA is designated SEQ ID:4890, and is provided hereinbelow with reference to the sequence listing part.

[30467] VGAM2179 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2179 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2179 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30468] VGAM2179 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2179 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2179 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed

sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2179 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2179 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30469] The complementary binding of VGAM2179 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2179 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2179 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2179 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target

protein is therefore outlined by a broken line.

[30470] It is appreciated that VGAM2179 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2179 host target genes. The mRNA of each one of this plurality of VGAM2179 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2179 RNA, herein designated VGAM RNA, and which when bound by VGAM2179 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2179 host target proteins.

[30471] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2179 gene, herein designated VGAM GENE, on one or more VGAM2179 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30472] It is yet further appreciated that a function of VGAM2179 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2179 include diagnosis, prevention and treatment of viral infection by Rabbit fibroma virus. Specific functions, and accordingly utilities, of VGAM2179 correlate with, and may be deduced from, the identity of the host target genes which VGAM2179 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[30473] Nucleotide sequences of the VGAM2179 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2179 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2179 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2179 are further described hereinbelow with reference to Table 1.

[30474] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2179 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[30475] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2180 (VGAM2180) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[30476] VGAM2180 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2180 was detected is described hereinabove with reference to Figs. 2-8.

[30477] VGAM2180 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Yaba-like disease virus. VGAM2180 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[30478] VGAM2180 gene, herein designated VGAM GENE, encodes a VGAM2180 precursor RNA, herein designated VGAM

PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2180 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2180 precursor RNA is designated SEQ ID:2166, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2166 is located at position 128284 relative to the genome of Yaba-like disease virus.

[30479] VGAM2180 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2180 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30480] An enzyme complex designated DICER COMPLEX, dices the VGAM2180 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2180 RNA, herein designated VGAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2180 RNA is designated SEQ ID:4891, and is provided hereinbelow with reference to the sequence listing part.

[30481] VGAM2180 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2180 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2180 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30482] VGAM2180 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2180 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2180 RNA, herein designated

VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2180 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2180 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30483] The complementary binding of VGAM2180 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2180 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2180 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2180 host target protein, herein desig-

nated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[30484] It is appreciated that VGAM2180 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2180 host target genes. The mRNA of each one of this plurality of VGAM2180 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2180 RNA, herein designated VGAM RNA, and which when bound by VGAM2180 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2180 host target proteins.

[30485] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2180 gene, herein designated VGAM GENE, on one or more VGAM2180 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30486] It is yet further appreciated that a function of VGAM2180 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2180 include diagnosis, prevention and treatment of viral infection by Yaba-like disease virus. Specific functions, and accordingly utilities, of VGAM2180 correlate with, and may be deduced from, the identity of the host target genes which VGAM2180 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[30487] Nucleotide sequences of the VGAM2180 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2180 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2180 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2180 are further described hereinbelow with reference to Table 1.

[30488] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2180 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[30489] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2181 (VGAM2181) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[30490] VGAM2181 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2181 was detected is described hereinabove with reference to Figs. 2-8.

[30491] VGAM2181 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Yaba-like disease virus. VGAM2181 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[30492] VGAM2181 gene, herein designated VGAM GENE, encodes

a VGAM2181 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2181 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2181 precursor RNA is designated SEQ ID:2167, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2167 is located at position 125843 relative to the genome of Yaba-like disease virus.

[30493] VGAM2181 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2181 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30494] An enzyme complex designated DICER COMPLEX, dices the VGAM2181 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2181 RNA,

herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 75%) nucleotide sequence of VGAM2181 RNA is designated SEQ ID:4892, and is provided hereinbelow with reference to the sequence listing part.

[30495] VGAM2181 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2181 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2181 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30496] VGAM2181 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2181 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM2181 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2181 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2181 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30497] The complementary binding of VGAM2181 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2181 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2181 host target RNA, herein designated VGAM HOST TARGET

RNA, into VGAM2181 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[30498] It is appreciated that VGAM2181 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2181 host target genes. The mRNA of each one of this plurality of VGAM2181 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2181 RNA, herein designated VGAM RNA, and which when bound by VGAM2181 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2181 host target proteins.

[30499] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2181 gene, herein designated VGAM GENE, on one or more VGAM2181 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30500] It is yet further appreciated that a function of VGAM2181 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2181 include diagnosis, prevention and treatment of viral infection by Yaba-like disease virus. Specific functions, and accordingly utilities, of VGAM2181 correlate with, and may be deduced from, the identity of the host target genes which VGAM2181 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[30501] Nucleotide sequences of the VGAM2181 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2181 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2181 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2181 are further

described hereinbelow with reference to Table 1.

[30502] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2181 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[30503] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2182 (VGAM2182) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[30504] VGAM2182 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2182 was detected is described hereinabove with reference to Figs. 2-8.

[30505] VGAM2182 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Yaba-like disease virus. VGAM2182 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[30506] VGAM2182 gene, herein designated VGAM GENE, encodes a VGAM2182 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2182 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2182 precursor RNA is designated SEQ ID:2168, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2168 is located at position 132254 relative to the genome of Yaba-like disease virus.

[30507] VGAM2182 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2182 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30508] An enzyme complex designated DICER COMPLEX, dices the VGAM2182 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, into VGAM2182 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2182 RNA is designated SEQ ID:4893, and is provided hereinbelow with reference to the sequence listing part.

[30509] VGAM2182 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2182 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2182 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30510] VGAM2182 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2182 host target RNA, herein designated VGAM HOST TARGET RNA. This

complementary binding is due to the fact that the nucleotide sequence of VGAM2182 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2182 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2182 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30511] The complementary binding of VGAM2182 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2182 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2182

host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2182 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[30512] It is appreciated that VGAM2182 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2182 host target genes. The mRNA of each one of this plurality of VGAM2182 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2182 RNA, herein designated VGAM RNA, and which when bound by VGAM2182 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2182 host target proteins.

[30513] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2182 gene, herein designated VGAM GENE, on one or more VGAM2182 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30514] It is yet further appreciated that a function of VGAM2182 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2182 include diagnosis, prevention and treatment of viral infection by Yaba-like disease virus. Specific functions, and accordingly utilities, of VGAM2182 correlate with, and may be deduced from, the identity of the host target genes which VGAM2182 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[30515] Nucleotide sequences of the VGAM2182 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2182 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2182 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM2182 are further described hereinbelow with reference to Table 1.

[30516] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2182 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[30517] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2183 (VGAM2183) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[30518] VGAM2183 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2183 was detected is described hereinabove with reference to Figs. 2-8.

[30519] VGAM2183 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Yaba-like disease virus. VGAM2183 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the

human genome.

[30520] VGAM2183 gene, herein designated VGAM GENE, encodes a VGAM2183 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2183 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2183 precursor RNA is designated SEQ ID:2169, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2169 is located at position 135497 relative to the genome of Yaba-like disease virus.

[30521] VGAM2183 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2183 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30522] An enzyme complex designated DICER COMPLEX, dices

the VGAM2183 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2183 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2183 RNA is designated SEQ ID:4894, and is provided hereinbelow with reference to the sequence listing part.

[30523] VGAM2183 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2183 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2183 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30524] VGAM2183 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2183 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2183 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2183 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2183 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30525] The complementary binding of VGAM2183 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2183 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM2183 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2183 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[30526] It is appreciated that VGAM2183 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2183 host target genes. The mRNA of each one of this plurality of VGAM2183 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2183 RNA, herein designated VGAM RNA, and which when bound by VGAM2183 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2183 host target proteins.

[30527] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2183 gene, herein designated VGAM GENE, on one or more VGAM2183 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30528] It is yet further appreciated that a function of VGAM2183 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2183 include diagnosis, prevention and treatment of viral infection by Yaba-like disease virus. Specific functions, and accordingly utilities, of VGAM2183 correlate with, and may be deduced from, the identity of the host target genes which VGAM2183 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[30529] Nucleotide sequences of the VGAM2183 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2183 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of

VGAM2183 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2183 are further described hereinbelow with reference to Table 1.

[30530] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2183 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[30531] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2184 (VGAM2184) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[30532] VGAM2184 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2184 was detected is described hereinabove with reference to Figs. 2-8.

[30533] VGAM2184 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Monkeypox virus. VGAM2184 host target gene, herein designated VGAM

HOST TARGET GENE, is a human gene contained in the human genome.

[30534] VGAM2184 gene, herein designated VGAM GENE, encodes a VGAM2184 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2184 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2184 precursor RNA is designated SEQ ID:2170, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2170 is located at position 187541 relative to the genome of Monkeypox virus.

[30535] VGAM2184 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2184 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30536] An enzyme complex designated DICER COMPLEX, dices the VGAM2184 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2184 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2184 RNA is designated SEQ ID:4895, and is provided hereinbelow with reference to the sequence listing part.

[30537] VGAM2184 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2184 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2184 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30538] VGAM2184 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites

located in untranslated regions of VGAM2184 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2184 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2184 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2184 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30539] The complementary binding of VGAM2184 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2184 host target RNA, herein designated VGAM

HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2184 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2184 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[30540] It is appreciated that VGAM2184 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2184 host target genes. The mRNA of each one of this plurality of VGAM2184 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2184 RNA, herein designated VGAM RNA, and which when bound by VGAM2184 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2184 host target proteins.

[30541] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2184 gene, herein designated VGAM GENE, on one or more VGAM2184 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove

with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30542] It is yet further appreciated that a function of VGAM2184 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2184 include diagnosis, prevention and treatment of viral infection by Monkeypox virus. Specific functions, and accordingly utilities, of VGAM2184 correlate with, and may be deduced from, the identity of the host target genes which VGAM2184 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[30543] Nucleotide sequences of the VGAM2184 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2184 RNA, herein designated VGAM RNA, and

a schematic representation of the secondary folding of VGAM2184 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2184 are further described hereinbelow with reference to Table 1.

[30544] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2184 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[30545] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2185 (VGAM2185) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[30546] VGAM2185 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2185 was detected is described hereinabove with reference to Figs. 2-8.

[30547] VGAM2185 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Camelpox virus.

VGAM2185 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[30548] VGAM2185 gene, herein designated VGAM GENE, encodes a VGAM2185 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2185 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2185 precursor RNA is designated SEQ ID:2171, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2171 is located at position 195252 relative to the genome of Camelpox virus.

[30549] VGAM2185 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2185 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[30550] An enzyme complex designated DICER COMPLEX, dices the VGAM2185 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2185 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 52%) nucleotide sequence of VGAM2185 RNA is designated SEQ ID:4896, and is provided hereinbelow with reference to the sequence listing part.

[30551] VGAM2185 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2185 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2185 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30552] VGAM2185 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM2185 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2185 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2185 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2185 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30553] The complementary binding of VGAM2185 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM2185 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2185 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2185 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[30554] It is appreciated that VGAM2185 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2185 host target genes. The mRNA of each one of this plurality of VGAM2185 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2185 RNA, herein designated VGAM RNA, and which when bound by VGAM2185 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2185 host target proteins.

[30555] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2185 gene, herein designated VGAM GENE, on one or more VGAM2185 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30556] It is yet further appreciated that a function of VGAM2185 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2185 include diagnosis, prevention and treatment of viral infection by Camelpox virus. Specific functions, and accordingly utilities, of VGAM2185 correlate with, and may be deduced from, the identity of the host target genes which VGAM2185 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[30557] Nucleotide sequences of the VGAM2185 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

diced VGAM2185 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2185 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2185 are further described hereinbelow with reference to Table 1.

[30558] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2185 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[30559] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2186 (VGAM2186) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[30560] VGAM2186 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2186 was detected is described hereinabove with reference to Figs. 2-8.

[30561] VGAM2186 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of Monkeypox virus. VGAM2186 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[30562] VGAM2186 gene, herein designated VGAM GENE, encodes a VGAM2186 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2186 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2186 precursor RNA is designated SEQ ID:2172, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2172 is located at position 184211 relative to the genome of Monkeypox virus.

[30563] VGAM2186 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2186 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30564] An enzyme complex designated DICER COMPLEX, dices the VGAM2186 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2186 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 65%) nucleotide sequence of VGAM2186 RNA is designated SEQ ID:4897, and is provided hereinbelow with reference to the sequence listing part.

[30565] VGAM2186 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2186 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2186 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30566] VGAM2186 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2186 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2186 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2186 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2186 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30567] The complementary binding of VGAM2186 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM2186 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2186 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2186 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[30568] It is appreciated that VGAM2186 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2186 host target genes. The mRNA of each one of this plurality of VGAM2186 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2186 RNA, herein designated VGAM RNA, and which when bound by VGAM2186 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2186 host target proteins.

[30569] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2186 gene, herein designated VGAM GENE, on one or more VGAM2186 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30570] It is yet further appreciated that a function of VGAM2186 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2186 include diagnosis, prevention and treatment of viral infection by Monkeypox virus. Specific functions, and accordingly utilities, of VGAM2186 correlate with, and may be deduced from, the identity of the host target genes which VGAM2186 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[30571] Nucleotide sequences of the VGAM2186 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the diced VGAM2186 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2186 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2186 are further described hereinbelow with reference to Table 1.

[30572] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2186 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[30573] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2187 (VGAM2187) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[30574] VGAM2187 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2187 was detected is described hereinabove with reference to Figs. 2-8.

[30575] VGAM2187 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Monkeypox virus. VGAM2187 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[30576] VGAM2187 gene, herein designated VGAM GENE, encodes a VGAM2187 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2187 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2187 precursor RNA is designated SEQ ID:2173, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2173 is located at position 186422 relative to the genome of Monkeypox virus.

[30577] VGAM2187 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2187 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30578] An enzyme complex designated DICER COMPLEX, dices the VGAM2187 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2187 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2187 RNA is designated SEQ ID:4898, and is provided hereinbelow with reference to the sequence listing part.

[30579] VGAM2187 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2187 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2187 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN COD-

ING and 3UTR respectively.

[30580] VGAM2187 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2187 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2187 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2187 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2187 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30581] The complementary binding of VGAM2187 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2187 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2187 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2187 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[30582] It is appreciated that VGAM2187 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2187 host target genes. The mRNA of each one of this plurality of VGAM2187 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2187 RNA, herein designated VGAM RNA, and which when bound by VGAM2187 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2187 host target proteins.

[30583] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2187 gene, herein designated VGAM GENE, on one

or more VGAM2187 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30584] It is yet further appreciated that a function of VGAM2187 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2187 include diagnosis, prevention and treatment of viral infection by Monkeypox virus. Specific functions, and accordingly utilities, of VGAM2187 correlate with, and may be deduced from, the identity of the host target genes which VGAM2187 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[30585] Nucleotide sequences of the VGAM2187 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2187 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2187 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2187 are further described hereinbelow with reference to Table 1.

[30586] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2187 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[30587] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2188 (VGAM2188) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[30588] VGAM2188 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2188 was detected is de-

scribed hereinabove with reference to Figs. 2-8.

[30589] VGAM2188 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Monkeypox virus. VGAM2188 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[30590] VGAM2188 gene, herein designated VGAM GENE, encodes a VGAM2188 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2188 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2188 precursor RNA is designated SEQ ID:2174, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2174 is located at position 185906 relative to the genome of Monkeypox virus.

[30591] VGAM2188 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2188 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30592] An enzyme complex designated DICER COMPLEX, dices the VGAM2188 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2188 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide sequence of VGAM2188 RNA is designated SEQ ID:4899, and is provided hereinbelow with reference to the sequence listing part.

[30593] VGAM2188 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2188 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2188 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN COD-

ING and 3UTR respectively.

[30594] VGAM2188 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2188 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2188 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2188 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2188 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30595] The complementary binding of VGAM2188 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2188 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2188 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2188 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[30596] It is appreciated that VGAM2188 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2188 host target genes. The mRNA of each one of this plurality of VGAM2188 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2188 RNA, herein designated VGAM RNA, and which when bound by VGAM2188 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2188 host target proteins.

[30597] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2188 gene, herein designated VGAM GENE, on one

or more VGAM2188 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30598] It is yet further appreciated that a function of VGAM2188 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2188 include diagnosis, prevention and treatment of viral infection by Monkeypox virus. Specific functions, and accordingly utilities, of VGAM2188 correlate with, and may be deduced from, the identity of the host target genes which VGAM2188 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[30599] Nucleotide sequences of the VGAM2188 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2188 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2188 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2188 are further described hereinbelow with reference to Table 1.

[30600] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2188 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[30601] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2189 (VGAM2189) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[30602] VGAM2189 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2189 was detected is de-

scribed hereinabove with reference to Figs. 2-8.

[30603] VGAM2189 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Monkeypox virus. VGAM2189 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[30604] VGAM2189 gene, herein designated VGAM GENE, encodes a VGAM2189 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2189 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2189 precursor RNA is designated SEQ ID:2175, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2175 is located at position 189835 relative to the genome of Monkeypox virus.

[30605] VGAM2189 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2189 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30606] An enzyme complex designated DICER COMPLEX, dices the VGAM2189 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2189 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2189 RNA is designated SEQ ID:4900, and is provided hereinbelow with reference to the sequence listing part.

[30607] VGAM2189 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2189 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2189 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and

a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30608] VGAM2189 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2189 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2189 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2189 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2189 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both

3UTR and 5UTR regions.

[30609] The complementary binding of VGAM2189 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2189 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2189 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2189 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[30610] It is appreciated that VGAM2189 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2189 host target genes. The mRNA of each one of this plurality of VGAM2189 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2189 RNA, herein designated VGAM RNA, and which when bound by VGAM2189 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2189 host target proteins.

[30611] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM2189 gene, herein designated VGAM GENE, on one or more VGAM2189 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30612] It is yet further appreciated that a function of VGAM2189 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2189 include diagnosis, prevention and treatment of viral infection by Monkeypox virus. Specific functions, and accordingly utilities, of VGAM2189 correlate with, and may be deduced from, the identity of the host target genes which VGAM2189 binds and inhibits, and the function of these host target genes, as elaborated

hereinbelow.

[30613] Nucleotide sequences of the VGAM2189 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2189 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2189 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2189 are further described hereinbelow with reference to Table 1.

[30614] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2189 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[30615] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2190 (VGAM2190) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[30616] VGAM2190 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene.

The method by which VGAM2190 was detected is described hereinabove with reference to Figs. 2-8.

[30617] VGAM2190 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Monkeypox virus. VGAM2190 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[30618] VGAM2190 gene, herein designated VGAM GENE, encodes a VGAM2190 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2190 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2190 precursor RNA is designated SEQ ID:2176, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2176 is located at position 181733 relative to the genome of Monkeypox virus.

[30619] VGAM2190 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2190 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30620] An enzyme complex designated DICER COMPLEX, dices the VGAM2190 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2190 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2190 RNA is designated SEQ ID:4901, and is provided hereinbelow with reference to the sequence listing part.

[30621] VGAM2190 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2190 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2190 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding

gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30622] VGAM2190 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2190 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2190 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2190 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2190 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be lo-

cated in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30623] The complementary binding of VGAM2190 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2190 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2190 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2190 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[30624] It is appreciated that VGAM2190 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2190 host target genes. The mRNA of each one of this plurality of VGAM2190 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2190 RNA, herein designated VGAM RNA, and which when bound by VGAM2190 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2190 host target proteins.

[30625] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM2190 gene, herein designated VGAM GENE, on one or more VGAM2190 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30626] It is yet further appreciated that a function of VGAM2190 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2190 include diagnosis, prevention and treatment of viral infection by Monkeypox virus. Specific functions, and accordingly utilities, of VGAM2190 correlate with, and may be deduced from, the identity of the host target genes which VGAM2190 binds and inhibits,

and the function of these host target genes, as elaborated hereinbelow.

[30627] Nucleotide sequences of the VGAM2190 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2190 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2190 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2190 are further described hereinbelow with reference to Table 1.

[30628] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2190 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[30629] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2191 (VGAM2191) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[30630] VGAM2191 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2191 was detected is described hereinabove with reference to Figs. 2-8.

[30631] VGAM2191 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Monkeypox virus. VGAM2191 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[30632] VGAM2191 gene, herein designated VGAM GENE, encodes a VGAM2191 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2191 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2191 precursor RNA is designated SEQ ID:2177, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2177 is located at position 812 relative to the genome of Monkeypox virus.

[30633] VGAM2191 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2191 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30634] An enzyme complex designated DICER COMPLEX, dices the VGAM2191 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2191 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2191 RNA is designated SEQ ID:4902, and is provided hereinbelow with reference to the sequence listing part.

[30635] VGAM2191 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2191 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2191 host target RNA, herein designated VGAM HOST TARGET RNA, comprises

three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30636] VGAM2191 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2191 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2191 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2191 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2191 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an

example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30637] The complementary binding of VGAM2191 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2191 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2191 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2191 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[30638] It is appreciated that VGAM2191 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2191 host target genes. The mRNA of each one of this plurality of VGAM2191 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2191 RNA, herein designated VGAM RNA, and which when bound by VGAM2191 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2191 host target proteins.

[30639] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2191 gene, herein designated VGAM GENE, on one or more VGAM2191 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30640] It is yet further appreciated that a function of VGAM2191 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2191 include diagnosis, prevention and treatment of viral infection by Monkeypox virus. Specific functions, and accordingly utilities, of VGAM2191 correlate with, and may be deduced from, the identity of the

host target genes which VGAM2191 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[30641] Nucleotide sequences of the VGAM2191 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2191 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2191 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2191 are further described hereinbelow with reference to Table 1.

[30642] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2191 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[30643] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2192 (VGAM2192) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[30644] VGAM2192 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2192 was detected is described hereinabove with reference to Figs. 2-8.

[30645] VGAM2192 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Monkeypox virus. VGAM2192 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[30646] VGAM2192 gene, herein designated VGAM GENE, encodes a VGAM2192 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2192 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2192 precursor RNA is designated SEQ ID:2178, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2178 is located at position 2502 relative to the genome of Monkeypox virus.

[30647] VGAM2192 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2192 folded precursor RNA, herein designated VGAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30648] An enzyme complex designated DICER COMPLEX, dices the VGAM2192 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2192 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2192 RNA is designated SEQ ID:4903, and is provided hereinbelow with reference to the sequence listing part.

[30649] VGAM2192 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2192 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2192 host target RNA,

herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30650] VGAM2192 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2192 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2192 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2192 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2192 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host tar-

get binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30651] The complementary binding of VGAM2192 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2192 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2192 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2192 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[30652] It is appreciated that VGAM2192 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2192 host target genes. The mRNA of each one of this plurality of VGAM2192 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2192 RNA, herein designated VGAM RNA, and which when bound by VGAM2192 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2192 host target proteins.

[30653] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2192 gene, herein designated VGAM GENE, on one or more VGAM2192 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30654] It is yet further appreciated that a function of VGAM2192 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2192 include diagnosis, prevention and treatment of viral infection by Monkeypox virus. Specific functions, and accordingly utilities, of VGAM2192 corre-

late with, and may be deduced from, the identity of the host target genes which VGAM2192 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[30655] Nucleotide sequences of the VGAM2192 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2192 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2192 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2192 are further described hereinbelow with reference to Table 1.

[30656] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2192 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[30657] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2193 (VGAM2193) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the

art.

[30658] VGAM2193 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2193 was detected is described hereinabove with reference to Figs. 2-8.

[30659] VGAM2193 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cowpox virus. VGAM2193 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[30660] VGAM2193 gene, herein designated VGAM GENE, encodes a VGAM2193 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2193 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2193 precursor RNA is designated SEQ ID:2179, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2179 is located at position 18641 relative to the genome of Cowpox virus.

[30661] VGAM2193 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2193 folded

precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30662] An enzyme complex designated DICER COMPLEX, dices the VGAM2193 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2193 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 56%) nucleotide sequence of VGAM2193 RNA is designated SEQ ID:4904, and is provided hereinbelow with reference to the sequence listing part.

[30663] VGAM2193 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2193 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM2193 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30664] VGAM2193 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2193 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2193 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2193 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2193 host target RNA, herein designated VGAM HOST TARGET RNA.

It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30665] The complementary binding of VGAM2193 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2193 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2193 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2193 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[30666] It is appreciated that VGAM2193 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2193 host target genes. The mRNA of each one of this plurality of VGAM2193 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2193 RNA, herein designated VGAM RNA, and which when bound by VGAM2193 RNA, herein designated VGAM RNA, causes inhibition of translation of

respective one or more VGAM2193 host target proteins.

[30667] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2193 gene, herein designated VGAM GENE, on one or more VGAM2193 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30668] It is yet further appreciated that a function of VGAM2193 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2193 include diagnosis, prevention and treatment of viral infection by Cowpox virus. Specific

functions, and accordingly utilities, of VGAM2193 correlate with, and may be deduced from, the identity of the host target genes which VGAM2193 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[30669] Nucleotide sequences of the VGAM2193 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2193 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2193 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2193 are further described hereinbelow with reference to Table 1.

[30670] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2193 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[30671] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2194 (VGAM2194) viral gene, which modulates expression of respective host target genes thereof, the func-

tion and utility of which host target genes is known in the art.

[30672] VGAM2194 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2194 was detected is described hereinabove with reference to Figs. 2-8.

[30673] VGAM2194 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Monkeypox virus. VGAM2194 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[30674] VGAM2194 gene, herein designated VGAM GENE, encodes a VGAM2194 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2194 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2194 precursor RNA is designated SEQ ID:2180, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2180 is located at position 269 relative to the genome of Monkeypox virus.

[30675] VGAM2194 precursor RNA, herein designated VGAM PRE-

CURSOR RNA, folds onto itself, forming VGAM2194 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30676] An enzyme complex designated DICER COMPLEX, dices the VGAM2194 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2194 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2194 RNA is designated SEQ ID:4905, and is provided hereinbelow with reference to the sequence listing part.

[30677] VGAM2194 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM2194 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2194 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30678] VGAM2194 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2194 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2194 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2194 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2194 host

target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30679] The complementary binding of VGAM2194 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2194 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2194 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2194 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[30680] It is appreciated that VGAM2194 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2194 host target genes. The mRNA of each one of this plurality of VGAM2194 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2194 RNA, herein designated VGAM RNA, and which when bound by VGAM2194 RNA, herein

designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2194 host target proteins.

[30681] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2194 gene, herein designated VGAM GENE, on one or more VGAM2194 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30682] It is yet further appreciated that a function of VGAM2194 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2194 include diagnosis, prevention and

treatment of viral infection by Monkeypox virus. Specific functions, and accordingly utilities, of VGAM2194 correlate with, and may be deduced from, the identity of the host target genes which VGAM2194 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[30683] Nucleotide sequences of the VGAM2194 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2194 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2194 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2194 are further described hereinbelow with reference to Table 1.

[30684] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2194 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[30685] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2195 (VGAM2195) viral gene, which modulates ex-

pression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[30686] VGAM2195 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2195 was detected is described hereinabove with reference to Figs. 2-8.

[30687] VGAM2195 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Yaba-like disease virus. VGAM2195 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[30688] VGAM2195 gene, herein designated VGAM GENE, encodes a VGAM2195 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2195 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2195 precursor RNA is designated SEQ ID:2181, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2181 is located at position 9471 relative to the genome of Yaba-like disease virus.

[30689] VGAM2195 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2195 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30690] An enzyme complex designated DICER COMPLEX, dices the VGAM2195 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2195 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 52%) nucleotide sequence of VGAM2195 RNA is designated SEQ ID:4906, and is provided hereinbelow with reference to the sequence listing part.

[30691] VGAM2195 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2195 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2195 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30692] VGAM2195 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2195 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2195 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2195 RNA, herein designated VGAM RNA, may have a different number of host target

binding sites in untranslated regions of a VGAM2195 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30693] The complementary binding of VGAM2195 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2195 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2195 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2195 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[30694] It is appreciated that VGAM2195 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2195 host target genes. The mRNA of each one of this plurality of VGAM2195 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2195 RNA, herein designated VGAM

RNA, and which when bound by VGAM2195 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2195 host target proteins.

[30695] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2195 gene, herein designated VGAM GENE, on one or more VGAM2195 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30696] It is yet further appreciated that a function of VGAM2195 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM2195 include diagnosis, prevention and treatment of viral infection by Yaba-like disease virus. Specific functions, and accordingly utilities, of VGAM2195 correlate with, and may be deduced from, the identity of the host target genes which VGAM2195 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[30697] Nucleotide sequences of the VGAM2195 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2195 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2195 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2195 are further described hereinbelow with reference to Table 1.

[30698] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2195 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[30699] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Mes-

senger 2196 (VGAM2196) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[30700] VGAM2196 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2196 was detected is described hereinabove with reference to Figs. 2-8.

[30701] VGAM2196 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Yaba-like disease virus. VGAM2196 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[30702] VGAM2196 gene, herein designated VGAM GENE, encodes a VGAM2196 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2196 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2196 precursor RNA is designated SEQ ID:2182, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2182 is located at position

11842 relative to the genome of Yaba-like disease virus.

[30703] VGAM2196 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2196 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30704] An enzyme complex designated DICER COMPLEX, dices the VGAM2196 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2196 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2196 RNA is designated SEQ ID:4907, and is provided hereinbelow with reference to the sequence listing part.

[30705] VGAM2196 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2196 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2196 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30706] VGAM2196 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2196 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2196 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2196 RNA, herein designated

VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2196 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30707] The complementary binding of VGAM2196 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2196 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2196 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2196 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[30708] It is appreciated that VGAM2196 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2196 host target genes. The mRNA of each one of this plurality of VGAM2196 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM2196 RNA, herein designated VGAM RNA, and which when bound by VGAM2196 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2196 host target proteins.

[30709] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2196 gene, herein designated VGAM GENE, on one or more VGAM2196 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30710] It is yet further appreciated that a function of VGAM2196 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2196 include diagnosis, prevention and treatment of viral infection by Yaba-like disease virus. Specific functions, and accordingly utilities, of VGAM2196 correlate with, and may be deduced from, the identity of the host target genes which VGAM2196 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[30711] Nucleotide sequences of the VGAM2196 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2196 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2196 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2196 are further described hereinbelow with reference to Table 1.

[30712] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2196 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[30713] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present

invention, referred to here as Viral Genomic Address Messenger 2197 (VGAM2197) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[30714] VGAM2197 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2197 was detected is described hereinabove with reference to Figs. 2-8.

[30715] VGAM2197 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Yaba-like disease virus. VGAM2197 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[30716] VGAM2197 gene, herein designated VGAM GENE, encodes a VGAM2197 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2197 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2197 precursor RNA is designated SEQ ID:2183, and is provided hereinbelow with reference to the sequence listing part. Nu-

cleotide sequence SEQ ID:2183 is located at position 6543 relative to the genome of Yaba-like disease virus.

[30717] VGAM2197 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2197 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30718] An enzyme complex designated DICER COMPLEX, dices the VGAM2197 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2197 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2197 RNA is designated SEQ ID:4908, and is provided hereinbelow with reference to the sequence

listing part.

[30719] VGAM2197 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2197 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2197 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30720] VGAM2197 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2197 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2197 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not

meant to be limiting VGAM2197 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2197 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30721] The complementary binding of VGAM2197 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2197 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2197 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2197 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[30722] It is appreciated that VGAM2197 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2197 host target genes. The mRNA of each one of this plurality of VGAM2197 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2197 RNA, herein designated VGAM RNA, and which when bound by VGAM2197 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2197 host target proteins.

[30723] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2197 gene, herein designated VGAM GENE, on one or more VGAM2197 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30724] It is yet further appreciated that a function of VGAM2197

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2197 include diagnosis, prevention and treatment of viral infection by Yaba-like disease virus. Specific functions, and accordingly utilities, of VGAM2197 correlate with, and may be deduced from, the identity of the host target genes which VGAM2197 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[30725] Nucleotide sequences of the VGAM2197 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2197 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2197 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2197 are further described hereinbelow with reference to Table 1.

[30726] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2197 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[30727] Fig. 1 further provides a conceptual description of another

novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2198 (VGAM2198) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[30728] VGAM2198 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2198 was detected is described hereinabove with reference to Figs. 2-8.

[30729] VGAM2198 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Yaba-like disease virus. VGAM2198 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[30730] VGAM2198 gene, herein designated VGAM GENE, encodes a VGAM2198 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2198 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2198 precursor RNA is designated SEQ ID:2184, and is provided here-

inbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2184 is located at position 22309 relative to the genome of Yaba-like disease virus.

[30731] VGAM2198 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2198 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30732] An enzyme complex designated DICER COMPLEX, dices the VGAM2198 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2198 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2198 RNA is designated SEQ ID:4909, and

is provided hereinbelow with reference to the sequence listing part.

[30733] VGAM2198 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2198 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2198 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30734] VGAM2198 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2198 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2198 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites

shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2198 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2198 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30735] The complementary binding of VGAM2198 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2198 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2198 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2198 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[30736] It is appreciated that VGAM2198 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2198 host target genes. The mRNA of each one of this plurality of VGAM2198 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2198 RNA, herein designated VGAM RNA, and which when bound by VGAM2198 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2198 host target proteins.

[30737] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2198 gene, herein designated VGAM GENE, on one or more VGAM2198 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30738] It is yet further appreciated that a function of VGAM2198 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2198 include diagnosis, prevention and treatment of viral infection by Yaba-like disease virus. Specific functions, and accordingly utilities, of VGAM2198 correlate with, and may be deduced from, the identity of the host target genes which VGAM2198 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[30739] Nucleotide sequences of the VGAM2198 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2198 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2198 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2198 are further described hereinbelow with reference to Table 1.

[30740] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2198 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[30741] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2199 (VGAM2199) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[30742] VGAM2199 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2199 was detected is described hereinabove with reference to Figs. 2-8.

[30743] VGAM2199 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Yaba-like disease virus. VGAM2199 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[30744] VGAM2199 gene, herein designated VGAM GENE, encodes a VGAM2199 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2199 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2199 precur-

sor RNA is designated SEQ ID:2185, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2185 is located at position 3375 relative to the genome of Yaba-like disease virus.

[30745] VGAM2199 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2199 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30746] An enzyme complex designated DICER COMPLEX, dices the VGAM2199 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2199 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide se-

quence of VGAM2199 RNA is designated SEQ ID:4910, and is provided hereinbelow with reference to the sequence listing part.

[30747] VGAM2199 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2199 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2199 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30748] VGAM2199 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2199 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2199 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is ap-

preciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2199 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2199 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30749] The complementary binding of VGAM2199 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2199 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2199 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2199 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[30750] It is appreciated that VGAM2199 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2199 host target genes. The mRNA of

each one of this plurality of VGAM2199 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2199 RNA, herein designated VGAM RNA, and which when bound by VGAM2199 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2199 host target proteins.

[30751] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2199 gene, herein designated VGAM GENE, on one or more VGAM2199 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science

294,779 (2001)).

[30752] It is yet further appreciated that a function of VGAM2199 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2199 include diagnosis, prevention and treatment of viral infection by Yaba-like disease virus. Specific functions, and accordingly utilities, of VGAM2199 correlate with, and may be deduced from, the identity of the host target genes which VGAM2199 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[30753] Nucleotide sequences of the VGAM2199 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2199 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2199 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2199 are further described hereinbelow with reference to Table 1.

[30754] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2199 RNA, herein designated VGAM RNA, are de-

scribed hereinbelow with reference to Table 2.

[30755] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2200 (VGAM2200) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[30756] VGAM2200 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2200 was detected is described hereinabove with reference to Figs. 2-8.

[30757] VGAM2200 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cowpox virus.
VGAM2200 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[30758] VGAM2200 gene, herein designated VGAM GENE, encodes a VGAM2200 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2200 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly

similar to the nucleotide sequence of VGAM2200 precursor RNA is designated SEQ ID:2186, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2186 is located at position 184637 relative to the genome of Cowpox virus.

[30759] VGAM2200 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2200 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30760] An enzyme complex designated DICER COMPLEX, dices the VGAM2200 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2200 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 70%) nucleotide sequence of VGAM2200 RNA is designated SEQ ID:4911, and is provided hereinbelow with reference to the sequence listing part.

[30761] VGAM2200 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2200 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2200 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30762] VGAM2200 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2200 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2200 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I,

BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2200 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2200 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30763] The complementary binding of VGAM2200 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2200 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2200 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2200 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[30764] It is appreciated that VGAM2200 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM2200 host target genes. The mRNA of each one of this plurality of VGAM2200 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2200 RNA, herein designated VGAM RNA, and which when bound by VGAM2200 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2200 host target proteins.

[30765] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2200 gene, herein designated VGAM GENE, on one or more VGAM2200 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30766] It is yet further appreciated that a function of VGAM2200 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2200 include diagnosis, prevention and treatment of viral infection by Cowpox virus. Specific functions, and accordingly utilities, of VGAM2200 correlate with, and may be deduced from, the identity of the host target genes which VGAM2200 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[30767] Nucleotide sequences of the VGAM2200 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2200 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2200 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2200 are further described hereinbelow with reference to Table 1.

[30768] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites

to VGAM2200 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[30769] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2201 (VGAM2201) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[30770] VGAM2201 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2201 was detected is described hereinabove with reference to Figs. 2-8.

[30771] VGAM2201 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cowpox virus.
VGAM2201 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[30772] VGAM2201 gene, herein designated VGAM GENE, encodes a VGAM2201 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2201 precursor RNA, herein designated VGAM PRECURSOR RNA, does not en-

code a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2201 precursor RNA is designated SEQ ID:2187, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2187 is located at position 185848 relative to the genome of Cowpox virus.

[30773] VGAM2201 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2201 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30774] An enzyme complex designated DICER COMPLEX, dices the VGAM2201 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2201 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2201 RNA is designated SEQ ID:4912, and is provided hereinbelow with reference to the sequence listing part.

[30775] VGAM2201 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2201 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2201 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30776] VGAM2201 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2201 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2201 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3

such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2201 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2201 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30777] The complementary binding of VGAM2201 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2201 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2201 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2201 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[30778] It is appreciated that VGAM2201 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2201 host target genes. The mRNA of each one of this plurality of VGAM2201 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2201 RNA, herein designated VGAM RNA, and which when bound by VGAM2201 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2201 host target proteins.

[30779] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2201 gene, herein designated VGAM GENE, on one or more VGAM2201 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30780] It is yet further appreciated that a function of VGAM2201 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2201 include diagnosis, prevention and treatment of viral infection by Cowpox virus. Specific functions, and accordingly utilities, of VGAM2201 correlate with, and may be deduced from, the identity of the host target genes which VGAM2201 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[30781] Nucleotide sequences of the VGAM2201 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2201 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2201 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2201 are further described hereinbelow with reference to Table 1.

[30782] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the

complementarity of each of these host target binding sites to VGAM2201 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[30783] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2202 (VGAM2202) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[30784] VGAM2202 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2202 was detected is described hereinabove with reference to Figs. 2-8.

[30785] VGAM2202 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Camelpox virus. VGAM2202 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[30786] VGAM2202 gene, herein designated VGAM GENE, encodes a VGAM2202 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2202 precursor RNA,

herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2202 precursor RNA is designated SEQ ID:2188, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2188 is located at position 162506 relative to the genome of Camelpox virus.

[30787] VGAM2202 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2202 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30788] An enzyme complex designated DICER COMPLEX, dices the VGAM2202 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2202 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of VGAM2202 RNA is designated SEQ ID:4913, and is provided hereinbelow with reference to the sequence listing part.

[30789] VGAM2202 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2202 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2202 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30790] VGAM2202 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2202 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2202 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host

target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2202 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2202 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30791] The complementary binding of VGAM2202 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2202 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2202 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2202 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[30792] It is appreciated that VGAM2202 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2202 host target genes. The mRNA of each one of this plurality of VGAM2202 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2202 RNA, herein designated VGAM RNA, and which when bound by VGAM2202 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2202 host target proteins.

[30793] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2202 gene, herein designated VGAM GENE, on one or more VGAM2202 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30794] It is yet further appreciated that a function of VGAM2202 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2202 include diagnosis, prevention and treatment of viral infection by Camelpox virus. Specific functions, and accordingly utilities, of VGAM2202 correlate with, and may be deduced from, the identity of the host target genes which VGAM2202 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[30795] Nucleotide sequences of the VGAM2202 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2202 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2202 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2202 are further described hereinbelow with reference to Table 1.

[30796] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2202 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[30797] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2203 (VGAM2203) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[30798] VGAM2203 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2203 was detected is described hereinabove with reference to Figs. 2-8.

[30799] VGAM2203 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cowpox virus. VGAM2203 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[30800] VGAM2203 gene, herein designated VGAM GENE, encodes a VGAM2203 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and un-

like most ordinary genes, VGAM2203 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2203 precursor RNA is designated SEQ ID:2189, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2189 is located at position 173794 relative to the genome of Cowpox virus.

[30801] VGAM2203 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2203 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30802] An enzyme complex designated DICER COMPLEX, dices the VGAM2203 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2203 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2203 RNA is designated SEQ ID:4914, and is provided hereinbelow with reference to the sequence listing part.

[30803] VGAM2203 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2203 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2203 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30804] VGAM2203 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2203 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2203 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed

sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2203 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2203 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30805] The complementary binding of VGAM2203 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2203 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2203 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2203 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target

protein is therefore outlined by a broken line.

[30806] It is appreciated that VGAM2203 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2203 host target genes. The mRNA of each one of this plurality of VGAM2203 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2203 RNA, herein designated VGAM RNA, and which when bound by VGAM2203 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2203 host target proteins.

[30807] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2203 gene, herein designated VGAM GENE, on one or more VGAM2203 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30808] It is yet further appreciated that a function of VGAM2203 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2203 include diagnosis, prevention and treatment of viral infection by Cowpox virus. Specific functions, and accordingly utilities, of VGAM2203 correlate with, and may be deduced from, the identity of the host target genes which VGAM2203 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[30809] Nucleotide sequences of the VGAM2203 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2203 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2203 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2203 are further described hereinbelow with reference to Table 1.

[30810] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2203 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[30811] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2204 (VGAM2204) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[30812] VGAM2204 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2204 was detected is described hereinabove with reference to Figs. 2-8.

[30813] VGAM2204 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cowpox virus.
VGAM2204 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[30814] VGAM2204 gene, herein designated VGAM GENE, encodes a VGAM2204 precursor RNA, herein designated VGAM

PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2204 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2204 precursor RNA is designated SEQ ID:2190, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2190 is located at position 183474 relative to the genome of Cowpox virus.

[30815] VGAM2204 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2204 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30816] An enzyme complex designated DICER COMPLEX, dices the VGAM2204 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2204 RNA, herein designated VGAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2204 RNA is designated SEQ ID:4915, and is provided hereinbelow with reference to the sequence listing part.

[30817] VGAM2204 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2204 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2204 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30818] VGAM2204 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2204 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2204 RNA, herein designated

VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2204 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2204 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30819] The complementary binding of VGAM2204 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2204 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2204 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2204 host target protein, herein desig-

nated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[30820] It is appreciated that VGAM2204 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2204 host target genes. The mRNA of each one of this plurality of VGAM2204 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2204 RNA, herein designated VGAM RNA, and which when bound by VGAM2204 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2204 host target proteins.

[30821] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2204 gene, herein designated VGAM GENE, on one or more VGAM2204 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30822] It is yet further appreciated that a function of VGAM2204 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2204 include diagnosis, prevention and treatment of viral infection by Cowpox virus. Specific functions, and accordingly utilities, of VGAM2204 correlate with, and may be deduced from, the identity of the host target genes which VGAM2204 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[30823] Nucleotide sequences of the VGAM2204 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2204 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2204 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2204 are further described hereinbelow with reference to Table 1.

[30824] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2204 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[30825] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2205 (VGAM2205) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[30826] VGAM2205 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2205 was detected is described hereinabove with reference to Figs. 2-8.

[30827] VGAM2205 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cowpox virus.
VGAM2205 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[30828] VGAM2205 gene, herein designated VGAM GENE, encodes

a VGAM2205 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2205 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2205 precursor RNA is designated SEQ ID:2191, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2191 is located at position 188975 relative to the genome of Cowpox virus.

[30829] VGAM2205 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2205 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30830] An enzyme complex designated DICER COMPLEX, dices the VGAM2205 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2205 RNA,

herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2205 RNA is designated SEQ ID:4916, and is provided hereinbelow with reference to the sequence listing part.

[30831] VGAM2205 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2205 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2205 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30832] VGAM2205 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2205 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM2205 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2205 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2205 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30833] The complementary binding of VGAM2205 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2205 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2205 host target RNA, herein designated VGAM HOST TARGET

RNA, into VGAM2205 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[30834] It is appreciated that VGAM2205 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2205 host target genes. The mRNA of each one of this plurality of VGAM2205 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2205 RNA, herein designated VGAM RNA, and which when bound by VGAM2205 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2205 host target proteins.

[30835] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2205 gene, herein designated VGAM GENE, on one or more VGAM2205 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30836] It is yet further appreciated that a function of VGAM2205 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2205 include diagnosis, prevention and treatment of viral infection by Cowpox virus. Specific functions, and accordingly utilities, of VGAM2205 correlate with, and may be deduced from, the identity of the host target genes which VGAM2205 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[30837] Nucleotide sequences of the VGAM2205 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2205 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2205 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2205 are further

described hereinbelow with reference to Table 1.

[30838] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2205 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[30839] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2206 (VGAM2206) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[30840] VGAM2206 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2206 was detected is described hereinabove with reference to Figs. 2-8.

[30841] VGAM2206 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cowpox virus.
VGAM2206 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[30842] VGAM2206 gene, herein designated VGAM GENE, encodes a VGAM2206 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2206 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2206 precursor RNA is designated SEQ ID:2192, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2192 is located at position 178296 relative to the genome of Cowpox virus.

[30843] VGAM2206 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2206 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30844] An enzyme complex designated DICER COMPLEX, dices the VGAM2206 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, into VGAM2206 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 63%) nucleotide sequence of VGAM2206 RNA is designated SEQ ID:4917, and is provided hereinbelow with reference to the sequence listing part.

[30845] VGAM2206 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2206 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2206 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30846] VGAM2206 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2206 host target RNA, herein designated VGAM HOST TARGET RNA. This

complementary binding is due to the fact that the nucleotide sequence of VGAM2206 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2206 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2206 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30847] The complementary binding of VGAM2206 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2206 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2206

host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2206 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[30848] It is appreciated that VGAM2206 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2206 host target genes. The mRNA of each one of this plurality of VGAM2206 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2206 RNA, herein designated VGAM RNA, and which when bound by VGAM2206 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2206 host target proteins.

[30849] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2206 gene, herein designated VGAM GENE, on one or more VGAM2206 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30850] It is yet further appreciated that a function of VGAM2206 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2206 include diagnosis, prevention and treatment of viral infection by Cowpox virus. Specific functions, and accordingly utilities, of VGAM2206 correlate with, and may be deduced from, the identity of the host target genes which VGAM2206 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[30851] Nucleotide sequences of the VGAM2206 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2206 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2206 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM2206 are further described hereinbelow with reference to Table 1.

[30852] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2206 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[30853] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2207 (VGAM2207) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[30854] VGAM2207 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2207 was detected is described hereinabove with reference to Figs. 2-8.

[30855] VGAM2207 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Myxoma virus. VGAM2207 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the

human genome.

[30856] VGAM2207 gene, herein designated VGAM GENE, encodes a VGAM2207 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2207 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2207 precursor RNA is designated SEQ ID:2193, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2193 is located at position 11555 relative to the genome of Myxoma virus.

[30857] VGAM2207 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2207 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30858] An enzyme complex designated DICER COMPLEX, dices

the VGAM2207 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2207 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2207 RNA is designated SEQ ID:4918, and is provided hereinbelow with reference to the sequence listing part.

[30859] VGAM2207 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2207 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2207 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30860] VGAM2207 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2207 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2207 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2207 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2207 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30861] The complementary binding of VGAM2207 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2207 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM2207 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2207 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[30862] It is appreciated that VGAM2207 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2207 host target genes. The mRNA of each one of this plurality of VGAM2207 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2207 RNA, herein designated VGAM RNA, and which when bound by VGAM2207 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2207 host target proteins.

[30863] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2207 gene, herein designated VGAM GENE, on one or more VGAM2207 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30864] It is yet further appreciated that a function of VGAM2207 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2207 include diagnosis, prevention and treatment of viral infection by Myxoma virus. Specific functions, and accordingly utilities, of VGAM2207 correlate with, and may be deduced from, the identity of the host target genes which VGAM2207 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[30865] Nucleotide sequences of the VGAM2207 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2207 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of

VGAM2207 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2207 are further described hereinbelow with reference to Table 1.

[30866] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2207 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[30867] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2208 (VGAM2208) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[30868] VGAM2208 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2208 was detected is described hereinabove with reference to Figs. 2-8.

[30869] VGAM2208 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Myxoma virus. VGAM2208 host target gene, herein designated VGAM

HOST TARGET GENE, is a human gene contained in the human genome.

[30870] VGAM2208 gene, herein designated VGAM GENE, encodes a VGAM2208 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2208 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2208 precursor RNA is designated SEQ ID:2194, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2194 is located at position 21539 relative to the genome of Myxoma virus.

[30871] VGAM2208 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2208 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30872] An enzyme complex designated DICER COMPLEX, dices the VGAM2208 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2208 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2208 RNA is designated SEQ ID:4919, and is provided hereinbelow with reference to the sequence listing part.

[30873] VGAM2208 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2208 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2208 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30874] VGAM2208 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites

located in untranslated regions of VGAM2208 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2208 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2208 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2208 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30875] The complementary binding of VGAM2208 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2208 host target RNA, herein designated VGAM

HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2208 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2208 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[30876] It is appreciated that VGAM2208 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2208 host target genes. The mRNA of each one of this plurality of VGAM2208 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2208 RNA, herein designated VGAM RNA, and which when bound by VGAM2208 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2208 host target proteins.

[30877] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2208 gene, herein designated VGAM GENE, on one or more VGAM2208 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove

with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30878] It is yet further appreciated that a function of VGAM2208 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2208 include diagnosis, prevention and treatment of viral infection by Myxoma virus. Specific functions, and accordingly utilities, of VGAM2208 correlate with, and may be deduced from, the identity of the host target genes which VGAM2208 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[30879] Nucleotide sequences of the VGAM2208 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2208 RNA, herein designated VGAM RNA, and

a schematic representation of the secondary folding of VGAM2208 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2208 are further described hereinbelow with reference to Table 1.

[30880] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2208 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[30881] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2209 (VGAM2209) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[30882] VGAM2209 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2209 was detected is described hereinabove with reference to Figs. 2-8.

[30883] VGAM2209 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Myxoma virus.

VGAM2209 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[30884] VGAM2209 gene, herein designated VGAM GENE, encodes a VGAM2209 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2209 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2209 precursor RNA is designated SEQ ID:2195, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2195 is located at position 1250 relative to the genome of Myxoma virus.

[30885] VGAM2209 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2209 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[30886] An enzyme complex designated DICER COMPLEX, dices the VGAM2209 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2209 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2209 RNA is designated SEQ ID:4920, and is provided hereinbelow with reference to the sequence listing part.

[30887] VGAM2209 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2209 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2209 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30888] VGAM2209 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM2209 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2209 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2209 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2209 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30889] The complementary binding of VGAM2209 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM2209 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2209 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2209 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[30890] It is appreciated that VGAM2209 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2209 host target genes. The mRNA of each one of this plurality of VGAM2209 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2209 RNA, herein designated VGAM RNA, and which when bound by VGAM2209 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2209 host target proteins.

[30891] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2209 gene, herein designated VGAM GENE, on one or more VGAM2209 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30892] It is yet further appreciated that a function of VGAM2209 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2209 include diagnosis, prevention and treatment of viral infection by Myxoma virus. Specific functions, and accordingly utilities, of VGAM2209 correlate with, and may be deduced from, the identity of the host target genes which VGAM2209 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[30893] Nucleotide sequences of the VGAM2209 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

diced VGAM2209 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2209 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2209 are further described hereinbelow with reference to Table 1.

[30894] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2209 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[30895] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2210 (VGAM2210) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[30896] VGAM2210 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2210 was detected is described hereinabove with reference to Figs. 2-8.

[30897] VGAM2210 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of Myxoma virus. VGAM2210 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[30898] VGAM2210 gene, herein designated VGAM GENE, encodes a VGAM2210 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2210 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2210 precursor RNA is designated SEQ ID:2196, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2196 is located at position 12338 relative to the genome of Myxoma virus.

[30899] VGAM2210 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2210 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30900] An enzyme complex designated DICER COMPLEX, dices the VGAM2210 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2210 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2210 RNA is designated SEQ ID:4921, and is provided hereinbelow with reference to the sequence listing part.

[30901] VGAM2210 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2210 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2210 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30902] VGAM2210 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2210 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2210 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2210 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2210 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30903] The complementary binding of VGAM2210 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM2210 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2210 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2210 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[30904] It is appreciated that VGAM2210 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2210 host target genes. The mRNA of each one of this plurality of VGAM2210 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2210 RNA, herein designated VGAM RNA, and which when bound by VGAM2210 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2210 host target proteins.

[30905] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2210 gene, herein designated VGAM GENE, on one or more VGAM2210 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30906] It is yet further appreciated that a function of VGAM2210 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2210 include diagnosis, prevention and treatment of viral infection by Myxoma virus. Specific functions, and accordingly utilities, of VGAM2210 correlate with, and may be deduced from, the identity of the host target genes which VGAM2210 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[30907] Nucleotide sequences of the VGAM2210 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the diced VGAM2210 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2210 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2210 are further described hereinbelow with reference to Table 1.

[30908] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2210 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[30909] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2211 (VGAM2211) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[30910] VGAM2211 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2211 was detected is described hereinabove with reference to Figs. 2-8.

[30911] VGAM2211 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Myxoma virus. VGAM2211 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[30912] VGAM2211 gene, herein designated VGAM GENE, encodes a VGAM2211 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2211 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2211 precursor RNA is designated SEQ ID:2197, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2197 is located at position 17880 relative to the genome of Myxoma virus.

[30913] VGAM2211 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2211 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30914] An enzyme complex designated DICER COMPLEX, dices the VGAM2211 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2211 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2211 RNA is designated SEQ ID:4922, and is provided hereinbelow with reference to the sequence listing part.

[30915] VGAM2211 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2211 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2211 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN COD-

ING and 3UTR respectively.

[30916] VGAM2211 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2211 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2211 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2211 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2211 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30917] The complementary binding of VGAM2211 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2211 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2211 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2211 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[30918] It is appreciated that VGAM2211 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2211 host target genes. The mRNA of each one of this plurality of VGAM2211 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2211 RNA, herein designated VGAM RNA, and which when bound by VGAM2211 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2211 host target proteins.

[30919] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2211 gene, herein designated VGAM GENE, on one

or more VGAM2211 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30920] It is yet further appreciated that a function of VGAM2211 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2211 include diagnosis, prevention and treatment of viral infection by Myxoma virus. Specific functions, and accordingly utilities, of VGAM2211 correlate with, and may be deduced from, the identity of the host target genes which VGAM2211 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[30921] Nucleotide sequences of the VGAM2211 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2211 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2211 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2211 are further described hereinbelow with reference to Table 1.

[30922] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2211 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[30923] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2212 (VGAM2212) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[30924] VGAM2212 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2212 was detected is de-

scribed hereinabove with reference to Figs. 2-8.

[30925] VGAM2212 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Myxoma virus. VGAM2212 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[30926] VGAM2212 gene, herein designated VGAM GENE, encodes a VGAM2212 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2212 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2212 precursor RNA is designated SEQ ID:2198, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2198 is located at position 11366 relative to the genome of Myxoma virus.

[30927] VGAM2212 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2212 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30928] An enzyme complex designated DICER COMPLEX, dices the VGAM2212 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2212 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 66%) nucleotide sequence of VGAM2212 RNA is designated SEQ ID:4923, and is provided hereinbelow with reference to the sequence listing part.

[30929] VGAM2212 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2212 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2212 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and

a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30930] VGAM2212 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2212 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2212 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2212 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2212 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both

3UTR and 5UTR regions.

[30931] The complementary binding of VGAM2212 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2212 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2212 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2212 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[30932] It is appreciated that VGAM2212 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2212 host target genes. The mRNA of each one of this plurality of VGAM2212 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2212 RNA, herein designated VGAM RNA, and which when bound by VGAM2212 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2212 host target proteins.

[30933] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM2212 gene, herein designated VGAM GENE, on one or more VGAM2212 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30934] It is yet further appreciated that a function of VGAM2212 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2212 include diagnosis, prevention and treatment of viral infection by Myxoma virus. Specific functions, and accordingly utilities, of VGAM2212 correlate with, and may be deduced from, the identity of the host target genes which VGAM2212 binds and inhibits, and the function of these host target genes, as elaborated

hereinbelow.

[30935] Nucleotide sequences of the VGAM2212 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2212 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2212 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2212 are further described hereinbelow with reference to Table 1.

[30936] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2212 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[30937] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2213 (VGAM2213) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[30938] VGAM2213 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene.

The method by which VGAM2213 was detected is described hereinabove with reference to Figs. 2-8.

[30939] VGAM2213 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Myxoma virus. VGAM2213 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[30940] VGAM2213 gene, herein designated VGAM GENE, encodes a VGAM2213 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2213 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2213 precursor RNA is designated SEQ ID:2199, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2199 is located at position 12976 relative to the genome of Myxoma virus.

[30941] VGAM2213 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2213 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30942] An enzyme complex designated DICER COMPLEX, dices the VGAM2213 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2213 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 83%) nucleotide sequence of VGAM2213 RNA is designated SEQ ID:4924, and is provided hereinbelow with reference to the sequence listing part.

[30943] VGAM2213 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2213 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2213 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding

gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30944] VGAM2213 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2213 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2213 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2213 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2213 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be lo-

cated in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30945] The complementary binding of VGAM2213 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2213 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2213 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2213 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[30946] It is appreciated that VGAM2213 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2213 host target genes. The mRNA of each one of this plurality of VGAM2213 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2213 RNA, herein designated VGAM RNA, and which when bound by VGAM2213 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2213 host target proteins.

[30947] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM2213 gene, herein designated VGAM GENE, on one or more VGAM2213 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30948] It is yet further appreciated that a function of VGAM2213 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2213 include diagnosis, prevention and treatment of viral infection by Myxoma virus. Specific functions, and accordingly utilities, of VGAM2213 correlate with, and may be deduced from, the identity of the host target genes which VGAM2213 binds and inhibits,

and the function of these host target genes, as elaborated hereinbelow.

[30949] Nucleotide sequences of the VGAM2213 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2213 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2213 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2213 are further described hereinbelow with reference to Table 1.

[30950] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2213 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[30951] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2214 (VGAM2214) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[30952] VGAM2214 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2214 was detected is described hereinabove with reference to Figs. 2-8.

[30953] VGAM2214 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Myxoma virus. VGAM2214 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[30954] VGAM2214 gene, herein designated VGAM GENE, encodes a VGAM2214 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2214 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2214 precursor RNA is designated SEQ ID:2200, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2200 is located at position 20836 relative to the genome of Myxoma virus.

[30955] VGAM2214 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2214 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30956] An enzyme complex designated DICER COMPLEX, dices the VGAM2214 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2214 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2214 RNA is designated SEQ ID:4925, and is provided hereinbelow with reference to the sequence listing part.

[30957] VGAM2214 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2214 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2214 host target RNA, herein designated VGAM HOST TARGET RNA, comprises

three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30958] VGAM2214 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2214 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2214 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2214 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2214 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an

example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30959] The complementary binding of VGAM2214 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2214 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2214 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2214 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[30960] It is appreciated that VGAM2214 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2214 host target genes. The mRNA of each one of this plurality of VGAM2214 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2214 RNA, herein designated VGAM RNA, and which when bound by VGAM2214 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2214 host target proteins.

[30961] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2214 gene, herein designated VGAM GENE, on one or more VGAM2214 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30962] It is yet further appreciated that a function of VGAM2214 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2214 include diagnosis, prevention and treatment of viral infection by Myxoma virus. Specific functions, and accordingly utilities, of VGAM2214 correlate with, and may be deduced from, the identity of the

host target genes which VGAM2214 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[30963] Nucleotide sequences of the VGAM2214 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2214 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2214 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2214 are further described hereinbelow with reference to Table 1.

[30964] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2214 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[30965] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2215 (VGAM2215) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[30966] VGAM2215 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2215 was detected is described hereinabove with reference to Figs. 2-8.

[30967] VGAM2215 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia virus. VGAM2215 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[30968] VGAM2215 gene, herein designated VGAM GENE, encodes a VGAM2215 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2215 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2215 precursor RNA is designated SEQ ID:2201, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2201 is located at position 9138 relative to the genome of Ectromelia virus.

[30969] VGAM2215 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2215 folded precursor RNA, herein designated VGAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30970] An enzyme complex designated DICER COMPLEX, dices the VGAM2215 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2215 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide sequence of VGAM2215 RNA is designated SEQ ID:4926, and is provided hereinbelow with reference to the sequence listing part.

[30971] VGAM2215 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2215 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2215 host target RNA,

herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30972] VGAM2215 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2215 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2215 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2215 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2215 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host tar-

get binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30973] The complementary binding of VGAM2215 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2215 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2215 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2215 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[30974] It is appreciated that VGAM2215 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2215 host target genes. The mRNA of each one of this plurality of VGAM2215 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2215 RNA, herein designated VGAM RNA, and which when bound by VGAM2215 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2215 host target proteins.

[30975] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2215 gene, herein designated VGAM GENE, on one or more VGAM2215 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30976] It is yet further appreciated that a function of VGAM2215 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2215 include diagnosis, prevention and treatment of viral infection by Ectromelia virus. Specific functions, and accordingly utilities, of VGAM2215 corre-

late with, and may be deduced from, the identity of the host target genes which VGAM2215 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[30977] Nucleotide sequences of the VGAM2215 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2215 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2215 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2215 are further described hereinbelow with reference to Table 1.

[30978] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2215 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[30979] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2216 (VGAM2216) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the

art.

[30980] VGAM2216 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2216 was detected is described hereinabove with reference to Figs. 2-8.

[30981] VGAM2216 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia virus. VGAM2216 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[30982] VGAM2216 gene, herein designated VGAM GENE, encodes a VGAM2216 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2216 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2216 precursor RNA is designated SEQ ID:2202, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2202 is located at position 192667 relative to the genome of Ectromelia virus.

[30983] VGAM2216 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2216 folded

precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30984] An enzyme complex designated DICER COMPLEX, dices the VGAM2216 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2216 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2216 RNA is designated SEQ ID:4927, and is provided hereinbelow with reference to the sequence listing part.

[30985] VGAM2216 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2216 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM2216 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30986] VGAM2216 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2216 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2216 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2216 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2216 host target RNA, herein designated VGAM HOST TARGET RNA.

It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30987] The complementary binding of VGAM2216 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2216 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2216 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2216 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[30988] It is appreciated that VGAM2216 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2216 host target genes. The mRNA of each one of this plurality of VGAM2216 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2216 RNA, herein designated VGAM RNA, and which when bound by VGAM2216 RNA, herein designated VGAM RNA, causes inhibition of translation of

respective one or more VGAM2216 host target proteins.

[30989] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2216 gene, herein designated VGAM GENE, on one or more VGAM2216 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30990] It is yet further appreciated that a function of VGAM2216 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2216 include diagnosis, prevention and treatment of viral infection by Ectromelia virus. Specific

functions, and accordingly utilities, of VGAM2216 correlate with, and may be deduced from, the identity of the host target genes which VGAM2216 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[30991] Nucleotide sequences of the VGAM2216 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2216 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2216 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2216 are further described hereinbelow with reference to Table 1.

[30992] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2216 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[30993] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2217 (VGAM2217) viral gene, which modulates expression of respective host target genes thereof, the func-

tion and utility of which host target genes is known in the art.

[30994] VGAM2217 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2217 was detected is described hereinabove with reference to Figs. 2-8.

[30995] VGAM2217 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia virus. VGAM2217 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[30996] VGAM2217 gene, herein designated VGAM GENE, encodes a VGAM2217 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2217 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2217 precursor RNA is designated SEQ ID:2203, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2203 is located at position 198184 relative to the genome of Ectromelia virus.

[30997] VGAM2217 precursor RNA, herein designated VGAM PRE-

CURSOR RNA, folds onto itself, forming VGAM2217 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30998] An enzyme complex designated DICER COMPLEX, dices the VGAM2217 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2217 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2217 RNA is designated SEQ ID:4928, and is provided hereinbelow with reference to the sequence listing part.

[30999] VGAM2217 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM2217 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2217 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31000] VGAM2217 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2217 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2217 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2217 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2217 host

target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31001] The complementary binding of VGAM2217 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2217 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2217 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2217 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[31002] It is appreciated that VGAM2217 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2217 host target genes. The mRNA of each one of this plurality of VGAM2217 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2217 RNA, herein designated VGAM RNA, and which when bound by VGAM2217 RNA, herein

designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2217 host target proteins.

[31003] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2217 gene, herein designated VGAM GENE, on one or more VGAM2217 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31004] It is yet further appreciated that a function of VGAM2217 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2217 include diagnosis, prevention and

treatment of viral infection by Ectromelia virus. Specific functions, and accordingly utilities, of VGAM2217 correlate with, and may be deduced from, the identity of the host target genes which VGAM2217 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[31005] Nucleotide sequences of the VGAM2217 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2217 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2217 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2217 are further described hereinbelow with reference to Table 1.

[31006] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2217 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[31007] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2218 (VGAM2218) viral gene, which modulates ex-

pression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[31008] VGAM2218 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2218 was detected is described hereinabove with reference to Figs. 2-8.

[31009] VGAM2218 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia virus. VGAM2218 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[31010] VGAM2218 gene, herein designated VGAM GENE, encodes a VGAM2218 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2218 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2218 precursor RNA is designated SEQ ID:2204, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2204 is located at position 188178 relative to the genome of Ectromelia virus.

[31011] VGAM2218 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2218 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31012] An enzyme complex designated DICER COMPLEX, dices the VGAM2218 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2218 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2218 RNA is designated SEQ ID:4929, and is provided hereinbelow with reference to the sequence listing part.

[31013] VGAM2218 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2218 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2218 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31014] VGAM2218 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2218 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2218 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2218 RNA, herein designated VGAM RNA, may have a different number of host target

binding sites in untranslated regions of a VGAM2218 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31015] The complementary binding of VGAM2218 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2218 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2218 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2218 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[31016] It is appreciated that VGAM2218 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2218 host target genes. The mRNA of each one of this plurality of VGAM2218 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2218 RNA, herein designated VGAM

RNA, and which when bound by VGAM2218 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2218 host target proteins.

[31017] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2218 gene, herein designated VGAM GENE, on one or more VGAM2218 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31018] It is yet further appreciated that a function of VGAM2218 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM2218 include diagnosis, prevention and treatment of viral infection by Ectromelia virus. Specific functions, and accordingly utilities, of VGAM2218 correlate with, and may be deduced from, the identity of the host target genes which VGAM2218 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[31019] Nucleotide sequences of the VGAM2218 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2218 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2218 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2218 are further described hereinbelow with reference to Table 1.

[31020] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2218 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[31021] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Mes-

senger 2219 (VGAM2219) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[31022] VGAM2219 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2219 was detected is described hereinabove with reference to Figs. 2-8.

[31023] VGAM2219 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia virus. VGAM2219 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[31024] VGAM2219 gene, herein designated VGAM GENE, encodes a VGAM2219 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2219 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2219 precursor RNA is designated SEQ ID:2205, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2205 is located at position

190763 relative to the genome of Ectromelia virus.

[31025] VGAM2219 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2219 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31026] An enzyme complex designated DICER COMPLEX, dices the VGAM2219 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2219 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 51%) nucleotide sequence of VGAM2219 RNA is designated SEQ ID:4930, and is provided hereinbelow with reference to the sequence listing part.

[31027] VGAM2219 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2219 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2219 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31028] VGAM2219 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2219 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2219 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2219 RNA, herein designated

VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2219 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31029] The complementary binding of VGAM2219 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2219 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2219 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2219 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[31030] It is appreciated that VGAM2219 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2219 host target genes. The mRNA of each one of this plurality of VGAM2219 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM2219 RNA, herein designated VGAM RNA, and which when bound by VGAM2219 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2219 host target proteins.

[31031] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2219 gene, herein designated VGAM GENE, on one or more VGAM2219 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31032] It is yet further appreciated that a function of VGAM2219 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2219 include diagnosis, prevention and treatment of viral infection by Ectromelia virus. Specific functions, and accordingly utilities, of VGAM2219 correlate with, and may be deduced from, the identity of the host target genes which VGAM2219 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[31033] Nucleotide sequences of the VGAM2219 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2219 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2219 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2219 are further described hereinbelow with reference to Table 1.

[31034] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2219 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[31035] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present

invention, referred to here as Viral Genomic Address Messenger 2220 (VGAM2220) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[31036] VGAM2220 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2220 was detected is described hereinabove with reference to Figs. 2-8.

[31037] VGAM2220 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia virus. VGAM2220 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[31038] VGAM2220 gene, herein designated VGAM GENE, encodes a VGAM2220 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2220 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2220 precursor RNA is designated SEQ ID:2206, and is provided hereinbelow with reference to the sequence listing part. Nu-

cleotide sequence SEQ ID:2206 is located at position 196292 relative to the genome of Ectromelia virus.

[31039] VGAM2220 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2220 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31040] An enzyme complex designated DICER COMPLEX, dices the VGAM2220 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2220 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2220 RNA is designated SEQ ID:4931, and is provided hereinbelow with reference to the sequence

listing part.

[31041] VGAM2220 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2220 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2220 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31042] VGAM2220 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2220 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2220 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not

meant to be limiting VGAM2220 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2220 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31043] The complementary binding of VGAM2220 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2220 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2220 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2220 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[31044] It is appreciated that VGAM2220 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2220 host target genes. The mRNA of each one of this plurality of VGAM2220 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2220 RNA, herein designated VGAM RNA, and which when bound by VGAM2220 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2220 host target proteins.

[31045] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2220 gene, herein designated VGAM GENE, on one or more VGAM2220 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31046] It is yet further appreciated that a function of VGAM2220

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2220 include diagnosis, prevention and treatment of viral infection by Ectromelia virus. Specific functions, and accordingly utilities, of VGAM2220 correlate with, and may be deduced from, the identity of the host target genes which VGAM2220 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[31047] Nucleotide sequences of the VGAM2220 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2220 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2220 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2220 are further described hereinbelow with reference to Table 1.

[31048] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2220 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[31049] Fig. 1 further provides a conceptual description of another

novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2221 (VGAM2221) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[31050] VGAM2221 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2221 was detected is described hereinabove with reference to Figs. 2-8.

[31051] VGAM2221 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine herpesvirus 2. VGAM2221 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[31052] VGAM2221 gene, herein designated VGAM GENE, encodes a VGAM2221 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2221 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2221 precursor RNA is designated SEQ ID:2207, and is provided here-

inbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2207 is located at position 161928 relative to the genome of Equine herpesvirus 2.

[31053] VGAM2221 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2221 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31054] An enzyme complex designated DICER COMPLEX, dices the VGAM2221 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2221 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 82%) nucleotide sequence of VGAM2221 RNA is designated SEQ ID:4932, and

is provided hereinbelow with reference to the sequence listing part.

[31055] VGAM2221 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2221 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2221 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31056] VGAM2221 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2221 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2221 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites

shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2221 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2221 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31057] The complementary binding of VGAM2221 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2221 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2221 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2221 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[31058] It is appreciated that VGAM2221 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2221 host target genes. The mRNA of each one of this plurality of VGAM2221 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2221 RNA, herein designated VGAM RNA, and which when bound by VGAM2221 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2221 host target proteins.

[31059] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2221 gene, herein designated VGAM GENE, on one or more VGAM2221 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31060] It is yet further appreciated that a function of VGAM2221 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2221 include diagnosis, prevention and treatment of viral infection by Equine herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2221 correlate with, and may be deduced from, the identity of the host target genes which VGAM2221 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[31061] Nucleotide sequences of the VGAM2221 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2221 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2221 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2221 are further described hereinbelow with reference to Table 1.

[31062] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2221 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[31063] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2222 (VGAM2222) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[31064] VGAM2222 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2222 was detected is described hereinabove with reference to Figs. 2-8.

[31065] VGAM2222 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine herpesvirus 2. VGAM2222 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[31066] VGAM2222 gene, herein designated VGAM GENE, encodes a VGAM2222 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2222 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2222 precur-

sor RNA is designated SEQ ID:2208, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2208 is located at position 11521 relative to the genome of Equine herpesvirus 2.

[31067] VGAM2222 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2222 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31068] An enzyme complex designated DICER COMPLEX, dices the VGAM2222 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2222 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 61%) nucleotide se-

quence of VGAM2222 RNA is designated SEQ ID:4933, and is provided hereinbelow with reference to the sequence listing part.

[31069] VGAM2222 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2222 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2222 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31070] VGAM2222 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2222 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2222 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is ap-

preciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2222 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2222 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31071] The complementary binding of VGAM2222 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2222 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2222 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2222 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[31072] It is appreciated that VGAM2222 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2222 host target genes. The mRNA of

each one of this plurality of VGAM2222 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2222 RNA, herein designated VGAM RNA, and which when bound by VGAM2222 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2222 host target proteins.

[31073] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2222 gene, herein designated VGAM GENE, on one or more VGAM2222 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science

294,779 (2001)).

[31074] It is yet further appreciated that a function of VGAM2222 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2222 include diagnosis, prevention and treatment of viral infection by Equine herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2222 correlate with, and may be deduced from, the identity of the host target genes which VGAM2222 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[31075] Nucleotide sequences of the VGAM2222 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2222 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2222 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2222 are further described hereinbelow with reference to Table 1.

[31076] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2222 RNA, herein designated VGAM RNA, are de-

scribed hereinbelow with reference to Table 2.

[31077] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2223 (VGAM2223) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[31078] VGAM2223 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2223 was detected is described hereinabove with reference to Figs. 2-8.

[31079] VGAM2223 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine herpesvirus 2. VGAM2223 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[31080] VGAM2223 gene, herein designated VGAM GENE, encodes a VGAM2223 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2223 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly

similar to the nucleotide sequence of VGAM2223 precursor RNA is designated SEQ ID:2209, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2209 is located at position 2065 relative to the genome of Equine herpesvirus 2.

[31081] VGAM2223 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2223 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31082] An enzyme complex designated DICER COMPLEX, dices the VGAM2223 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2223 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 47%) nucleotide sequence of VGAM2223 RNA is designated SEQ ID:4934, and is provided hereinbelow with reference to the sequence listing part.

[31083] VGAM2223 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2223 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2223 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31084] VGAM2223 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2223 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2223 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I,

BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2223 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2223 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31085] The complementary binding of VGAM2223 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2223 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2223 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2223 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[31086] It is appreciated that VGAM2223 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM2223 host target genes. The mRNA of each one of this plurality of VGAM2223 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2223 RNA, herein designated VGAM RNA, and which when bound by VGAM2223 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2223 host target proteins.

[31087] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2223 gene, herein designated VGAM GENE, on one or more VGAM2223 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31088] It is yet further appreciated that a function of VGAM2223 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2223 include diagnosis, prevention and treatment of viral infection by Equine herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2223 correlate with, and may be deduced from, the identity of the host target genes which VGAM2223 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[31089] Nucleotide sequences of the VGAM2223 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2223 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2223 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2223 are further described hereinbelow with reference to Table 1.

[31090] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites

to VGAM2223 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[31091] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2224 (VGAM2224) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[31092] VGAM2224 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2224 was detected is described hereinabove with reference to Figs. 2-8.

[31093] VGAM2224 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine herpesvirus 2. VGAM2224 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[31094] VGAM2224 gene, herein designated VGAM GENE, encodes a VGAM2224 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2224 precursor RNA, herein designated VGAM PRECURSOR RNA, does not en-

code a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2224 precursor RNA is designated SEQ ID:2210, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2210 is located at position 2628 relative to the genome of Equine herpesvirus 2.

[31095] VGAM2224 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2224 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31096] An enzyme complex designated DICER COMPLEX, dices the VGAM2224 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2224 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 52%) nucleotide sequence of VGAM2224 RNA is designated SEQ ID:4935, and is provided hereinbelow with reference to the sequence listing part.

[31097] VGAM2224 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2224 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2224 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31098] VGAM2224 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2224 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2224 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3

such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2224 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2224 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31099] The complementary binding of VGAM2224 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2224 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2224 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2224 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[31100] It is appreciated that VGAM2224 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2224 host target genes. The mRNA of each one of this plurality of VGAM2224 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2224 RNA, herein designated VGAM RNA, and which when bound by VGAM2224 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2224 host target proteins.

[31101] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2224 gene, herein designated VGAM GENE, on one or more VGAM2224 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31102] It is yet further appreciated that a function of VGAM2224 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2224 include diagnosis, prevention and treatment of viral infection by Equine herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2224 correlate with, and may be deduced from, the identity of the host target genes which VGAM2224 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[31103] Nucleotide sequences of the VGAM2224 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2224 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2224 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2224 are further described hereinbelow with reference to Table 1.

[31104] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the

complementarity of each of these host target binding sites to VGAM2224 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[31105] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2225 (VGAM2225) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[31106] VGAM2225 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2225 was detected is described hereinabove with reference to Figs. 2-8.

[31107] VGAM2225 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine herpesvirus 2. VGAM2225 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[31108] VGAM2225 gene, herein designated VGAM GENE, encodes a VGAM2225 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2225 precursor RNA,

herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2225 precursor RNA is designated SEQ ID:2211, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2211 is located at position 9536 relative to the genome of Equine herpesvirus 2.

[31109] VGAM2225 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2225 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31110] An enzyme complex designated DICER COMPLEX, dices the VGAM2225 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2225 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2225 RNA is designated SEQ ID:4936, and is provided hereinbelow with reference to the sequence listing part.

[31111] VGAM2225 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2225 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2225 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31112] VGAM2225 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2225 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2225 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host

target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2225 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2225 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31113] The complementary binding of VGAM2225 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2225 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2225 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2225 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[31114] It is appreciated that VGAM2225 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2225 host target genes. The mRNA of each one of this plurality of VGAM2225 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2225 RNA, herein designated VGAM RNA, and which when bound by VGAM2225 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2225 host target proteins.

[31115] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2225 gene, herein designated VGAM GENE, on one or more VGAM2225 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31116] It is yet further appreciated that a function of VGAM2225 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2225 include diagnosis, prevention and treatment of viral infection by Equine herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2225 correlate with, and may be deduced from, the identity of the host target genes which VGAM2225 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[31117] Nucleotide sequences of the VGAM2225 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2225 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2225 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2225 are further described hereinbelow with reference to Table 1.

[31118] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2225 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[31119] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2226 (VGAM2226) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[31120] VGAM2226 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2226 was detected is described hereinabove with reference to Figs. 2-8.

[31121] VGAM2226 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine herpesvirus 2. VGAM2226 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[31122] VGAM2226 gene, herein designated VGAM GENE, encodes a VGAM2226 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and un-

like most ordinary genes, VGAM2226 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2226 precursor RNA is designated SEQ ID:2212, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2212 is located at position 161798 relative to the genome of Equine herpesvirus 2.

[31123] VGAM2226 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2226 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31124] An enzyme complex designated DICER COMPLEX, dices the VGAM2226 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2226 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2226 RNA is designated SEQ ID:4937, and is provided hereinbelow with reference to the sequence listing part.

[31125] VGAM2226 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2226 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2226 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31126] VGAM2226 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2226 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2226 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed

sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2226 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2226 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31127] The complementary binding of VGAM2226 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2226 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2226 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2226 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target

protein is therefore outlined by a broken line.

[31128] It is appreciated that VGAM2226 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2226 host target genes. The mRNA of each one of this plurality of VGAM2226 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2226 RNA, herein designated VGAM RNA, and which when bound by VGAM2226 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2226 host target proteins.

[31129] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2226 gene, herein designated VGAM GENE, on one or more VGAM2226 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31130] It is yet further appreciated that a function of VGAM2226 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2226 include diagnosis, prevention and treatment of viral infection by Equine herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2226 correlate with, and may be deduced from, the identity of the host target genes which VGAM2226 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[31131] Nucleotide sequences of the VGAM2226 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2226 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2226 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2226 are further described hereinbelow with reference to Table 1.

[31132] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2226 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[31133] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2227 (VGAM2227) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[31134] VGAM2227 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2227 was detected is described hereinabove with reference to Figs. 2-8.

[31135] VGAM2227 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine herpesvirus 2. VGAM2227 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[31136] VGAM2227 gene, herein designated VGAM GENE, encodes a VGAM2227 precursor RNA, herein designated VGAM

PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2227 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2227 precursor RNA is designated SEQ ID:2213, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2213 is located at position 161250 relative to the genome of Equine herpesvirus 2.

[31137] VGAM2227 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2227 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31138] An enzyme complex designated DICER COMPLEX, dices the VGAM2227 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2227 RNA, herein designated VGAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2227 RNA is designated SEQ ID:4938, and is provided hereinbelow with reference to the sequence listing part.

[31139] VGAM2227 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2227 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2227 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31140] VGAM2227 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2227 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2227 RNA, herein designated

VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2227 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2227 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31141] The complementary binding of VGAM2227 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2227 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2227 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2227 host target protein, herein desig-

nated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[31142] It is appreciated that VGAM2227 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2227 host target genes. The mRNA of each one of this plurality of VGAM2227 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2227 RNA, herein designated VGAM RNA, and which when bound by VGAM2227 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2227 host target proteins.

[31143] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2227 gene, herein designated VGAM GENE, on one or more VGAM2227 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31144] It is yet further appreciated that a function of VGAM2227 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2227 include diagnosis, prevention and treatment of viral infection by Equine herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2227 correlate with, and may be deduced from, the identity of the host target genes which VGAM2227 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[31145] Nucleotide sequences of the VGAM2227 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2227 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2227 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2227 are further described hereinbelow with reference to Table 1.

[31146] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2227 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[31147] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2228 (VGAM2228) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[31148] VGAM2228 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2228 was detected is described hereinabove with reference to Figs. 2-8.

[31149] VGAM2228 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine herpesvirus 2. VGAM2228 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[31150] VGAM2228 gene, herein designated VGAM GENE, encodes

a VGAM2228 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2228 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2228 precursor RNA is designated SEQ ID:2214, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2214 is located at position 162465 relative to the genome of Equine herpesvirus 2.

[31151] VGAM2228 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2228 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31152] An enzyme complex designated DICER COMPLEX, dices the VGAM2228 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2228 RNA,

herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2228 RNA is designated SEQ ID:4939, and is provided hereinbelow with reference to the sequence listing part.

[31153] VGAM2228 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2228 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2228 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31154] VGAM2228 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2228 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM2228 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2228 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2228 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31155] The complementary binding of VGAM2228 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2228 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2228 host target RNA, herein designated VGAM HOST TARGET

RNA, into VGAM2228 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[31156] It is appreciated that VGAM2228 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2228 host target genes. The mRNA of each one of this plurality of VGAM2228 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2228 RNA, herein designated VGAM RNA, and which when bound by VGAM2228 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2228 host target proteins.

[31157] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2228 gene, herein designated VGAM GENE, on one or more VGAM2228 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31158] It is yet further appreciated that a function of VGAM2228 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2228 include diagnosis, prevention and treatment of viral infection by Equine herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2228 correlate with, and may be deduced from, the identity of the host target genes which VGAM2228 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[31159] Nucleotide sequences of the VGAM2228 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2228 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2228 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2228 are further

described hereinbelow with reference to Table 1.

[31160] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2228 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[31161] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2229 (VGAM2229) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[31162] VGAM2229 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2229 was detected is described hereinabove with reference to Figs. 2-8.

[31163] VGAM2229 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Potato aucuba mosaic virus. VGAM2229 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[31164] VGAM2229 gene, herein designated VGAM GENE, encodes a VGAM2229 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2229 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2229 precursor RNA is designated SEQ ID:2215, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2215 is located at position 827 relative to the genome of Potato aucuba mosaic virus.

[31165] VGAM2229 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2229 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31166] An enzyme complex designated DICER COMPLEX, dices the VGAM2229 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, into VGAM2229 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of VGAM2229 RNA is designated SEQ ID:4940, and is provided hereinbelow with reference to the sequence listing part.

[31167] VGAM2229 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2229 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2229 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31168] VGAM2229 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2229 host target RNA, herein designated VGAM HOST TARGET RNA. This

complementary binding is due to the fact that the nucleotide sequence of VGAM2229 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2229 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2229 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31169] The complementary binding of VGAM2229 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2229 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2229

host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2229 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[31170] It is appreciated that VGAM2229 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2229 host target genes. The mRNA of each one of this plurality of VGAM2229 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2229 RNA, herein designated VGAM RNA, and which when bound by VGAM2229 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2229 host target proteins.

[31171] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2229 gene, herein designated VGAM GENE, on one or more VGAM2229 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31172] It is yet further appreciated that a function of VGAM2229 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2229 include diagnosis, prevention and treatment of viral infection by Potato aucuba mosaic virus. Specific functions, and accordingly utilities, of VGAM2229 correlate with, and may be deduced from, the identity of the host target genes which VGAM2229 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[31173] Nucleotide sequences of the VGAM2229 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2229 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2229 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM2229 are further described hereinbelow with reference to Table 1.

[31174] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2229 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[31175] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2230 (VGAM2230) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[31176] VGAM2230 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2230 was detected is described hereinabove with reference to Figs. 2-8.

[31177] VGAM2230 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Potato aucuba mosaic virus. VGAM2230 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in

the human genome.

[31178] VGAM2230 gene, herein designated VGAM GENE, encodes a VGAM2230 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2230 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2230 precursor RNA is designated SEQ ID:2216, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2216 is located at position 1300 relative to the genome of Potato aucuba mosaic virus.

[31179] VGAM2230 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2230 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31180] An enzyme complex designated DICER COMPLEX, dices

the VGAM2230 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2230 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2230 RNA is designated SEQ ID:4941, and is provided hereinbelow with reference to the sequence listing part.

[31181] VGAM2230 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2230 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2230 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31182] VGAM2230 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2230 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2230 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2230 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2230 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31183] The complementary binding of VGAM2230 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2230 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM2230 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2230 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[31184] It is appreciated that VGAM2230 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2230 host target genes. The mRNA of each one of this plurality of VGAM2230 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2230 RNA, herein designated VGAM RNA, and which when bound by VGAM2230 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2230 host target proteins.

[31185] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2230 gene, herein designated VGAM GENE, on one or more VGAM2230 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31186] It is yet further appreciated that a function of VGAM2230 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2230 include diagnosis, prevention and treatment of viral infection by Potato aucuba mosaic virus. Specific functions, and accordingly utilities, of VGAM2230 correlate with, and may be deduced from, the identity of the host target genes which VGAM2230 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[31187] Nucleotide sequences of the VGAM2230 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2230 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of

VGAM2230 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2230 are further described hereinbelow with reference to Table 1.

[31188] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2230 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[31189] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2231 (VGAM2231) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[31190] VGAM2231 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2231 was detected is described hereinabove with reference to Figs. 2-8.

[31191] VGAM2231 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Potato aucuba mosaic virus. VGAM2231 host target gene, herein designated

VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[31192] VGAM2231 gene, herein designated VGAM GENE, encodes a VGAM2231 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2231 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2231 precursor RNA is designated SEQ ID:2217, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2217 is located at position 1079 relative to the genome of Potato aucuba mosaic virus.

[31193] VGAM2231 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2231 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31194] An enzyme complex designated DICER COMPLEX, dices the VGAM2231 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2231 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2231 RNA is designated SEQ ID:4942, and is provided hereinbelow with reference to the sequence listing part.

[31195] VGAM2231 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2231 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2231 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31196] VGAM2231 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites

located in untranslated regions of VGAM2231 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2231 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2231 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2231 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31197] The complementary binding of VGAM2231 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2231 host target RNA, herein designated VGAM

HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2231 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2231 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[31198] It is appreciated that VGAM2231 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2231 host target genes. The mRNA of each one of this plurality of VGAM2231 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2231 RNA, herein designated VGAM RNA, and which when bound by VGAM2231 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2231 host target proteins.

[31199] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2231 gene, herein designated VGAM GENE, on one or more VGAM2231 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove

with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31200] It is yet further appreciated that a function of VGAM2231 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2231 include diagnosis, prevention and treatment of viral infection by Potato aucuba mosaic virus. Specific functions, and accordingly utilities, of VGAM2231 correlate with, and may be deduced from, the identity of the host target genes which VGAM2231 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[31201] Nucleotide sequences of the VGAM2231 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2231 RNA, herein designated VGAM RNA, and

a schematic representation of the secondary folding of VGAM2231 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2231 are further described hereinbelow with reference to Table 1.

[31202] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2231 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[31203] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2232 (VGAM2232) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[31204] VGAM2232 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2232 was detected is described hereinabove with reference to Figs. 2-8.

[31205] VGAM2232 gene, herein designated VGAM GENE, is a viral gene contained in the genome of porcine epidemic diar-

rhea virus. VGAM2232 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[31206] VGAM2232 gene, herein designated VGAM GENE, encodes a VGAM2232 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2232 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2232 precursor RNA is designated SEQ ID:2218, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2218 is located at position 2170 relative to the genome of porcine epidemic diarrhea virus.

[31207] VGAM2232 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2232 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[31208] An enzyme complex designated DICER COMPLEX, dices the VGAM2232 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2232 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2232 RNA is designated SEQ ID:4943, and is provided hereinbelow with reference to the sequence listing part.

[31209] VGAM2232 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2232 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2232 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31210] VGAM2232 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM2232 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2232 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2232 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2232 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31211] The complementary binding of VGAM2232 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM2232 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2232 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2232 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[31212] It is appreciated that VGAM2232 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2232 host target genes. The mRNA of each one of this plurality of VGAM2232 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2232 RNA, herein designated VGAM RNA, and which when bound by VGAM2232 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2232 host target proteins.

[31213] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2232 gene, herein designated VGAM GENE, on one or more VGAM2232 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31214] It is yet further appreciated that a function of VGAM2232 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2232 include diagnosis, prevention and treatment of viral infection by porcine epidemic diarrhea virus. Specific functions, and accordingly utilities, of VGAM2232 correlate with, and may be deduced from, the identity of the host target genes which VGAM2232 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[31215] Nucleotide sequences of the VGAM2232 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

diced VGAM2232 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2232 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2232 are further described hereinbelow with reference to Table 1.

[31216] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2232 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[31217] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2233 (VGAM2233) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[31218] VGAM2233 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2233 was detected is described hereinabove with reference to Figs. 2-8.

[31219] VGAM2233 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of porcine epidemic diarrhea virus. VGAM2233 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[31220] VGAM2233 gene, herein designated VGAM GENE, encodes a VGAM2233 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2233 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2233 precursor RNA is designated SEQ ID:2219, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2219 is located at position 17365 relative to the genome of porcine epidemic diarrhea virus.

[31221] VGAM2233 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2233 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31222] An enzyme complex designated DICER COMPLEX, dices the VGAM2233 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2233 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2233 RNA is designated SEQ ID:4944, and is provided hereinbelow with reference to the sequence listing part.

[31223] VGAM2233 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2233 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2233 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN COD-

ING and 3UTR respectively.

[31224] VGAM2233 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2233 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2233 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2233 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2233 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31225] The complementary binding of VGAM2233 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2233 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2233 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2233 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[31226] It is appreciated that VGAM2233 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2233 host target genes. The mRNA of each one of this plurality of VGAM2233 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2233 RNA, herein designated VGAM RNA, and which when bound by VGAM2233 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2233 host target proteins.

[31227] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2233 gene, herein designated VGAM GENE, on one

or more VGAM2233 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31228] It is yet further appreciated that a function of VGAM2233 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2233 include diagnosis, prevention and treatment of viral infection by porcine epidemic diarrhea virus. Specific functions, and accordingly utilities, of VGAM2233 correlate with, and may be deduced from, the identity of the host target genes which VGAM2233 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[31229] Nucleotide sequences of the VGAM2233 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2233 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2233 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2233 are further described hereinbelow with reference to Table 1.

[31230] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2233 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[31231] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2234 (VGAM2234) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[31232] VGAM2234 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2234 was detected is de-

scribed hereinabove with reference to Figs. 2-8.

[31233] VGAM2234 gene, herein designated VGAM GENE, is a viral gene contained in the genome of porcine epidemic diarrhea virus. VGAM2234 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[31234] VGAM2234 gene, herein designated VGAM GENE, encodes a VGAM2234 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2234 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2234 precursor RNA is designated SEQ ID:2220, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2220 is located at position 15172 relative to the genome of porcine epidemic diarrhea virus.

[31235] VGAM2234 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2234 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31236] An enzyme complex designated DICER COMPLEX, dices the VGAM2234 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2234 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2234 RNA is designated SEQ ID:4945, and is provided hereinbelow with reference to the sequence listing part.

[31237] VGAM2234 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2234 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2234 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding

gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31238] VGAM2234 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2234 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2234 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2234 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2234 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be lo-

cated in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31239] The complementary binding of VGAM2234 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2234 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2234 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2234 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[31240] It is appreciated that VGAM2234 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2234 host target genes. The mRNA of each one of this plurality of VGAM2234 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2234 RNA, herein designated VGAM RNA, and which when bound by VGAM2234 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2234 host target proteins.

[31241] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM2234 gene, herein designated VGAM GENE, on one or more VGAM2234 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31242] It is yet further appreciated that a function of VGAM2234 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2234 include diagnosis, prevention and treatment of viral infection by porcine epidemic diarrhea virus. Specific functions, and accordingly utilities, of VGAM2234 correlate with, and may be deduced from, the identity of the host target genes which VGAM2234 binds

and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[31243] Nucleotide sequences of the VGAM2234 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2234 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2234 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2234 are further described hereinbelow with reference to Table 1.

[31244] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2234 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[31245] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2235 (VGAM2235) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[31246] VGAM2235 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2235 was detected is described hereinabove with reference to Figs. 2-8.

[31247] VGAM2235 gene, herein designated VGAM GENE, is a viral gene contained in the genome of porcine epidemic diarrhea virus. VGAM2235 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[31248] VGAM2235 gene, herein designated VGAM GENE, encodes a VGAM2235 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2235 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2235 precursor RNA is designated SEQ ID:2221, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2221 is located at position 19252 relative to the genome of porcine epidemic diarrhea virus.

[31249] VGAM2235 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2235 folded precursor RNA, herein designated VGAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31250] An enzyme complex designated DICER COMPLEX, dices the VGAM2235 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2235 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2235 RNA is designated SEQ ID:4946, and is provided hereinbelow with reference to the sequence listing part.

[31251] VGAM2235 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2235 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2235 host target RNA,

herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31252] VGAM2235 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2235 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2235 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2235 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2235 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host tar-

get binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31253] The complementary binding of VGAM2235 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2235 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2235 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2235 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[31254] It is appreciated that VGAM2235 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2235 host target genes. The mRNA of each one of this plurality of VGAM2235 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2235 RNA, herein designated VGAM RNA, and which when bound by VGAM2235 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2235 host target proteins.

[31255] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2235 gene, herein designated VGAM GENE, on one or more VGAM2235 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31256] It is yet further appreciated that a function of VGAM2235 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2235 include diagnosis, prevention and treatment of viral infection by porcine epidemic diarrhea virus. Specific functions, and accordingly utilities, of

VGAM2235 correlate with, and may be deduced from, the identity of the host target genes which VGAM2235 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[31257] Nucleotide sequences of the VGAM2235 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2235 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2235 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2235 are further described hereinbelow with reference to Table 1.

[31258] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2235 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[31259] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2236 (VGAM2236) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the

art.

[31260] VGAM2236 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2236 was detected is described hereinabove with reference to Figs. 2-8.

[31261] VGAM2236 gene, herein designated VGAM GENE, is a viral gene contained in the genome of porcine epidemic diarrhea virus. VGAM2236 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[31262] VGAM2236 gene, herein designated VGAM GENE, encodes a VGAM2236 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2236 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2236 precursor RNA is designated SEQ ID:2222, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2222 is located at position 3556 relative to the genome of porcine epidemic diarrhea virus.

[31263] VGAM2236 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2236 folded

precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31264] An enzyme complex designated DICER COMPLEX, dices the VGAM2236 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2236 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 66%) nucleotide sequence of VGAM2236 RNA is designated SEQ ID:4947, and is provided hereinbelow with reference to the sequence listing part.

[31265] VGAM2236 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2236 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM2236 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31266] VGAM2236 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2236 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2236 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2236 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2236 host target RNA, herein designated VGAM HOST TARGET RNA.

It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31267] The complementary binding of VGAM2236 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2236 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2236 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2236 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[31268] It is appreciated that VGAM2236 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2236 host target genes. The mRNA of each one of this plurality of VGAM2236 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2236 RNA, herein designated VGAM RNA, and which when bound by VGAM2236 RNA, herein designated VGAM RNA, causes inhibition of translation of

respective one or more VGAM2236 host target proteins.

[31269] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2236 gene, herein designated VGAM GENE, on one or more VGAM2236 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31270] It is yet further appreciated that a function of VGAM2236 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2236 include diagnosis, prevention and treatment of viral infection by porcine epidemic diarrhea

virus. Specific functions, and accordingly utilities, of VGAM2236 correlate with, and may be deduced from, the identity of the host target genes which VGAM2236 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[31271] Nucleotide sequences of the VGAM2236 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2236 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2236 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2236 are further described hereinbelow with reference to Table 1.

[31272] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2236 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[31273] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2237 (VGAM2237) viral gene, which modulates expression of respective host target genes thereof, the func-

tion and utility of which host target genes is known in the art.

[31274] VGAM2237 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2237 was detected is described hereinabove with reference to Figs. 2-8.

[31275] VGAM2237 gene, herein designated VGAM GENE, is a viral gene contained in the genome of porcine epidemic diarrhea virus. VGAM2237 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[31276] VGAM2237 gene, herein designated VGAM GENE, encodes a VGAM2237 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2237 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2237 precursor RNA is designated SEQ ID:2223, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2223 is located at position 26770 relative to the genome of porcine epidemic diarrhea virus.

[31277] VGAM2237 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2237 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31278] An enzyme complex designated DICER COMPLEX, dices the VGAM2237 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2237 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 49%) nucleotide sequence of VGAM2237 RNA is designated SEQ ID:4948, and is provided hereinbelow with reference to the sequence listing part.

[31279] VGAM2237 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2237 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2237 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31280] VGAM2237 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2237 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2237 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2237 RNA, herein designated VGAM RNA, may have a different number of host target

binding sites in untranslated regions of a VGAM2237 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31281] The complementary binding of VGAM2237 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2237 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2237 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2237 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[31282] It is appreciated that VGAM2237 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2237 host target genes. The mRNA of each one of this plurality of VGAM2237 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2237 RNA, herein designated VGAM

RNA, and which when bound by VGAM2237 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2237 host target proteins.

[31283] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2237 gene, herein designated VGAM GENE, on one or more VGAM2237 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31284] It is yet further appreciated that a function of VGAM2237 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM2237 include diagnosis, prevention and treatment of viral infection by porcine epidemic diarrhea virus. Specific functions, and accordingly utilities, of VGAM2237 correlate with, and may be deduced from, the identity of the host target genes which VGAM2237 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[31285] Nucleotide sequences of the VGAM2237 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2237 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2237 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2237 are further described hereinbelow with reference to Table 1.

[31286] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2237 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[31287] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Mes-

senger 2238 (VGAM2238) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[31288] VGAM2238 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2238 was detected is described hereinabove with reference to Figs. 2-8.

[31289] VGAM2238 gene, herein designated VGAM GENE, is a viral gene contained in the genome of porcine epidemic diarrhea virus. VGAM2238 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[31290] VGAM2238 gene, herein designated VGAM GENE, encodes a VGAM2238 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2238 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2238 precursor RNA is designated SEQ ID:2224, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2224 is located at position 7462

relative to the genome of porcine epidemic diarrhea virus.

[31291] VGAM2238 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2238 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31292] An enzyme complex designated DICER COMPLEX, dices the VGAM2238 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2238 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2238 RNA is designated SEQ ID:4949, and is provided hereinbelow with reference to the sequence listing part.

[31293] VGAM2238 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2238 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2238 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31294] VGAM2238 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2238 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2238 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2238 RNA, herein designated

VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2238 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31295] The complementary binding of VGAM2238 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2238 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2238 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2238 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[31296] It is appreciated that VGAM2238 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2238 host target genes. The mRNA of each one of this plurality of VGAM2238 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM2238 RNA, herein designated VGAM RNA, and which when bound by VGAM2238 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2238 host target proteins.

[31297] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2238 gene, herein designated VGAM GENE, on one or more VGAM2238 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31298] It is yet further appreciated that a function of VGAM2238 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2238 include diagnosis, prevention and treatment of viral infection by porcine epidemic diarrhea virus. Specific functions, and accordingly utilities, of VGAM2238 correlate with, and may be deduced from, the identity of the host target genes which VGAM2238 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[31299] Nucleotide sequences of the VGAM2238 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2238 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2238 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2238 are further described hereinbelow with reference to Table 1.

[31300] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2238 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[31301] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present

invention, referred to here as Viral Genomic Address Messenger 2239 (VGAM2239) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[31302] VGAM2239 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2239 was detected is described hereinabove with reference to Figs. 2-8.

[31303] VGAM2239 gene, herein designated VGAM GENE, is a viral gene contained in the genome of porcine epidemic diarrhea virus. VGAM2239 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[31304] VGAM2239 gene, herein designated VGAM GENE, encodes a VGAM2239 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2239 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2239 precursor RNA is designated SEQ ID:2225, and is provided hereinbelow with reference to the sequence listing part. Nu-

cleotide sequence SEQ ID:2225 is located at position 11663 relative to the genome of porcine epidemic diarrhea virus.

[31305] VGAM2239 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2239 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31306] An enzyme complex designated DICER COMPLEX, dices the VGAM2239 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2239 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 67%) nucleotide sequence of VGAM2239 RNA is designated SEQ ID:4950, and

is provided hereinbelow with reference to the sequence listing part.

[31307] VGAM2239 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2239 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2239 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31308] VGAM2239 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2239 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2239 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites

shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2239 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2239 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31309] The complementary binding of VGAM2239 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2239 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2239 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2239 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[31310] It is appreciated that VGAM2239 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2239 host target genes. The mRNA of each one of this plurality of VGAM2239 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2239 RNA, herein designated VGAM RNA, and which when bound by VGAM2239 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2239 host target proteins.

[31311] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2239 gene, herein designated VGAM GENE, on one or more VGAM2239 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31312] It is yet further appreciated that a function of VGAM2239 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2239 include diagnosis, prevention and treatment of viral infection by porcine epidemic diarrhea virus. Specific functions, and accordingly utilities, of VGAM2239 correlate with, and may be deduced from, the identity of the host target genes which VGAM2239 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[31313] Nucleotide sequences of the VGAM2239 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2239 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2239 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2239 are further described hereinbelow with reference to Table 1.

[31314] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2239 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[31315] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2240 (VGAM2240) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[31316] VGAM2240 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2240 was detected is described hereinabove with reference to Figs. 2-8.

[31317] VGAM2240 gene, herein designated VGAM GENE, is a viral gene contained in the genome of porcine epidemic diarrhea virus. VGAM2240 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[31318] VGAM2240 gene, herein designated VGAM GENE, encodes a VGAM2240 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2240 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2240 precur-

sor RNA is designated SEQ ID:2226, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2226 is located at position 27326 relative to the genome of porcine epidemic diarrhea virus.

[31319] VGAM2240 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2240 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31320] An enzyme complex designated DICER COMPLEX, dices the VGAM2240 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2240 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 77%) nucleotide sequence of VGAM2240 RNA is designated SEQ ID:4951, and is provided hereinbelow with reference to the sequence listing part.

[31321] VGAM2240 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2240 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2240 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31322] VGAM2240 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2240 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2240 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I,

BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2240 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2240 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31323] The complementary binding of VGAM2240 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2240 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2240 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2240 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[31324] It is appreciated that VGAM2240 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM2240 host target genes. The mRNA of each one of this plurality of VGAM2240 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2240 RNA, herein designated VGAM RNA, and which when bound by VGAM2240 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2240 host target proteins.

[31325] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2240 gene, herein designated VGAM GENE, on one or more VGAM2240 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31326] It is yet further appreciated that a function of VGAM2240 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2240 include diagnosis, prevention and treatment of viral infection by porcine epidemic diarrhea virus. Specific functions, and accordingly utilities, of VGAM2240 correlate with, and may be deduced from, the identity of the host target genes which VGAM2240 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[31327] Nucleotide sequences of the VGAM2240 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2240 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2240 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2240 are further described hereinbelow with reference to Table 1.

[31328] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites

to VGAM2240 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[31329] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2241 (VGAM2241) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[31330] VGAM2241 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2241 was detected is described hereinabove with reference to Figs. 2-8.

[31331] VGAM2241 gene, herein designated VGAM GENE, is a viral gene contained in the genome of porcine epidemic diarrhea virus. VGAM2241 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[31332] VGAM2241 gene, herein designated VGAM GENE, encodes a VGAM2241 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2241 precursor RNA, herein designated VGAM PRECURSOR RNA, does not en-

code a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2241 precursor RNA is designated SEQ ID:2227, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2227 is located at position 14383 relative to the genome of porcine epidemic diarrhea virus.

[31333] VGAM2241 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2241 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31334] An enzyme complex designated DICER COMPLEX, dices the VGAM2241 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2241 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2241 RNA is designated SEQ ID:4952, and is provided hereinbelow with reference to the sequence listing part.

[31335] VGAM2241 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2241 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2241 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31336] VGAM2241 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2241 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2241 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host

target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2241 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2241 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31337] The complementary binding of VGAM2241 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2241 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2241 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2241 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[31338] It is appreciated that VGAM2241 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2241 host target genes. The mRNA of each one of this plurality of VGAM2241 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2241 RNA, herein designated VGAM RNA, and which when bound by VGAM2241 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2241 host target proteins.

[31339] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2241 gene, herein designated VGAM GENE, on one or more VGAM2241 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31340] It is yet further appreciated that a function of VGAM2241 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2241 include diagnosis, prevention and treatment of viral infection by porcine epidemic diarrhea virus. Specific functions, and accordingly utilities, of VGAM2241 correlate with, and may be deduced from, the identity of the host target genes which VGAM2241 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[31341] Nucleotide sequences of the VGAM2241 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2241 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2241 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2241 are further described hereinbelow with reference to Table 1.

[31342] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2241 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[31343] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2242 (VGAM2242) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[31344] VGAM2242 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2242 was detected is described hereinabove with reference to Figs. 2-8.

[31345] VGAM2242 gene, herein designated VGAM GENE, is a viral gene contained in the genome of porcine epidemic diarrhea virus. VGAM2242 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[31346] VGAM2242 gene, herein designated VGAM GENE, encodes a VGAM2242 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and un-

like most ordinary genes, VGAM2242 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2242 precursor RNA is designated SEQ ID:2228, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2228 is located at position 2414 relative to the genome of porcine epidemic diarrhea virus.

[31347] VGAM2242 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2242 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31348] An enzyme complex designated DICER COMPLEX, dices the VGAM2242 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2242 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2242 RNA is designated SEQ ID:4953, and is provided hereinbelow with reference to the sequence listing part.

[31349] VGAM2242 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2242 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2242 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31350] VGAM2242 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2242 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2242 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed

sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2242 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2242 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31351] The complementary binding of VGAM2242 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2242 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2242 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2242 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target

protein is therefore outlined by a broken line.

[31352] It is appreciated that VGAM2242 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2242 host target genes. The mRNA of each one of this plurality of VGAM2242 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2242 RNA, herein designated VGAM RNA, and which when bound by VGAM2242 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2242 host target proteins.

[31353] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2242 gene, herein designated VGAM GENE, on one or more VGAM2242 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31354] It is yet further appreciated that a function of VGAM2242 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2242 include diagnosis, prevention and treatment of viral infection by porcine epidemic diarrhea virus. Specific functions, and accordingly utilities, of VGAM2242 correlate with, and may be deduced from, the identity of the host target genes which VGAM2242 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[31355] Nucleotide sequences of the VGAM2242 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2242 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2242 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2242 are further described hereinbelow with reference to Table 1.

[31356] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2242 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[31357] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2243 (VGAM2243) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[31358] VGAM2243 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2243 was detected is described hereinabove with reference to Figs. 2-8.

[31359] VGAM2243 gene, herein designated VGAM GENE, is a viral gene contained in the genome of porcine epidemic diarrhea virus. VGAM2243 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[31360] VGAM2243 gene, herein designated VGAM GENE, encodes a VGAM2243 precursor RNA, herein designated VGAM

PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2243 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2243 precursor RNA is designated SEQ ID:2229, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2229 is located at position 19645 relative to the genome of porcine epidemic diarrhea virus.

[31361] VGAM2243 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2243 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31362] An enzyme complex designated DICER COMPLEX, dices the VGAM2243 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2243 RNA,

herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2243 RNA is designated SEQ ID:4954, and is provided hereinbelow with reference to the sequence listing part.

[31363] VGAM2243 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2243 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2243 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31364] VGAM2243 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2243 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM2243 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2243 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2243 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31365] The complementary binding of VGAM2243 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2243 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2243 host target RNA, herein designated VGAM HOST TARGET

RNA, into VGAM2243 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[31366] It is appreciated that VGAM2243 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2243 host target genes. The mRNA of each one of this plurality of VGAM2243 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2243 RNA, herein designated VGAM RNA, and which when bound by VGAM2243 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2243 host target proteins.

[31367] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2243 gene, herein designated VGAM GENE, on one or more VGAM2243 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31368] It is yet further appreciated that a function of VGAM2243 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2243 include diagnosis, prevention and treatment of viral infection by porcine epidemic diarrhea virus. Specific functions, and accordingly utilities, of VGAM2243 correlate with, and may be deduced from, the identity of the host target genes which VGAM2243 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[31369] Nucleotide sequences of the VGAM2243 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2243 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2243 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2243 are further

described hereinbelow with reference to Table 1.

[31370] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2243 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[31371] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2244 (VGAM2244) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[31372] VGAM2244 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2244 was detected is described hereinabove with reference to Figs. 2-8.

[31373] VGAM2244 gene, herein designated VGAM GENE, is a viral gene contained in the genome of porcine epidemic diarrhea virus. VGAM2244 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[31374] VGAM2244 gene, herein designated VGAM GENE, encodes a VGAM2244 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2244 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2244 precursor RNA is designated SEQ ID:2230, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2230 is located at position 23117 relative to the genome of porcine epidemic diarrhea virus.

[31375] VGAM2244 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2244 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31376] An enzyme complex designated DICER COMPLEX, dices

the VGAM2244 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2244 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2244 RNA is designated SEQ ID:4955, and is provided hereinbelow with reference to the sequence listing part.

[31377] VGAM2244 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2244 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2244 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31378] VGAM2244 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2244 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2244 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2244 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2244 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31379] The complementary binding of VGAM2244 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2244 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM2244 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2244 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[31380] It is appreciated that VGAM2244 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2244 host target genes. The mRNA of each one of this plurality of VGAM2244 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2244 RNA, herein designated VGAM RNA, and which when bound by VGAM2244 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2244 host target proteins.

[31381] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2244 gene, herein designated VGAM GENE, on one or more VGAM2244 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31382] It is yet further appreciated that a function of VGAM2244 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2244 include diagnosis, prevention and treatment of viral infection by porcine epidemic diarrhea virus. Specific functions, and accordingly utilities, of VGAM2244 correlate with, and may be deduced from, the identity of the host target genes which VGAM2244 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[31383] Nucleotide sequences of the VGAM2244 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2244 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of

VGAM2244 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2244 are further described hereinbelow with reference to Table 1.

[31384] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2244 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[31385] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2245 (VGAM2245) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[31386] VGAM2245 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2245 was detected is described hereinabove with reference to Figs. 2-8.

[31387] VGAM2245 gene, herein designated VGAM GENE, is a viral gene contained in the genome of porcine epidemic diarrhea virus. VGAM2245 host target gene, herein desig-

nated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[31388] VGAM2245 gene, herein designated VGAM GENE, encodes a VGAM2245 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2245 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2245 precursor RNA is designated SEQ ID:2231, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2231 is located at position 11817 relative to the genome of porcine epidemic diarrhea virus.

[31389] VGAM2245 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2245 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[31390] An enzyme complex designated DICER COMPLEX, dices the VGAM2245 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2245 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2245 RNA is designated SEQ ID:4956, and is provided hereinbelow with reference to the sequence listing part.

[31391] VGAM2245 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2245 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2245 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31392] VGAM2245 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM2245 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2245 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2245 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2245 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31393] The complementary binding of VGAM2245 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM2245 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2245 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2245 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[31394] It is appreciated that VGAM2245 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2245 host target genes. The mRNA of each one of this plurality of VGAM2245 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2245 RNA, herein designated VGAM RNA, and which when bound by VGAM2245 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2245 host target proteins.

[31395] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2245 gene, herein designated VGAM GENE, on one or more VGAM2245 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31396] It is yet further appreciated that a function of VGAM2245 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2245 include diagnosis, prevention and treatment of viral infection by porcine epidemic diarrhea virus. Specific functions, and accordingly utilities, of VGAM2245 correlate with, and may be deduced from, the identity of the host target genes which VGAM2245 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[31397] Nucleotide sequences of the VGAM2245 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

diced VGAM2245 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2245 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2245 are further described hereinbelow with reference to Table 1.

[31398] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2245 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[31399] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2246 (VGAM2246) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[31400] VGAM2246 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2246 was detected is described hereinabove with reference to Figs. 2-8.

[31401] VGAM2246 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of porcine epidemic diarrhea virus. VGAM2246 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[31402] VGAM2246 gene, herein designated VGAM GENE, encodes a VGAM2246 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2246 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2246 precursor RNA is designated SEQ ID:2232, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2232 is located at position 4217 relative to the genome of porcine epidemic diarrhea virus.

[31403] VGAM2246 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2246 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31404] An enzyme complex designated DICER COMPLEX, dices the VGAM2246 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2246 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 71%) nucleotide sequence of VGAM2246 RNA is designated SEQ ID:4957, and is provided hereinbelow with reference to the sequence listing part.

[31405] VGAM2246 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2246 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2246 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31406] VGAM2246 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2246 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2246 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2246 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2246 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31407] The complementary binding of VGAM2246 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM2246 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2246 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2246 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[31408] It is appreciated that VGAM2246 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2246 host target genes. The mRNA of each one of this plurality of VGAM2246 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2246 RNA, herein designated VGAM RNA, and which when bound by VGAM2246 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2246 host target proteins.

[31409] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2246 gene, herein designated VGAM GENE, on one or more VGAM2246 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31410] It is yet further appreciated that a function of VGAM2246 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2246 include diagnosis, prevention and treatment of viral infection by porcine epidemic diarrhea virus. Specific functions, and accordingly utilities, of VGAM2246 correlate with, and may be deduced from, the identity of the host target genes which VGAM2246 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[31411] Nucleotide sequences of the VGAM2246 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the diced VGAM2246 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2246 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2246 are further described hereinbelow with reference to Table 1.

[31412] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2246 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[31413] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2247 (VGAM2247) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[31414] VGAM2247 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2247 was detected is described hereinabove with reference to Figs. 2-8.

[31415] VGAM2247 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Transmissible gastroenteritis virus. VGAM2247 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[31416] VGAM2247 gene, herein designated VGAM GENE, encodes a VGAM2247 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2247 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2247 precursor RNA is designated SEQ ID:2233, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2233 is located at position 6648 relative to the genome of Transmissible gastroenteritis virus.

[31417] VGAM2247 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2247 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31418] An enzyme complex designated DICER COMPLEX, dices the VGAM2247 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2247 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 71%) nucleotide sequence of VGAM2247 RNA is designated SEQ ID:4958, and is provided hereinbelow with reference to the sequence listing part.

[31419] VGAM2247 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2247 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2247 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and

a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31420] VGAM2247 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2247 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2247 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2247 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2247 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both

3UTR and 5UTR regions.

[31421] The complementary binding of VGAM2247 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2247 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2247 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2247 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[31422] It is appreciated that VGAM2247 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2247 host target genes. The mRNA of each one of this plurality of VGAM2247 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2247 RNA, herein designated VGAM RNA, and which when bound by VGAM2247 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2247 host target proteins.

[31423] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM2247 gene, herein designated VGAM GENE, on one or more VGAM2247 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31424] It is yet further appreciated that a function of VGAM2247 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2247 include diagnosis, prevention and treatment of viral infection by Transmissible gastroenteritis virus. Specific functions, and accordingly utilities, of VGAM2247 correlate with, and may be deduced from, the identity of the host target genes which VGAM2247 binds and inhibits, and the function of these host target genes,

as elaborated hereinbelow.

[31425] Nucleotide sequences of the VGAM2247 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2247 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2247 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2247 are further described hereinbelow with reference to Table 1.

[31426] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2247 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[31427] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2248 (VGAM2248) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[31428] VGAM2248 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene.

The method by which VGAM2248 was detected is described hereinabove with reference to Figs. 2-8.

[31429] VGAM2248 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Transmissible gastroenteritis virus. VGAM2248 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[31430] VGAM2248 gene, herein designated VGAM GENE, encodes a VGAM2248 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2248 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2248 precursor RNA is designated SEQ ID:2234, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2234 is located at position 10637 relative to the genome of Transmissible gastroenteritis virus.

[31431] VGAM2248 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2248 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31432] An enzyme complex designated DICER COMPLEX, dices the VGAM2248 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2248 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2248 RNA is designated SEQ ID:4959, and is provided hereinbelow with reference to the sequence listing part.

[31433] VGAM2248 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2248 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2248 host target RNA, herein designated VGAM HOST TARGET RNA, comprises

three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31434] VGAM2248 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2248 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2248 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2248 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2248 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an

example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31435] The complementary binding of VGAM2248 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2248 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2248 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2248 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[31436] It is appreciated that VGAM2248 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2248 host target genes. The mRNA of each one of this plurality of VGAM2248 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2248 RNA, herein designated VGAM RNA, and which when bound by VGAM2248 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2248 host target proteins.

[31437] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2248 gene, herein designated VGAM GENE, on one or more VGAM2248 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31438] It is yet further appreciated that a function of VGAM2248 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2248 include diagnosis, prevention and treatment of viral infection by Transmissible gastroenteritis virus. Specific functions, and accordingly utilities, of VGAM2248 correlate with, and may be deduced from, the

identity of the host target genes which VGAM2248 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[31439] Nucleotide sequences of the VGAM2248 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2248 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2248 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2248 are further described hereinbelow with reference to Table 1.

[31440] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2248 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[31441] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2249 (VGAM2249) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[31442] VGAM2249 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2249 was detected is described hereinabove with reference to Figs. 2-8.

[31443] VGAM2249 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Transmissible gastroenteritis virus. VGAM2249 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[31444] VGAM2249 gene, herein designated VGAM GENE, encodes a VGAM2249 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2249 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2249 precursor RNA is designated SEQ ID:2235, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2235 is located at position 7046 relative to the genome of Transmissible gastroenteritis virus.

[31445] VGAM2249 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2249 folded

precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31446] An enzyme complex designated DICER COMPLEX, dices the VGAM2249 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2249 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2249 RNA is designated SEQ ID:4960, and is provided hereinbelow with reference to the sequence listing part.

[31447] VGAM2249 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2249 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM2249 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31448] VGAM2249 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2249 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2249 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2249 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2249 host target RNA, herein designated VGAM HOST TARGET RNA.

It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31449] The complementary binding of VGAM2249 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2249 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2249 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2249 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[31450] It is appreciated that VGAM2249 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2249 host target genes. The mRNA of each one of this plurality of VGAM2249 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2249 RNA, herein designated VGAM RNA, and which when bound by VGAM2249 RNA, herein designated VGAM RNA, causes inhibition of translation of

respective one or more VGAM2249 host target proteins.

[31451] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2249 gene, herein designated VGAM GENE, on one or more VGAM2249 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31452] It is yet further appreciated that a function of VGAM2249 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2249 include diagnosis, prevention and treatment of viral infection by Transmissible gastroenteri-

tis virus. Specific functions, and accordingly utilities, of VGAM2249 correlate with, and may be deduced from, the identity of the host target genes which VGAM2249 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[31453] Nucleotide sequences of the VGAM2249 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2249 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2249 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2249 are further described hereinbelow with reference to Table 1.

[31454] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2249 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[31455] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2250 (VGAM2250) viral gene, which modulates expression of respective host target genes thereof, the func-

tion and utility of which host target genes is known in the art.

[31456] VGAM2250 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2250 was detected is described hereinabove with reference to Figs. 2-8.

[31457] VGAM2250 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Transmissible gastroenteritis virus. VGAM2250 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[31458] VGAM2250 gene, herein designated VGAM GENE, encodes a VGAM2250 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2250 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2250 precursor RNA is designated SEQ ID:2236, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2236 is located at position 14152 relative to the genome of Transmissible gastroenteritis virus.

[31459] VGAM2250 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2250 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31460] An enzyme complex designated DICER COMPLEX, dices the VGAM2250 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2250 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2250 RNA is designated SEQ ID:4961, and is provided hereinbelow with reference to the sequence listing part.

[31461] VGAM2250 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2250 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2250 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31462] VGAM2250 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2250 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2250 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2250 RNA, herein designated VGAM RNA, may have a different number of host target

binding sites in untranslated regions of a VGAM2250 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31463] The complementary binding of VGAM2250 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2250 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2250 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2250 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[31464] It is appreciated that VGAM2250 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2250 host target genes. The mRNA of each one of this plurality of VGAM2250 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2250 RNA, herein designated VGAM

RNA, and which when bound by VGAM2250 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2250 host target proteins.

[31465] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2250 gene, herein designated VGAM GENE, on one or more VGAM2250 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31466] It is yet further appreciated that a function of VGAM2250 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM2250 include diagnosis, prevention and treatment of viral infection by Transmissible gastroenteritis virus. Specific functions, and accordingly utilities, of VGAM2250 correlate with, and may be deduced from, the identity of the host target genes which VGAM2250 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[31467] Nucleotide sequences of the VGAM2250 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2250 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2250 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2250 are further described hereinbelow with reference to Table 1.

[31468] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2250 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[31469] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Mes-

senger 2251 (VGAM2251) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[31470] VGAM2251 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2251 was detected is described hereinabove with reference to Figs. 2-8.

[31471] VGAM2251 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Transmissible gastroenteritis virus. VGAM2251 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[31472] VGAM2251 gene, herein designated VGAM GENE, encodes a VGAM2251 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2251 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2251 precursor RNA is designated SEQ ID:2237, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2237 is located at position 4728

relative to the genome of Transmissible gastroenteritis virus.

[31473] VGAM2251 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2251 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31474] An enzyme complex designated DICER COMPLEX, dices the VGAM2251 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2251 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2251 RNA is designated SEQ ID:4962, and is provided hereinbelow with reference to the sequence

listing part.

[31475] VGAM2251 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2251 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2251 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31476] VGAM2251 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2251 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2251 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not

meant to be limiting VGAM2251 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2251 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31477] The complementary binding of VGAM2251 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2251 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2251 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2251 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[31478] It is appreciated that VGAM2251 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2251 host target genes. The mRNA of each one of this plurality of VGAM2251 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2251 RNA, herein designated VGAM RNA, and which when bound by VGAM2251 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2251 host target proteins.

[31479] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2251 gene, herein designated VGAM GENE, on one or more VGAM2251 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31480] It is yet further appreciated that a function of VGAM2251

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2251 include diagnosis, prevention and treatment of viral infection by Transmissible gastroenteritis virus. Specific functions, and accordingly utilities, of VGAM2251 correlate with, and may be deduced from, the identity of the host target genes which VGAM2251 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[31481] Nucleotide sequences of the VGAM2251 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2251 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2251 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2251 are further described hereinbelow with reference to Table 1.

[31482] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2251 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[31483] Fig. 1 further provides a conceptual description of another

novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2252 (VGAM2252) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[31484] VGAM2252 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2252 was detected is described hereinabove with reference to Figs. 2-8.

[31485] VGAM2252 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Transmissible gastroenteritis virus. VGAM2252 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[31486] VGAM2252 gene, herein designated VGAM GENE, encodes a VGAM2252 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2252 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2252 precursor RNA is designated SEQ ID:2238, and is provided here-

inbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2238 is located at position 9049 relative to the genome of Transmissible gastroenteritis virus.

[31487] VGAM2252 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2252 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31488] An enzyme complex designated DICER COMPLEX, dices the VGAM2252 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2252 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 87%) nucleotide se-

quence of VGAM2252 RNA is designated SEQ ID:4963, and is provided hereinbelow with reference to the sequence listing part.

[31489] VGAM2252 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2252 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2252 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31490] VGAM2252 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2252 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2252 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is ap-

preciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2252 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2252 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31491] The complementary binding of VGAM2252 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2252 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2252 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2252 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[31492] It is appreciated that VGAM2252 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2252 host target genes. The mRNA of

each one of this plurality of VGAM2252 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2252 RNA, herein designated VGAM RNA, and which when bound by VGAM2252 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2252 host target proteins.

[31493] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2252 gene, herein designated VGAM GENE, on one or more VGAM2252 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science

294,779 (2001)).

[31494] It is yet further appreciated that a function of VGAM2252 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2252 include diagnosis, prevention and treatment of viral infection by Transmissible gastroenteritis virus. Specific functions, and accordingly utilities, of VGAM2252 correlate with, and may be deduced from, the identity of the host target genes which VGAM2252 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[31495] Nucleotide sequences of the VGAM2252 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2252 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2252 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2252 are further described hereinbelow with reference to Table 1.

[31496] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2252 RNA, herein designated VGAM RNA, are de-

scribed hereinbelow with reference to Table 2.

[31497] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2253 (VGAM2253) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[31498] VGAM2253 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2253 was detected is described hereinabove with reference to Figs. 2-8.

[31499] VGAM2253 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Transmissible gastroenteritis virus. VGAM2253 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[31500] VGAM2253 gene, herein designated VGAM GENE, encodes a VGAM2253 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2253 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly

similar to the nucleotide sequence of VGAM2253 precursor RNA is designated SEQ ID:2239, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2239 is located at position 2988 relative to the genome of Transmissible gastroenteritis virus.

[31501] VGAM2253 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2253 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31502] An enzyme complex designated DICER COMPLEX, dices the VGAM2253 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2253 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 64%) nucleotide sequence of VGAM2253 RNA is designated SEQ ID:4964, and is provided hereinbelow with reference to the sequence listing part.

[31503] VGAM2253 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2253 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2253 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31504] VGAM2253 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2253 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2253 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3

such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2253 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2253 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31505] The complementary binding of VGAM2253 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2253 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2253 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2253 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[31506] It is appreciated that VGAM2253 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2253 host target genes. The mRNA of each one of this plurality of VGAM2253 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2253 RNA, herein designated VGAM RNA, and which when bound by VGAM2253 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2253 host target proteins.

[31507] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2253 gene, herein designated VGAM GENE, on one or more VGAM2253 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31508] It is yet further appreciated that a function of VGAM2253 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2253 include diagnosis, prevention and treatment of viral infection by Transmissible gastroenteritis virus. Specific functions, and accordingly utilities, of VGAM2253 correlate with, and may be deduced from, the identity of the host target genes which VGAM2253 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[31509] Nucleotide sequences of the VGAM2253 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2253 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2253 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2253 are further described hereinbelow with reference to Table 1.

[31510] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the

complementarity of each of these host target binding sites to VGAM2253 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[31511] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2254 (VGAM2254) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[31512] VGAM2254 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2254 was detected is described hereinabove with reference to Figs. 2-8.

[31513] VGAM2254 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Transmissible gastroenteritis virus. VGAM2254 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[31514] VGAM2254 gene, herein designated VGAM GENE, encodes a VGAM2254 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2254 precursor RNA,

herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2254 precursor RNA is designated SEQ ID:2240, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2240 is located at position 9818 relative to the genome of Transmissible gastroenteritis virus.

[31515] VGAM2254 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2254 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31516] An enzyme complex designated DICER COMPLEX, dices the VGAM2254 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2254 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2254 RNA is designated SEQ ID:4965, and is provided hereinbelow with reference to the sequence listing part.

[31517] VGAM2254 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2254 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2254 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31518] VGAM2254 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2254 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2254 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed

sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2254 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2254 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31519] The complementary binding of VGAM2254 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2254 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2254 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2254 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target

protein is therefore outlined by a broken line.

[31520] It is appreciated that VGAM2254 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2254 host target genes. The mRNA of each one of this plurality of VGAM2254 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2254 RNA, herein designated VGAM RNA, and which when bound by VGAM2254 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2254 host target proteins.

[31521] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2254 gene, herein designated VGAM GENE, on one or more VGAM2254 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31522] It is yet further appreciated that a function of VGAM2254 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2254 include diagnosis, prevention and treatment of viral infection by Transmissible gastroenteritis virus. Specific functions, and accordingly utilities, of VGAM2254 correlate with, and may be deduced from, the identity of the host target genes which VGAM2254 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[31523] Nucleotide sequences of the VGAM2254 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2254 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2254 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2254 are further described hereinbelow with reference to Table 1.

[31524] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2254 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[31525] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2255 (VGAM2255) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[31526] VGAM2255 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2255 was detected is described hereinabove with reference to Figs. 2-8.

[31527] VGAM2255 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Transmissible gastroenteritis virus. VGAM2255 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[31528] VGAM2255 gene, herein designated VGAM GENE, encodes a VGAM2255 precursor RNA, herein designated VGAM

PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2255 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2255 precursor RNA is designated SEQ ID:2241, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2241 is located at position 11215 relative to the genome of Transmissible gastroenteritis virus.

[31529] VGAM2255 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2255 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31530] An enzyme complex designated DICER COMPLEX, dices the VGAM2255 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2255 RNA,

herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 47%) nucleotide sequence of VGAM2255 RNA is designated SEQ ID:4966, and is provided hereinbelow with reference to the sequence listing part.

[31531] VGAM2255 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2255 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2255 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31532] VGAM2255 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2255 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM2255 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2255 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2255 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31533] The complementary binding of VGAM2255 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2255 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2255 host target RNA, herein designated VGAM HOST TARGET

RNA, into VGAM2255 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[31534] It is appreciated that VGAM2255 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2255 host target genes. The mRNA of each one of this plurality of VGAM2255 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2255 RNA, herein designated VGAM RNA, and which when bound by VGAM2255 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2255 host target proteins.

[31535] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2255 gene, herein designated VGAM GENE, on one or more VGAM2255 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31536] It is yet further appreciated that a function of VGAM2255 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2255 include diagnosis, prevention and treatment of viral infection by Transmissible gastroenteritis virus. Specific functions, and accordingly utilities, of VGAM2255 correlate with, and may be deduced from, the identity of the host target genes which VGAM2255 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[31537] Nucleotide sequences of the VGAM2255 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2255 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2255 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2255 are further

described hereinbelow with reference to Table 1.

[31538] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2255 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[31539] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2256 (VGAM2256) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[31540] VGAM2256 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2256 was detected is described hereinabove with reference to Figs. 2-8.

[31541] VGAM2256 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Oat chlorotic stunt virus. VGAM2256 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[31542] VGAM2256 gene, herein designated VGAM GENE, encodes a VGAM2256 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2256 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2256 precursor RNA is designated SEQ ID:2242, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2242 is located at position 1813 relative to the genome of Oat chlorotic stunt virus.

[31543] VGAM2256 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2256 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31544] An enzyme complex designated DICER COMPLEX, dices the VGAM2256 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, into VGAM2256 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2256 RNA is designated SEQ ID:4967, and is provided hereinbelow with reference to the sequence listing part.

[31545] VGAM2256 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2256 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2256 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31546] VGAM2256 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2256 host target RNA, herein designated VGAM HOST TARGET RNA. This

complementary binding is due to the fact that the nucleotide sequence of VGAM2256 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2256 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2256 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31547] The complementary binding of VGAM2256 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2256 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2256

host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2256 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[31548] It is appreciated that VGAM2256 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2256 host target genes. The mRNA of each one of this plurality of VGAM2256 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2256 RNA, herein designated VGAM RNA, and which when bound by VGAM2256 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2256 host target proteins.

[31549] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2256 gene, herein designated VGAM GENE, on one or more VGAM2256 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31550] It is yet further appreciated that a function of VGAM2256 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2256 include diagnosis, prevention and treatment of viral infection by Oat chlorotic stunt virus. Specific functions, and accordingly utilities, of VGAM2256 correlate with, and may be deduced from, the identity of the host target genes which VGAM2256 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[31551] Nucleotide sequences of the VGAM2256 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2256 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2256 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM2256 are further described hereinbelow with reference to Table 1.

[31552] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2256 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[31553] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2257 (VGAM2257) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[31554] VGAM2257 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2257 was detected is described hereinabove with reference to Figs. 2-8.

[31555] VGAM2257 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Oat chlorotic stunt virus. VGAM2257 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the

human genome.

[31556] VGAM2257 gene, herein designated VGAM GENE, encodes a VGAM2257 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2257 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2257 precursor RNA is designated SEQ ID:2243, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2243 is located at position 987 relative to the genome of Oat chlorotic stunt virus.

[31557] VGAM2257 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2257 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31558] An enzyme complex designated DICER COMPLEX, dices

the VGAM2257 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2257 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 71%) nucleotide sequence of VGAM2257 RNA is designated SEQ ID:4968, and is provided hereinbelow with reference to the sequence listing part.

[31559] VGAM2257 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2257 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2257 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31560] VGAM2257 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2257 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2257 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2257 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2257 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31561] The complementary binding of VGAM2257 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2257 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM2257 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2257 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[31562] It is appreciated that VGAM2257 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2257 host target genes. The mRNA of each one of this plurality of VGAM2257 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2257 RNA, herein designated VGAM RNA, and which when bound by VGAM2257 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2257 host target proteins.

[31563] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2257 gene, herein designated VGAM GENE, on one or more VGAM2257 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31564] It is yet further appreciated that a function of VGAM2257 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2257 include diagnosis, prevention and treatment of viral infection by Oat chlorotic stunt virus. Specific functions, and accordingly utilities, of VGAM2257 correlate with, and may be deduced from, the identity of the host target genes which VGAM2257 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[31565] Nucleotide sequences of the VGAM2257 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2257 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of

VGAM2257 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2257 are further described hereinbelow with reference to Table 1.

[31566] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2257 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[31567] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2258 (VGAM2258) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[31568] VGAM2258 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2258 was detected is described hereinabove with reference to Figs. 2-8.

[31569] VGAM2258 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Oat chlorotic stunt virus. VGAM2258 host target gene, herein designated VGAM

HOST TARGET GENE, is a human gene contained in the human genome.

[31570] VGAM2258 gene, herein designated VGAM GENE, encodes a VGAM2258 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2258 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2258 precursor RNA is designated SEQ ID:2244, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2244 is located at position 1727 relative to the genome of Oat chlorotic stunt virus.

[31571] VGAM2258 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2258 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31572] An enzyme complex designated DICER COMPLEX, dices the VGAM2258 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2258 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 49%) nucleotide sequence of VGAM2258 RNA is designated SEQ ID:4969, and is provided hereinbelow with reference to the sequence listing part.

[31573] VGAM2258 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2258 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2258 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31574] VGAM2258 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites

located in untranslated regions of VGAM2258 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2258 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2258 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2258 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31575] The complementary binding of VGAM2258 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2258 host target RNA, herein designated VGAM

HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2258 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2258 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[31576] It is appreciated that VGAM2258 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2258 host target genes. The mRNA of each one of this plurality of VGAM2258 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2258 RNA, herein designated VGAM RNA, and which when bound by VGAM2258 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2258 host target proteins.

[31577] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2258 gene, herein designated VGAM GENE, on one or more VGAM2258 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove

with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31578] It is yet further appreciated that a function of VGAM2258 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2258 include diagnosis, prevention and treatment of viral infection by Oat chlorotic stunt virus. Specific functions, and accordingly utilities, of VGAM2258 correlate with, and may be deduced from, the identity of the host target genes which VGAM2258 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[31579] Nucleotide sequences of the VGAM2258 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2258 RNA, herein designated VGAM RNA, and

a schematic representation of the secondary folding of VGAM2258 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2258 are further described hereinbelow with reference to Table 1.

[31580] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2258 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[31581] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2259 (VGAM2259) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[31582] VGAM2259 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2259 was detected is described hereinabove with reference to Figs. 2-8.

[31583] VGAM2259 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Alcelaphine herpesvirus

1. VGAM2259 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[31584] VGAM2259 gene, herein designated VGAM GENE, encodes a VGAM2259 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2259 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2259 precursor RNA is designated SEQ ID:2245, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2245 is located at position 30401 relative to the genome of Alcelaphine herpesvirus 1.

[31585] VGAM2259 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2259 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31586] An enzyme complex designated DICER COMPLEX, dices the VGAM2259 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2259 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 72%) nucleotide sequence of VGAM2259 RNA is designated SEQ ID:4970, and is provided hereinbelow with reference to the sequence listing part.

[31587] VGAM2259 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2259 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2259 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31588] VGAM2259 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2259 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2259 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2259 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2259 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31589] The complementary binding of VGAM2259 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM2259 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2259 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2259 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[31590] It is appreciated that VGAM2259 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2259 host target genes. The mRNA of each one of this plurality of VGAM2259 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2259 RNA, herein designated VGAM RNA, and which when bound by VGAM2259 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2259 host target proteins.

[31591] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2259 gene, herein designated VGAM GENE, on one or more VGAM2259 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31592] It is yet further appreciated that a function of VGAM2259 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2259 include diagnosis, prevention and treatment of viral infection by Alcelaphine herpesvirus 1. Specific functions, and accordingly utilities, of VGAM2259 correlate with, and may be deduced from, the identity of the host target genes which VGAM2259 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[31593] Nucleotide sequences of the VGAM2259 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the diced VGAM2259 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2259 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2259 are further described hereinbelow with reference to Table 1.

[31594] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2259 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[31595] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2260 (VGAM2260) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[31596] VGAM2260 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2260 was detected is described hereinabove with reference to Figs. 2-8.

[31597] VGAM2260 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Alcelaphine herpesvirus 1. VGAM2260 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[31598] VGAM2260 gene, herein designated VGAM GENE, encodes a VGAM2260 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2260 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2260 precursor RNA is designated SEQ ID:2246, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2246 is located at position 26713 relative to the genome of Alcelaphine herpesvirus 1.

[31599] VGAM2260 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2260 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31600] An enzyme complex designated DICER COMPLEX, dices the VGAM2260 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2260 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 62%) nucleotide sequence of VGAM2260 RNA is designated SEQ ID:4971, and is provided hereinbelow with reference to the sequence listing part.

[31601] VGAM2260 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2260 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2260 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and

a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31602] VGAM2260 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2260 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2260 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2260 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2260 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both

3UTR and 5UTR regions.

[31603] The complementary binding of VGAM2260 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2260 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2260 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2260 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[31604] It is appreciated that VGAM2260 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2260 host target genes. The mRNA of each one of this plurality of VGAM2260 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2260 RNA, herein designated VGAM RNA, and which when bound by VGAM2260 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2260 host target proteins.

[31605] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM2260 gene, herein designated VGAM GENE, on one or more VGAM2260 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31606] It is yet further appreciated that a function of VGAM2260 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2260 include diagnosis, prevention and treatment of viral infection by Alcelaphine herpesvirus 1. Specific functions, and accordingly utilities, of VGAM2260 correlate with, and may be deduced from, the identity of the host target genes which VGAM2260 binds and inhibits, and the function of these host target genes, as

elaborated hereinbelow.

[31607] Nucleotide sequences of the VGAM2260 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2260 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2260 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2260 are further described hereinbelow with reference to Table 1.

[31608] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2260 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[31609] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2261 (VGAM2261) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[31610] VGAM2261 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2261 was detected is described hereinabove with reference to Figs. 2-8.

[31611] VGAM2261 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Alcelaphine herpesvirus 1. VGAM2261 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[31612] VGAM2261 gene, herein designated VGAM GENE, encodes

a VGAM2261 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2261 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2261 precursor RNA is designated SEQ ID:2247, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2247 is located at position 24763 relative to the genome of Alcelaphine herpesvirus 1.

[31613] VGAM2261 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2261 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31614] An enzyme complex designated DICER COMPLEX, dices the VGAM2261 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, into VGAM2261 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2261 RNA is designated SEQ ID:4972, and is provided hereinbelow with reference to the sequence listing part.

[31615] VGAM2261 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2261 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2261 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31616] VGAM2261 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2261 host target RNA, herein designated VGAM HOST TARGET RNA. This

complementary binding is due to the fact that the nucleotide sequence of VGAM2261 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2261 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2261 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31617] The complementary binding of VGAM2261 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2261 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2261

host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2261 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[31618] It is appreciated that VGAM2261 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2261 host target genes. The mRNA of each one of this plurality of VGAM2261 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2261 RNA, herein designated VGAM RNA, and which when bound by VGAM2261 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2261 host target proteins.

[31619] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2261 gene, herein designated VGAM GENE, on one or more VGAM2261 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31620] It is yet further appreciated that a function of VGAM2261 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2261 include diagnosis, prevention and treatment of viral infection by Alcelaphine herpesvirus 1. Specific functions, and accordingly utilities, of VGAM2261 correlate with, and may be deduced from, the identity of the host target genes which VGAM2261 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[31621] Nucleotide sequences of the VGAM2261 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2261 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2261 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM2261 are further described hereinbelow with reference to Table 1.

[31622] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2261 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[31623] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2262 (VGAM2262) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[31624] VGAM2262 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2262 was detected is described hereinabove with reference to Figs. 2-8.

[31625] VGAM2262 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Alcelaphine herpesvirus 1. VGAM2262 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the

human genome.

[31626] VGAM2262 gene, herein designated VGAM GENE, encodes a VGAM2262 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2262 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2262 precursor RNA is designated SEQ ID:2248, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2248 is located at position 17900 relative to the genome of Alcelaphine herpesvirus 1.

[31627] VGAM2262 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2262 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31628] An enzyme complex designated DICER COMPLEX, dices the VGAM2262 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2262 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 59%) nucleotide sequence of VGAM2262 RNA is designated SEQ ID:4973, and is provided hereinbelow with reference to the sequence listing part.

[31629] VGAM2262 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2262 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2262 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31630] VGAM2262 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites

located in untranslated regions of VGAM2262 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2262 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2262 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2262 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31631] The complementary binding of VGAM2262 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2262 host target RNA, herein designated VGAM

HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2262 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2262 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[31632] It is appreciated that VGAM2262 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2262 host target genes. The mRNA of each one of this plurality of VGAM2262 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2262 RNA, herein designated VGAM RNA, and which when bound by VGAM2262 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2262 host target proteins.

[31633] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2262 gene, herein designated VGAM GENE, on one or more VGAM2262 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove

with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31634] It is yet further appreciated that a function of VGAM2262 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2262 include diagnosis, prevention and treatment of viral infection by Alcelaphine herpesvirus 1. Specific functions, and accordingly utilities, of VGAM2262 correlate with, and may be deduced from, the identity of the host target genes which VGAM2262 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[31635] Nucleotide sequences of the VGAM2262 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2262 RNA, herein designated VGAM RNA, and

a schematic representation of the secondary folding of VGAM2262 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2262 are further described hereinbelow with reference to Table 1.

[31636] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2262 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[31637] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2263 (VGAM2263) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[31638] VGAM2263 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2263 was detected is described hereinabove with reference to Figs. 2-8.

[31639] VGAM2263 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Alcelaphine herpesvirus

1. VGAM2263 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[31640] VGAM2263 gene, herein designated VGAM GENE, encodes a VGAM2263 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2263 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2263 precursor RNA is designated SEQ ID:2249, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2249 is located at position 27186 relative to the genome of Alcelaphine herpesvirus 1.

[31641] VGAM2263 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2263 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31642] An enzyme complex designated DICER COMPLEX, dices the VGAM2263 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2263 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 71%) nucleotide sequence of VGAM2263 RNA is designated SEQ ID:4974, and is provided hereinbelow with reference to the sequence listing part.

[31643] VGAM2263 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2263 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2263 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31644] VGAM2263 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2263 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2263 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2263 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2263 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31645] The complementary binding of VGAM2263 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM2263 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2263 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2263 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[31646] It is appreciated that VGAM2263 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2263 host target genes. The mRNA of each one of this plurality of VGAM2263 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2263 RNA, herein designated VGAM RNA, and which when bound by VGAM2263 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2263 host target proteins.

[31647] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2263 gene, herein designated VGAM GENE, on one or more VGAM2263 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31648] It is yet further appreciated that a function of VGAM2263 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2263 include diagnosis, prevention and treatment of viral infection by Alcelaphine herpesvirus 1. Specific functions, and accordingly utilities, of VGAM2263 correlate with, and may be deduced from, the identity of the host target genes which VGAM2263 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[31649] Nucleotide sequences of the VGAM2263 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the diced VGAM2263 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2263 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2263 are further described hereinbelow with reference to Table 1.

[31650] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2263 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[31651] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2264 (VGAM2264) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[31652] VGAM2264 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2264 was detected is described hereinabove with reference to Figs. 2-8.

[31653] VGAM2264 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Alcelaphine herpesvirus 1. VGAM2264 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[31654] VGAM2264 gene, herein designated VGAM GENE, encodes a VGAM2264 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2264 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2264 precursor RNA is designated SEQ ID:2250, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2250 is located at position 20319 relative to the genome of Alcelaphine herpesvirus 1.

[31655] VGAM2264 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2264 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31656] An enzyme complex designated DICER COMPLEX, dices the VGAM2264 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2264 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2264 RNA is designated SEQ ID:4975, and is provided hereinbelow with reference to the sequence listing part.

[31657] VGAM2264 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2264 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2264 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and

a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31658] VGAM2264 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2264 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2264 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2264 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2264 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both

3UTR and 5UTR regions.

[31659] The complementary binding of VGAM2264 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2264 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2264 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2264 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[31660] It is appreciated that VGAM2264 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2264 host target genes. The mRNA of each one of this plurality of VGAM2264 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2264 RNA, herein designated VGAM RNA, and which when bound by VGAM2264 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2264 host target proteins.

[31661] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM2264 gene, herein designated VGAM GENE, on one or more VGAM2264 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31662] It is yet further appreciated that a function of VGAM2264 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2264 include diagnosis, prevention and treatment of viral infection by Alcelaphine herpesvirus 1. Specific functions, and accordingly utilities, of VGAM2264 correlate with, and may be deduced from, the identity of the host target genes which VGAM2264 binds and inhibits, and the function of these host target genes, as

elaborated hereinbelow.

[31663] Nucleotide sequences of the VGAM2264 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2264 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2264 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2264 are further described hereinbelow with reference to Table 1.

[31664] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2264 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[31665] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2265 (VGAM2265) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[31666] VGAM2265 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene.

The method by which VGAM2265 was detected is described hereinabove with reference to Figs. 2-8.

[31667] VGAM2265 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Alcelaphine herpesvirus 1. VGAM2265 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[31668] VGAM2265 gene, herein designated VGAM GENE, encodes a VGAM2265 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2265 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2265 precursor RNA is designated SEQ ID:2251, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2251 is located at position 27645 relative to the genome of Alcelaphine herpesvirus 1.

[31669] VGAM2265 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2265 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31670] An enzyme complex designated DICER COMPLEX, dices the VGAM2265 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2265 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide sequence of VGAM2265 RNA is designated SEQ ID:4976, and is provided hereinbelow with reference to the sequence listing part.

[31671] VGAM2265 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2265 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2265 host target RNA, herein designated VGAM HOST TARGET RNA, comprises

three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31672] VGAM2265 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2265 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2265 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2265 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2265 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an

example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31673] The complementary binding of VGAM2265 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2265 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2265 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2265 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[31674] It is appreciated that VGAM2265 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2265 host target genes. The mRNA of each one of this plurality of VGAM2265 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2265 RNA, herein designated VGAM RNA, and which when bound by VGAM2265 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2265 host target proteins.

[31675] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2265 gene, herein designated VGAM GENE, on one or more VGAM2265 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31676] It is yet further appreciated that a function of VGAM2265 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2265 include diagnosis, prevention and treatment of viral infection by Alcelaphine herpesvirus 1. Specific functions, and accordingly utilities, of VGAM2265 correlate with, and may be deduced from, the identity of

the host target genes which VGAM2265 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[31677] Nucleotide sequences of the VGAM2265 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2265 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2265 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2265 are further described hereinbelow with reference to Table 1.

[31678] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2265 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[31679] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2266 (VGAM2266) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[31680] VGAM2266 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2266 was detected is described hereinabove with reference to Figs. 2-8.

[31681] VGAM2266 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Alcelaphine herpesvirus 1. VGAM2266 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[31682] VGAM2266 gene, herein designated VGAM GENE, encodes a VGAM2266 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2266 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2266 precursor RNA is designated SEQ ID:2252, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2252 is located at position 27936 relative to the genome of Alcelaphine herpesvirus 1.

[31683] VGAM2266 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2266 folded

precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31684] An enzyme complex designated DICER COMPLEX, dices the VGAM2266 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2266 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2266 RNA is designated SEQ ID:4977, and is provided hereinbelow with reference to the sequence listing part.

[31685] VGAM2266 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2266 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM2266 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31686] VGAM2266 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2266 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2266 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2266 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2266 host target RNA, herein designated VGAM HOST TARGET RNA.

It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31687] The complementary binding of VGAM2266 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2266 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2266 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2266 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[31688] It is appreciated that VGAM2266 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2266 host target genes. The mRNA of each one of this plurality of VGAM2266 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2266 RNA, herein designated VGAM RNA, and which when bound by VGAM2266 RNA, herein designated VGAM RNA, causes inhibition of translation of

respective one or more VGAM2266 host target proteins.

[31689] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2266 gene, herein designated VGAM GENE, on one or more VGAM2266 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31690] It is yet further appreciated that a function of VGAM2266 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2266 include diagnosis, prevention and treatment of viral infection by Alcelaphine herpesvirus 1.

Specific functions, and accordingly utilities, of VGAM2266 correlate with, and may be deduced from, the identity of the host target genes which VGAM2266 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[31691] Nucleotide sequences of the VGAM2266 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2266 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2266 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2266 are further described hereinbelow with reference to Table 1.

[31692] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2266 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[31693] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2267 (VGAM2267) viral gene, which modulates expression of respective host target genes thereof, the func-

tion and utility of which host target genes is known in the art.

[31694] VGAM2267 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2267 was detected is described hereinabove with reference to Figs. 2-8.

[31695] VGAM2267 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Alcelaphine herpesvirus 1. VGAM2267 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[31696] VGAM2267 gene, herein designated VGAM GENE, encodes a VGAM2267 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2267 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2267 precursor RNA is designated SEQ ID:2253, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2253 is located at position 29434 relative to the genome of Alcelaphine herpesvirus 1.

[31697] VGAM2267 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2267 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31698] An enzyme complex designated DICER COMPLEX, dices the VGAM2267 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2267 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of VGAM2267 RNA is designated SEQ ID:4978, and is provided hereinbelow with reference to the sequence listing part.

[31699] VGAM2267 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2267 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2267 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31700] VGAM2267 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2267 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2267 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2267 RNA, herein designated VGAM RNA, may have a different number of host target

binding sites in untranslated regions of a VGAM2267 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31701] The complementary binding of VGAM2267 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2267 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2267 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2267 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[31702] It is appreciated that VGAM2267 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2267 host target genes. The mRNA of each one of this plurality of VGAM2267 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2267 RNA, herein designated VGAM

RNA, and which when bound by VGAM2267 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2267 host target proteins.

[31703] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2267 gene, herein designated VGAM GENE, on one or more VGAM2267 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31704] It is yet further appreciated that a function of VGAM2267 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM2267 include diagnosis, prevention and treatment of viral infection by Alcelaphine herpesvirus 1. Specific functions, and accordingly utilities, of VGAM2267 correlate with, and may be deduced from, the identity of the host target genes which VGAM2267 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[31705] Nucleotide sequences of the VGAM2267 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2267 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2267 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2267 are further described hereinbelow with reference to Table 1.

[31706] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2267 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[31707] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Mes-

senger 2268 (VGAM2268) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[31708] VGAM2268 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2268 was detected is described hereinabove with reference to Figs. 2-8.

[31709] VGAM2268 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Alcelaphine herpesvirus 1. VGAM2268 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[31710] VGAM2268 gene, herein designated VGAM GENE, encodes a VGAM2268 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2268 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2268 precursor RNA is designated SEQ ID:2254, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2254 is located at position

29021 relative to the genome of Alcelaphine herpesvirus 1.

[31711] VGAM2268 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2268 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31712] An enzyme complex designated DICER COMPLEX, dices the VGAM2268 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2268 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2268 RNA is designated SEQ ID:4979, and is provided hereinbelow with reference to the sequence

listing part.

[31713] VGAM2268 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2268 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2268 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31714] VGAM2268 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2268 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2268 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not

meant to be limiting VGAM2268 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2268 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31715] The complementary binding of VGAM2268 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2268 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2268 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2268 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[31716] It is appreciated that VGAM2268 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2268 host target genes. The mRNA of each one of this plurality of VGAM2268 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2268 RNA, herein designated VGAM RNA, and which when bound by VGAM2268 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2268 host target proteins.

[31717] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2268 gene, herein designated VGAM GENE, on one or more VGAM2268 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31718] It is yet further appreciated that a function of VGAM2268

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2268 include diagnosis, prevention and treatment of viral infection by Alcelaphine herpesvirus 1. Specific functions, and accordingly utilities, of VGAM2268 correlate with, and may be deduced from, the identity of the host target genes which VGAM2268 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[31719] Nucleotide sequences of the VGAM2268 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2268 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2268 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2268 are further described hereinbelow with reference to Table 1.

[31720] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2268 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[31721] Fig. 1 further provides a conceptual description of another

novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2269 (VGAM2269) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[31722] VGAM2269 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2269 was detected is described hereinabove with reference to Figs. 2-8.

[31723] VGAM2269 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Alcelaphine herpesvirus 1. VGAM2269 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[31724] VGAM2269 gene, herein designated VGAM GENE, encodes a VGAM2269 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2269 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2269 precursor RNA is designated SEQ ID:2255, and is provided here-

inbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2255 is located at position 30842 relative to the genome of Alcelaphine herpesvirus 1.

[31725] VGAM2269 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2269 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31726] An enzyme complex designated DICER COMPLEX, dices the VGAM2269 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2269 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 59%) nucleotide se-

quence of VGAM2269 RNA is designated SEQ ID:4980, and is provided hereinbelow with reference to the sequence listing part.

[31727] VGAM2269 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2269 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2269 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31728] VGAM2269 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2269 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2269 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is ap-

preciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2269 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2269 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31729] The complementary binding of VGAM2269 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2269 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2269 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2269 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[31730] It is appreciated that VGAM2269 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2269 host target genes. The mRNA of

each one of this plurality of VGAM2269 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2269 RNA, herein designated VGAM RNA, and which when bound by VGAM2269 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2269 host target proteins.

[31731] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2269 gene, herein designated VGAM GENE, on one or more VGAM2269 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science

294,779 (2001)).

[31732] It is yet further appreciated that a function of VGAM2269 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2269 include diagnosis, prevention and treatment of viral infection by Alcelaphine herpesvirus 1. Specific functions, and accordingly utilities, of VGAM2269 correlate with, and may be deduced from, the identity of the host target genes which VGAM2269 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[31733] Nucleotide sequences of the VGAM2269 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2269 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2269 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2269 are further described hereinbelow with reference to Table 1.

[31734] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2269 RNA, herein designated VGAM RNA, are de-

scribed hereinbelow with reference to Table 2.

[31735] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2270 (VGAM2270) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[31736] VGAM2270 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2270 was detected is described hereinabove with reference to Figs. 2-8.

[31737] VGAM2270 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Alcelaphine herpesvirus 1. VGAM2270 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[31738] VGAM2270 gene, herein designated VGAM GENE, encodes a VGAM2270 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2270 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly

similar to the nucleotide sequence of VGAM2270 precursor RNA is designated SEQ ID:2256, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2256 is located at position 26539 relative to the genome of Alcelaphine herpesvirus 1.

[31739] VGAM2270 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2270 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31740] An enzyme complex designated DICER COMPLEX, dices the VGAM2270 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2270 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2270 RNA is designated SEQ ID:4981, and is provided hereinbelow with reference to the sequence listing part.

[31741] VGAM2270 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2270 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2270 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31742] VGAM2270 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2270 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2270 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3

such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2270 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2270 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31743] The complementary binding of VGAM2270 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2270 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2270 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2270 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[31744] It is appreciated that VGAM2270 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2270 host target genes. The mRNA of each one of this plurality of VGAM2270 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2270 RNA, herein designated VGAM RNA, and which when bound by VGAM2270 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2270 host target proteins.

[31745] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2270 gene, herein designated VGAM GENE, on one or more VGAM2270 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31746] It is yet further appreciated that a function of VGAM2270 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2270 include diagnosis, prevention and treatment of viral infection by Alcelaphine herpesvirus 1. Specific functions, and accordingly utilities, of VGAM2270 correlate with, and may be deduced from, the identity of the host target genes which VGAM2270 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[31747] Nucleotide sequences of the VGAM2270 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2270 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2270 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2270 are further described hereinbelow with reference to Table 1.

[31748] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the

complementarity of each of these host target binding sites to VGAM2270 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[31749] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2271 (VGAM2271) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[31750] VGAM2271 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2271 was detected is described hereinabove with reference to Figs. 2-8.

[31751] VGAM2271 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Alcelaphine herpesvirus 1. VGAM2271 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[31752] VGAM2271 gene, herein designated VGAM GENE, encodes a VGAM2271 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2271 precursor RNA,

herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2271 precursor RNA is designated SEQ ID:2257, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2257 is located at position 29858 relative to the genome of Alcelaphine herpesvirus 1.

[31753] VGAM2271 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2271 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31754] An enzyme complex designated DICER COMPLEX, dices the VGAM2271 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2271 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2271 RNA is designated SEQ ID:4982, and is provided hereinbelow with reference to the sequence listing part.

[31755] VGAM2271 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2271 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2271 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31756] VGAM2271 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2271 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2271 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed

sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2271 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2271 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31757] The complementary binding of VGAM2271 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2271 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2271 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2271 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target

protein is therefore outlined by a broken line.

[31758] It is appreciated that VGAM2271 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2271 host target genes. The mRNA of each one of this plurality of VGAM2271 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2271 RNA, herein designated VGAM RNA, and which when bound by VGAM2271 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2271 host target proteins.

[31759] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2271 gene, herein designated VGAM GENE, on one or more VGAM2271 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31760] It is yet further appreciated that a function of VGAM2271 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2271 include diagnosis, prevention and treatment of viral infection by Alcelaphine herpesvirus 1. Specific functions, and accordingly utilities, of VGAM2271 correlate with, and may be deduced from, the identity of the host target genes which VGAM2271 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[31761] Nucleotide sequences of the VGAM2271 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2271 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2271 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2271 are further described hereinbelow with reference to Table 1.

[31762] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2271 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[31763] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2272 (VGAM2272) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[31764] VGAM2272 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2272 was detected is described hereinabove with reference to Figs. 2-8.

[31765] VGAM2272 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Alcelaphine herpesvirus 1. VGAM2272 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[31766] VGAM2272 gene, herein designated VGAM GENE, encodes a VGAM2272 precursor RNA, herein designated VGAM

PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2272 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2272 precursor RNA is designated SEQ ID:2258, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2258 is located at position 18433 relative to the genome of Alcelaphine herpesvirus 1.

[31767] VGAM2272 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2272 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31768] An enzyme complex designated DICER COMPLEX, dices the VGAM2272 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2272 RNA,

herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2272 RNA is designated SEQ ID:4983, and is provided hereinbelow with reference to the sequence listing part.

[31769] VGAM2272 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2272 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2272 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31770] VGAM2272 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2272 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM2272 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2272 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2272 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31771] The complementary binding of VGAM2272 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2272 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2272 host target RNA, herein designated VGAM HOST TARGET

RNA, into VGAM2272 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[31772] It is appreciated that VGAM2272 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2272 host target genes. The mRNA of each one of this plurality of VGAM2272 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2272 RNA, herein designated VGAM RNA, and which when bound by VGAM2272 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2272 host target proteins.

[31773] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2272 gene, herein designated VGAM GENE, on one or more VGAM2272 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31774] It is yet further appreciated that a function of VGAM2272 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2272 include diagnosis, prevention and treatment of viral infection by Alcelaphine herpesvirus 1. Specific functions, and accordingly utilities, of VGAM2272 correlate with, and may be deduced from, the identity of the host target genes which VGAM2272 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[31775] Nucleotide sequences of the VGAM2272 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2272 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2272 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2272 are further

described hereinbelow with reference to Table 1.

[31776] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2272 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[31777] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2273 (VGAM2273) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[31778] VGAM2273 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2273 was detected is described hereinabove with reference to Figs. 2-8.

[31779] VGAM2273 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Alcelaphine herpesvirus 1. VGAM2273 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[31780] VGAM2273 gene, herein designated VGAM GENE, encodes a VGAM2273 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2273 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2273 precursor RNA is designated SEQ ID:2259, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2259 is located at position 28077 relative to the genome of Alcelaphine herpesvirus 1.

[31781] VGAM2273 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2273 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31782] An enzyme complex designated DICER COMPLEX, dices

the VGAM2273 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2273 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 81%) nucleotide sequence of VGAM2273 RNA is designated SEQ ID:4984, and is provided hereinbelow with reference to the sequence listing part.

[31783] VGAM2273 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2273 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2273 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31784] VGAM2273 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2273 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2273 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2273 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2273 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31785] The complementary binding of VGAM2273 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2273 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM2273 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2273 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[31786] It is appreciated that VGAM2273 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2273 host target genes. The mRNA of each one of this plurality of VGAM2273 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2273 RNA, herein designated VGAM RNA, and which when bound by VGAM2273 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2273 host target proteins.

[31787] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2273 gene, herein designated VGAM GENE, on one or more VGAM2273 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31788] It is yet further appreciated that a function of VGAM2273 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2273 include diagnosis, prevention and treatment of viral infection by Alcelaphine herpesvirus 1. Specific functions, and accordingly utilities, of VGAM2273 correlate with, and may be deduced from, the identity of the host target genes which VGAM2273 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[31789] Nucleotide sequences of the VGAM2273 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2273 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of

VGAM2273 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2273 are further described hereinbelow with reference to Table 1.

[31790] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2273 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[31791] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2274 (VGAM2274) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[31792] VGAM2274 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2274 was detected is described hereinabove with reference to Figs. 2-8.

[31793] VGAM2274 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Alcelaphine herpesvirus 1. VGAM2274 host target gene, herein designated VGAM

HOST TARGET GENE, is a human gene contained in the human genome.

[31794] VGAM2274 gene, herein designated VGAM GENE, encodes a VGAM2274 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2274 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2274 precursor RNA is designated SEQ ID:2260, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2260 is located at position 31577 relative to the genome of Alcelaphine herpesvirus 1.

[31795] VGAM2274 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2274 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[31796] An enzyme complex designated DICER COMPLEX, dices the VGAM2274 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2274 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2274 RNA is designated SEQ ID:4985, and is provided hereinbelow with reference to the sequence listing part.

[31797] VGAM2274 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2274 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2274 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31798] VGAM2274 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM2274 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2274 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2274 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2274 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31799] The complementary binding of VGAM2274 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM2274 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2274 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2274 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[31800] It is appreciated that VGAM2274 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2274 host target genes. The mRNA of each one of this plurality of VGAM2274 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2274 RNA, herein designated VGAM RNA, and which when bound by VGAM2274 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2274 host target proteins.

[31801] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2274 gene, herein designated VGAM GENE, on one or more VGAM2274 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31802] It is yet further appreciated that a function of VGAM2274 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2274 include diagnosis, prevention and treatment of viral infection by Alcelaphine herpesvirus 1. Specific functions, and accordingly utilities, of VGAM2274 correlate with, and may be deduced from, the identity of the host target genes which VGAM2274 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[31803] Nucleotide sequences of the VGAM2274 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

diced VGAM2274 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2274 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2274 are further described hereinbelow with reference to Table 1.

[31804] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2274 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[31805] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2275 (VGAM2275) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[31806] VGAM2275 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2275 was detected is described hereinabove with reference to Figs. 2-8.

[31807] VGAM2275 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of Alcelaphine herpesvirus 1. VGAM2275 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[31808] VGAM2275 gene, herein designated VGAM GENE, encodes a VGAM2275 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2275 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2275 precursor RNA is designated SEQ ID:2261, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2261 is located at position 30158 relative to the genome of Alcelaphine herpesvirus 1.

[31809] VGAM2275 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2275 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31810] An enzyme complex designated DICER COMPLEX, dices the VGAM2275 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2275 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2275 RNA is designated SEQ ID:4986, and is provided hereinbelow with reference to the sequence listing part.

[31811] VGAM2275 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2275 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2275 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN COD-

ING and 3UTR respectively.

[31812] VGAM2275 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2275 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2275 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2275 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2275 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31813] The complementary binding of VGAM2275 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2275 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2275 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2275 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[31814] It is appreciated that VGAM2275 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2275 host target genes. The mRNA of each one of this plurality of VGAM2275 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2275 RNA, herein designated VGAM RNA, and which when bound by VGAM2275 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2275 host target proteins.

[31815] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2275 gene, herein designated VGAM GENE, on one

or more VGAM2275 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31816] It is yet further appreciated that a function of VGAM2275 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2275 include diagnosis, prevention and treatment of viral infection by Alcelaphine herpesvirus 1. Specific functions, and accordingly utilities, of VGAM2275 correlate with, and may be deduced from, the identity of the host target genes which VGAM2275 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[31817] Nucleotide sequences of the VGAM2275 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2275 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2275 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2275 are further described hereinbelow with reference to Table 1.

[31818] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2275 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[31819] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2276 (VGAM2276) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[31820] VGAM2276 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2276 was detected is de-

scribed hereinabove with reference to Figs. 2-8.

[31821] VGAM2276 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Alcelaphine herpesvirus 1. VGAM2276 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[31822] VGAM2276 gene, herein designated VGAM GENE, encodes a VGAM2276 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2276 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2276 precursor RNA is designated SEQ ID:2262, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2262 is located at position 30027 relative to the genome of Alcelaphine herpesvirus 1.

[31823] VGAM2276 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2276 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31824] An enzyme complex designated DICER COMPLEX, dices the VGAM2276 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2276 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 60%) nucleotide sequence of VGAM2276 RNA is designated SEQ ID:4987, and is provided hereinbelow with reference to the sequence listing part.

[31825] VGAM2276 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2276 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2276 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding

gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31826] VGAM2276 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2276 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2276 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2276 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2276 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be lo-

cated in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31827] The complementary binding of VGAM2276 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2276 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2276 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2276 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[31828] It is appreciated that VGAM2276 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2276 host target genes. The mRNA of each one of this plurality of VGAM2276 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2276 RNA, herein designated VGAM RNA, and which when bound by VGAM2276 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2276 host target proteins.

[31829] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM2276 gene, herein designated VGAM GENE, on one or more VGAM2276 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31830] It is yet further appreciated that a function of VGAM2276 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2276 include diagnosis, prevention and treatment of viral infection by Alcelaphine herpesvirus 1. Specific functions, and accordingly utilities, of VGAM2276 correlate with, and may be deduced from, the identity of the host target genes which VGAM2276 binds and in-

hibits, and the function of these host target genes, as elaborated hereinbelow.

[31831] Nucleotide sequences of the VGAM2276 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2276 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2276 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2276 are further described hereinbelow with reference to Table 1.

[31832] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2276 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[31833] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2277 (VGAM2277) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[31834] VGAM2277 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2277 was detected is described hereinabove with reference to Figs. 2-8.

[31835] VGAM2277 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Alcelaphine herpesvirus 1. VGAM2277 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[31836] VGAM2277 gene, herein designated VGAM GENE, encodes a VGAM2277 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2277 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2277 precursor RNA is designated SEQ ID:2263, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2263 is located at position 27286 relative to the genome of Alcelaphine herpesvirus 1.

[31837] VGAM2277 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2277 folded precursor RNA, herein designated VGAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31838] An enzyme complex designated DICER COMPLEX, dices the VGAM2277 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2277 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2277 RNA is designated SEQ ID:4988, and is provided hereinbelow with reference to the sequence listing part.

[31839] VGAM2277 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2277 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2277 host target RNA,

herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31840] VGAM2277 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2277 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2277 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2277 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2277 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host tar-

get binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31841] The complementary binding of VGAM2277 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2277 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2277 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2277 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[31842] It is appreciated that VGAM2277 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2277 host target genes. The mRNA of each one of this plurality of VGAM2277 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2277 RNA, herein designated VGAM RNA, and which when bound by VGAM2277 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2277 host target proteins.

[31843] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2277 gene, herein designated VGAM GENE, on one or more VGAM2277 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31844] It is yet further appreciated that a function of VGAM2277 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2277 include diagnosis, prevention and treatment of viral infection by Alcelaphine herpesvirus 1. Specific functions, and accordingly utilities, of VGAM2277

correlate with, and may be deduced from, the identity of the host target genes which VGAM2277 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[31845] Nucleotide sequences of the VGAM2277 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2277 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2277 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2277 are further described hereinbelow with reference to Table 1.

[31846] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2277 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[31847] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2278 (VGAM2278) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the

art.

[31848] VGAM2278 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2278 was detected is described hereinabove with reference to Figs. 2-8.

[31849] VGAM2278 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Alcelaphine herpesvirus 1. VGAM2278 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[31850] VGAM2278 gene, herein designated VGAM GENE, encodes a VGAM2278 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2278 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2278 precursor RNA is designated SEQ ID:2264, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2264 is located at position 29724 relative to the genome of Alcelaphine herpesvirus 1.

[31851] VGAM2278 precursor RNA, herein designated VGAM PRE-

CURSOR RNA, folds onto itself, forming VGAM2278 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31852] An enzyme complex designated DICER COMPLEX, dices the VGAM2278 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2278 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2278 RNA is designated SEQ ID:4989, and is provided hereinbelow with reference to the sequence listing part.

[31853] VGAM2278 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM2278 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2278 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31854] VGAM2278 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2278 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2278 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2278 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2278 host

target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31855] The complementary binding of VGAM2278 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2278 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2278 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2278 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[31856] It is appreciated that VGAM2278 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2278 host target genes. The mRNA of each one of this plurality of VGAM2278 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2278 RNA, herein designated VGAM RNA, and which when bound by VGAM2278 RNA, herein

designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2278 host target proteins.

[31857] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2278 gene, herein designated VGAM GENE, on one or more VGAM2278 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31858] It is yet further appreciated that a function of VGAM2278 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2278 include diagnosis, prevention and

treatment of viral infection by Alcelaphine herpesvirus 1. Specific functions, and accordingly utilities, of VGAM2278 correlate with, and may be deduced from, the identity of the host target genes which VGAM2278 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[31859] Nucleotide sequences of the VGAM2278 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2278 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2278 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2278 are further described hereinbelow with reference to Table 1.

[31860] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2278 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[31861] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2279 (VGAM2279) viral gene, which modulates ex-

pression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[31862] VGAM2279 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2279 was detected is described hereinabove with reference to Figs. 2-8.

[31863] VGAM2279 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Alcelaphine herpesvirus 1. VGAM2279 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[31864] VGAM2279 gene, herein designated VGAM GENE, encodes a VGAM2279 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2279 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2279 precursor RNA is designated SEQ ID:2265, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2265 is located at position 26039 relative to the genome of Alcelaphine herpesvirus

1.

[31865] VGAM2279 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2279 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31866] An enzyme complex designated DICER COMPLEX, dices the VGAM2279 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2279 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 49%) nucleotide sequence of VGAM2279 RNA is designated SEQ ID:4990, and is provided hereinbelow with reference to the sequence listing part.

[31867] VGAM2279 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2279 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2279 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31868] VGAM2279 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2279 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2279 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2279 RNA, herein designated

VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2279 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31869] The complementary binding of VGAM2279 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2279 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2279 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2279 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[31870] It is appreciated that VGAM2279 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2279 host target genes. The mRNA of each one of this plurality of VGAM2279 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM2279 RNA, herein designated VGAM RNA, and which when bound by VGAM2279 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2279 host target proteins.

[31871] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2279 gene, herein designated VGAM GENE, on one or more VGAM2279 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31872] It is yet further appreciated that a function of VGAM2279 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2279 include diagnosis, prevention and treatment of viral infection by Alcelaphine herpesvirus 1. Specific functions, and accordingly utilities, of VGAM2279 correlate with, and may be deduced from, the identity of the host target genes which VGAM2279 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[31873] Nucleotide sequences of the VGAM2279 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2279 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2279 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2279 are further described hereinbelow with reference to Table 1.

[31874] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2279 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[31875] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present

invention, referred to here as Viral Genomic Address Messenger 2280 (VGAM2280) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[31876] VGAM2280 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2280 was detected is described hereinabove with reference to Figs. 2-8.

[31877] VGAM2280 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Alcelaphine herpesvirus 1. VGAM2280 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[31878] VGAM2280 gene, herein designated VGAM GENE, encodes a VGAM2280 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2280 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2280 precursor RNA is designated SEQ ID:2266, and is provided hereinbelow with reference to the sequence listing part. Nu-

cleotide sequence SEQ ID:2266 is located at position 27049 relative to the genome of Alcelaphine herpesvirus 1.

[31879] VGAM2280 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2280 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31880] An enzyme complex designated DICER COMPLEX, dices the VGAM2280 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2280 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2280 RNA is designated SEQ ID:4991, and

is provided hereinbelow with reference to the sequence listing part.

[31881] VGAM2280 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2280 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2280 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31882] VGAM2280 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2280 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2280 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites

shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2280 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2280 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31883] The complementary binding of VGAM2280 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2280 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2280 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2280 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[31884] It is appreciated that VGAM2280 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2280 host target genes. The mRNA of each one of this plurality of VGAM2280 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2280 RNA, herein designated VGAM RNA, and which when bound by VGAM2280 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2280 host target proteins.

[31885] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2280 gene, herein designated VGAM GENE, on one or more VGAM2280 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31886] It is yet further appreciated that a function of VGAM2280 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2280 include diagnosis, prevention and treatment of viral infection by Alcelaphine herpesvirus 1. Specific functions, and accordingly utilities, of VGAM2280 correlate with, and may be deduced from, the identity of the host target genes which VGAM2280 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[31887] Nucleotide sequences of the VGAM2280 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2280 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2280 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2280 are further described hereinbelow with reference to Table 1.

[31888] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2280 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[31889] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2281 (VGAM2281) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[31890] VGAM2281 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2281 was detected is described hereinabove with reference to Figs. 2-8.

[31891] VGAM2281 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Murine hepatitis virus. VGAM2281 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[31892] VGAM2281 gene, herein designated VGAM GENE, encodes a VGAM2281 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2281 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2281 precur-

sor RNA is designated SEQ ID:2267, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2267 is located at position 22070 relative to the genome of Murine hepatitis virus.

[31893] VGAM2281 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2281 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31894] An enzyme complex designated DICER COMPLEX, dices the VGAM2281 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2281 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide se-

quence of VGAM2281 RNA is designated SEQ ID:4992, and is provided hereinbelow with reference to the sequence listing part.

[31895] VGAM2281 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2281 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2281 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31896] VGAM2281 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2281 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2281 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is ap-

preciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2281 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2281 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31897] The complementary binding of VGAM2281 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2281 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2281 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2281 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[31898] It is appreciated that VGAM2281 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2281 host target genes. The mRNA of

each one of this plurality of VGAM2281 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2281 RNA, herein designated VGAM RNA, and which when bound by VGAM2281 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2281 host target proteins.

[31899] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2281 gene, herein designated VGAM GENE, on one or more VGAM2281 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science

294,779 (2001)).

[31900] It is yet further appreciated that a function of VGAM2281 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2281 include diagnosis, prevention and treatment of viral infection by Murine hepatitis virus. Specific functions, and accordingly utilities, of VGAM2281 correlate with, and may be deduced from, the identity of the host target genes which VGAM2281 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[31901] Nucleotide sequences of the VGAM2281 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2281 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2281 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2281 are further described hereinbelow with reference to Table 1.

[31902] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2281 RNA, herein designated VGAM RNA, are de-

scribed hereinbelow with reference to Table 2.

[31903] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2282 (VGAM2282) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[31904] VGAM2282 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2282 was detected is described hereinabove with reference to Figs. 2-8.

[31905] VGAM2282 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Murine hepatitis virus. VGAM2282 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[31906] VGAM2282 gene, herein designated VGAM GENE, encodes a VGAM2282 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2282 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly

similar to the nucleotide sequence of VGAM2282 precursor RNA is designated SEQ ID:2268, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2268 is located at position 26667 relative to the genome of Murine hepatitis virus.

[31907] VGAM2282 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2282 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31908] An enzyme complex designated DICER COMPLEX, dices the VGAM2282 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2282 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2282 RNA is designated SEQ ID:4993, and is provided hereinbelow with reference to the sequence listing part.

[31909] VGAM2282 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2282 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2282 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31910] VGAM2282 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2282 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2282 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I,

BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2282 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2282 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31911] The complementary binding of VGAM2282 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2282 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2282 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2282 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[31912] It is appreciated that VGAM2282 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM2282 host target genes. The mRNA of each one of this plurality of VGAM2282 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2282 RNA, herein designated VGAM RNA, and which when bound by VGAM2282 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2282 host target proteins.

[31913] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2282 gene, herein designated VGAM GENE, on one or more VGAM2282 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31914] It is yet further appreciated that a function of VGAM2282 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2282 include diagnosis, prevention and treatment of viral infection by Murine hepatitis virus. Specific functions, and accordingly utilities, of VGAM2282 correlate with, and may be deduced from, the identity of the host target genes which VGAM2282 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[31915] Nucleotide sequences of the VGAM2282 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2282 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2282 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2282 are further described hereinbelow with reference to Table 1.

[31916] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites

to VGAM2282 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[31917] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2283 (VGAM2283) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[31918] VGAM2283 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2283 was detected is described hereinabove with reference to Figs. 2-8.

[31919] VGAM2283 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Murine hepatitis virus. VGAM2283 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[31920] VGAM2283 gene, herein designated VGAM GENE, encodes a VGAM2283 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2283 precursor RNA, herein designated VGAM PRECURSOR RNA, does not en-

code a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2283 precursor RNA is designated SEQ ID:2269, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2269 is located at position 23988 relative to the genome of Murine hepatitis virus.

[31921] VGAM2283 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2283 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31922] An enzyme complex designated DICER COMPLEX, dices the VGAM2283 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2283 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2283 RNA is designated SEQ ID:4994, and is provided hereinbelow with reference to the sequence listing part.

[31923] VGAM2283 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2283 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2283 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31924] VGAM2283 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2283 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2283 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3

such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2283 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2283 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31925] The complementary binding of VGAM2283 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2283 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2283 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2283 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[31926] It is appreciated that VGAM2283 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2283 host target genes. The mRNA of each one of this plurality of VGAM2283 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2283 RNA, herein designated VGAM RNA, and which when bound by VGAM2283 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2283 host target proteins.

[31927] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2283 gene, herein designated VGAM GENE, on one or more VGAM2283 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31928] It is yet further appreciated that a function of VGAM2283 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2283 include diagnosis, prevention and treatment of viral infection by Murine hepatitis virus. Specific functions, and accordingly utilities, of VGAM2283 correlate with, and may be deduced from, the identity of the host target genes which VGAM2283 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[31929] Nucleotide sequences of the VGAM2283 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2283 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2283 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2283 are further described hereinbelow with reference to Table 1.

[31930] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the

complementarity of each of these host target binding sites to VGAM2283 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[31931] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2284 (VGAM2284) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[31932] VGAM2284 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2284 was detected is described hereinabove with reference to Figs. 2-8.

[31933] VGAM2284 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Murine hepatitis virus. VGAM2284 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[31934] VGAM2284 gene, herein designated VGAM GENE, encodes a VGAM2284 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2284 precursor RNA,

herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2284 precursor RNA is designated SEQ ID:2270, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2270 is located at position 22470 relative to the genome of Murine hepatitis virus.

[31935] VGAM2284 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2284 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31936] An enzyme complex designated DICER COMPLEX, dices the VGAM2284 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2284 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2284 RNA is designated SEQ ID:4995, and is provided hereinbelow with reference to the sequence listing part.

[31937] VGAM2284 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2284 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2284 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31938] VGAM2284 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2284 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2284 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host

target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2284 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2284 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31939] The complementary binding of VGAM2284 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2284 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2284 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2284 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[31940] It is appreciated that VGAM2284 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2284 host target genes. The mRNA of each one of this plurality of VGAM2284 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2284 RNA, herein designated VGAM RNA, and which when bound by VGAM2284 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2284 host target proteins.

[31941] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2284 gene, herein designated VGAM GENE, on one or more VGAM2284 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31942] It is yet further appreciated that a function of VGAM2284 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2284 include diagnosis, prevention and treatment of viral infection by Murine hepatitis virus. Specific functions, and accordingly utilities, of VGAM2284 correlate with, and may be deduced from, the identity of the host target genes which VGAM2284 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[31943] Nucleotide sequences of the VGAM2284 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2284 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2284 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2284 are further described hereinbelow with reference to Table 1.

[31944] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2284 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[31945] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2285 (VGAM2285) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[31946] VGAM2285 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2285 was detected is described hereinabove with reference to Figs. 2-8.

[31947] VGAM2285 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Murine hepatitis virus. VGAM2285 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[31948] VGAM2285 gene, herein designated VGAM GENE, encodes a VGAM2285 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and un-

like most ordinary genes, VGAM2285 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2285 precursor RNA is designated SEQ ID:2271, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2271 is located at position 13151 relative to the genome of Murine hepatitis virus.

[31949] VGAM2285 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2285 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31950] An enzyme complex designated DICER COMPLEX, dices the VGAM2285 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2285 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2285 RNA is designated SEQ ID:4996, and is provided hereinbelow with reference to the sequence listing part.

[31951] VGAM2285 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2285 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2285 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31952] VGAM2285 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2285 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2285 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed

sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2285 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2285 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31953] The complementary binding of VGAM2285 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2285 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2285 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2285 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target

protein is therefore outlined by a broken line.

[31954] It is appreciated that VGAM2285 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2285 host target genes. The mRNA of each one of this plurality of VGAM2285 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2285 RNA, herein designated VGAM RNA, and which when bound by VGAM2285 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2285 host target proteins.

[31955] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2285 gene, herein designated VGAM GENE, on one or more VGAM2285 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31956] It is yet further appreciated that a function of VGAM2285 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2285 include diagnosis, prevention and treatment of viral infection by Murine hepatitis virus. Specific functions, and accordingly utilities, of VGAM2285 correlate with, and may be deduced from, the identity of the host target genes which VGAM2285 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[31957] Nucleotide sequences of the VGAM2285 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2285 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2285 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2285 are further described hereinbelow with reference to Table 1.

[31958] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2285 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[31959] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2286 (VGAM2286) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[31960] VGAM2286 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2286 was detected is described hereinabove with reference to Figs. 2-8.

[31961] VGAM2286 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Murine hepatitis virus. VGAM2286 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[31962] VGAM2286 gene, herein designated VGAM GENE, encodes a VGAM2286 precursor RNA, herein designated VGAM

PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2286 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2286 precursor RNA is designated SEQ ID:2272, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2272 is located at position 4778 relative to the genome of Murine hepatitis virus.

[31963] VGAM2286 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2286 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31964] An enzyme complex designated DICER COMPLEX, dices the VGAM2286 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2286 RNA, herein designated VGAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 54%) nucleotide sequence of VGAM2286 RNA is designated SEQ ID:4997, and is provided hereinbelow with reference to the sequence listing part.

[31965] VGAM2286 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2286 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2286 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31966] VGAM2286 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2286 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2286 RNA, herein designated

VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2286 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2286 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31967] The complementary binding of VGAM2286 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2286 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2286 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2286 host target protein, herein desig-

nated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[31968] It is appreciated that VGAM2286 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2286 host target genes. The mRNA of each one of this plurality of VGAM2286 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2286 RNA, herein designated VGAM RNA, and which when bound by VGAM2286 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2286 host target proteins.

[31969] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2286 gene, herein designated VGAM GENE, on one or more VGAM2286 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31970] It is yet further appreciated that a function of VGAM2286 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2286 include diagnosis, prevention and treatment of viral infection by Murine hepatitis virus. Specific functions, and accordingly utilities, of VGAM2286 correlate with, and may be deduced from, the identity of the host target genes which VGAM2286 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[31971] Nucleotide sequences of the VGAM2286 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2286 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2286 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2286 are further described hereinbelow with reference to Table 1.

[31972] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2286 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[31973] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2287 (VGAM2287) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[31974] VGAM2287 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2287 was detected is described hereinabove with reference to Figs. 2-8.

[31975] VGAM2287 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Murine hepatitis virus. VGAM2287 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[31976] VGAM2287 gene, herein designated VGAM GENE, encodes

a VGAM2287 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2287 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2287 precursor RNA is designated SEQ ID:2273, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2273 is located at position 3614 relative to the genome of Murine hepatitis virus.

[31977] VGAM2287 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2287 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31978] An enzyme complex designated DICER COMPLEX, dices the VGAM2287 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2287 RNA,

herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2287 RNA is designated SEQ ID:4998, and is provided hereinbelow with reference to the sequence listing part.

[31979] VGAM2287 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2287 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2287 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31980] VGAM2287 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2287 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM2287 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2287 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2287 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31981] The complementary binding of VGAM2287 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2287 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2287 host target RNA, herein designated VGAM HOST TARGET

RNA, into VGAM2287 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[31982] It is appreciated that VGAM2287 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2287 host target genes. The mRNA of each one of this plurality of VGAM2287 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2287 RNA, herein designated VGAM RNA, and which when bound by VGAM2287 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2287 host target proteins.

[31983] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2287 gene, herein designated VGAM GENE, on one or more VGAM2287 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31984] It is yet further appreciated that a function of VGAM2287 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2287 include diagnosis, prevention and treatment of viral infection by Murine hepatitis virus. Specific functions, and accordingly utilities, of VGAM2287 correlate with, and may be deduced from, the identity of the host target genes which VGAM2287 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[31985] Nucleotide sequences of the VGAM2287 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2287 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2287 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2287 are further

described hereinbelow with reference to Table 1.

[31986] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2287 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[31987] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2288 (VGAM2288) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[31988] VGAM2288 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2288 was detected is described hereinabove with reference to Figs. 2-8.

[31989] VGAM2288 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Murine hepatitis virus. VGAM2288 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[31990] VGAM2288 gene, herein designated VGAM GENE, encodes a VGAM2288 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2288 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2288 precursor RNA is designated SEQ ID:2274, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2274 is located at position 23052 relative to the genome of Murine hepatitis virus.

[31991] VGAM2288 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2288 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31992] An enzyme complex designated DICER COMPLEX, dices the VGAM2288 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, into VGAM2288 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2288 RNA is designated SEQ ID:4999, and is provided hereinbelow with reference to the sequence listing part.

[31993] VGAM2288 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2288 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2288 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31994] VGAM2288 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2288 host target RNA, herein designated VGAM HOST TARGET RNA. This

complementary binding is due to the fact that the nucleotide sequence of VGAM2288 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2288 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2288 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31995] The complementary binding of VGAM2288 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2288 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2288

host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2288 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[31996] It is appreciated that VGAM2288 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2288 host target genes. The mRNA of each one of this plurality of VGAM2288 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2288 RNA, herein designated VGAM RNA, and which when bound by VGAM2288 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2288 host target proteins.

[31997] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2288 gene, herein designated VGAM GENE, on one or more VGAM2288 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31998] It is yet further appreciated that a function of VGAM2288 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2288 include diagnosis, prevention and treatment of viral infection by Murine hepatitis virus. Specific functions, and accordingly utilities, of VGAM2288 correlate with, and may be deduced from, the identity of the host target genes which VGAM2288 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[31999] Nucleotide sequences of the VGAM2288 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2288 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2288 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM2288 are further described hereinbelow with reference to Table 1.

[32000] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2288 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[32001] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2289 (VGAM2289) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[32002] VGAM2289 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2289 was detected is described hereinabove with reference to Figs. 2-8.

[32003] VGAM2289 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Murine hepatitis virus. VGAM2289 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the

human genome.

[32004] VGAM2289 gene, herein designated VGAM GENE, encodes a VGAM2289 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2289 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2289 precursor RNA is designated SEQ ID:2275, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2275 is located at position 12369 relative to the genome of Murine hepatitis virus.

[32005] VGAM2289 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2289 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32006] An enzyme complex designated DICER COMPLEX, dices

the VGAM2289 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2289 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2289 RNA is designated SEQ ID:5000, and is provided hereinbelow with reference to the sequence listing part.

[32007] VGAM2289 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2289 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2289 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32008] VGAM2289 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2289 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2289 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2289 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2289 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32009] The complementary binding of VGAM2289 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2289 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM2289 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2289 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[32010] It is appreciated that VGAM2289 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2289 host target genes. The mRNA of each one of this plurality of VGAM2289 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2289 RNA, herein designated VGAM RNA, and which when bound by VGAM2289 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2289 host target proteins.

[32011] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2289 gene, herein designated VGAM GENE, on one or more VGAM2289 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32012] It is yet further appreciated that a function of VGAM2289 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2289 include diagnosis, prevention and treatment of viral infection by Murine hepatitis virus. Specific functions, and accordingly utilities, of VGAM2289 correlate with, and may be deduced from, the identity of the host target genes which VGAM2289 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[32013] Nucleotide sequences of the VGAM2289 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2289 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of

VGAM2289 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2289 are further described hereinbelow with reference to Table 1.

[32014] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2289 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[32015] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2290 (VGAM2290) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[32016] VGAM2290 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2290 was detected is described hereinabove with reference to Figs. 2-8.

[32017] VGAM2290 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Murine hepatitis virus. VGAM2290 host target gene, herein designated VGAM

HOST TARGET GENE, is a human gene contained in the human genome.

[32018] VGAM2290 gene, herein designated VGAM GENE, encodes a VGAM2290 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2290 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2290 precursor RNA is designated SEQ ID:2276, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2276 is located at position 16166 relative to the genome of Murine hepatitis virus.

[32019] VGAM2290 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2290 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32020] An enzyme complex designated DICER COMPLEX, dices the VGAM2290 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2290 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2290 RNA is designated SEQ ID:5001, and is provided hereinbelow with reference to the sequence listing part.

[32021] VGAM2290 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2290 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2290 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32022] VGAM2290 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites

located in untranslated regions of VGAM2290 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2290 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2290 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2290 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32023] The complementary binding of VGAM2290 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2290 host target RNA, herein designated VGAM

HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2290 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2290 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[32024] It is appreciated that VGAM2290 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2290 host target genes. The mRNA of each one of this plurality of VGAM2290 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2290 RNA, herein designated VGAM RNA, and which when bound by VGAM2290 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2290 host target proteins.

[32025] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2290 gene, herein designated VGAM GENE, on one or more VGAM2290 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove

with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32026] It is yet further appreciated that a function of VGAM2290 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2290 include diagnosis, prevention and treatment of viral infection by Murine hepatitis virus. Specific functions, and accordingly utilities, of VGAM2290 correlate with, and may be deduced from, the identity of the host target genes which VGAM2290 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[32027] Nucleotide sequences of the VGAM2290 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2290 RNA, herein designated VGAM RNA, and

a schematic representation of the secondary folding of VGAM2290 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2290 are further described hereinbelow with reference to Table 1.

[32028] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2290 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[32029] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2291 (VGAM2291) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[32030] VGAM2291 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2291 was detected is described hereinabove with reference to Figs. 2-8.

[32031] VGAM2291 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Murine hepatitis virus.

VGAM2291 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[32032] VGAM2291 gene, herein designated VGAM GENE, encodes a VGAM2291 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2291 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2291 precursor RNA is designated SEQ ID:2277, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2277 is located at position 15049 relative to the genome of Murine hepatitis virus.

[32033] VGAM2291 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2291 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[32034] An enzyme complex designated DICER COMPLEX, dices the VGAM2291 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2291 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2291 RNA is designated SEQ ID:5002, and is provided hereinbelow with reference to the sequence listing part.

[32035] VGAM2291 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2291 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2291 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32036] VGAM2291 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM2291 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2291 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2291 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2291 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32037] The complementary binding of VGAM2291 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM2291 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2291 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2291 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[32038] It is appreciated that VGAM2291 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2291 host target genes. The mRNA of each one of this plurality of VGAM2291 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2291 RNA, herein designated VGAM RNA, and which when bound by VGAM2291 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2291 host target proteins.

[32039] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2291 gene, herein designated VGAM GENE, on one or more VGAM2291 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32040] It is yet further appreciated that a function of VGAM2291 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2291 include diagnosis, prevention and treatment of viral infection by Murine hepatitis virus. Specific functions, and accordingly utilities, of VGAM2291 correlate with, and may be deduced from, the identity of the host target genes which VGAM2291 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[32041] Nucleotide sequences of the VGAM2291 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

diced VGAM2291 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2291 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2291 are further described hereinbelow with reference to Table 1.

[32042] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2291 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[32043] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2292 (VGAM2292) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[32044] VGAM2292 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2292 was detected is described hereinabove with reference to Figs. 2-8.

[32045] VGAM2292 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of Murine hepatitis virus. VGAM2292 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[32046] VGAM2292 gene, herein designated VGAM GENE, encodes a VGAM2292 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2292 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2292 precursor RNA is designated SEQ ID:2278, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2278 is located at position 5645 relative to the genome of Murine hepatitis virus.

[32047] VGAM2292 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2292 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32048] An enzyme complex designated DICER COMPLEX, dices the VGAM2292 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2292 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 49%) nucleotide sequence of VGAM2292 RNA is designated SEQ ID:5003, and is provided hereinbelow with reference to the sequence listing part.

[32049] VGAM2292 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2292 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2292 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32050] VGAM2292 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2292 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2292 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2292 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2292 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32051] The complementary binding of VGAM2292 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM2292 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2292 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2292 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[32052] It is appreciated that VGAM2292 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2292 host target genes. The mRNA of each one of this plurality of VGAM2292 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2292 RNA, herein designated VGAM RNA, and which when bound by VGAM2292 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2292 host target proteins.

[32053] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2292 gene, herein designated VGAM GENE, on one or more VGAM2292 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32054] It is yet further appreciated that a function of VGAM2292 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2292 include diagnosis, prevention and treatment of viral infection by Murine hepatitis virus. Specific functions, and accordingly utilities, of VGAM2292 correlate with, and may be deduced from, the identity of the host target genes which VGAM2292 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[32055] Nucleotide sequences of the VGAM2292 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the diced VGAM2292 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2292 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2292 are further described hereinbelow with reference to Table 1.

[32056] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2292 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[32057] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2293 (VGAM2293) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[32058] VGAM2293 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2293 was detected is described hereinabove with reference to Figs. 2-8.

[32059] VGAM2293 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Murine hepatitis virus. VGAM2293 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[32060] VGAM2293 gene, herein designated VGAM GENE, encodes a VGAM2293 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2293 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2293 precursor RNA is designated SEQ ID:2279, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2279 is located at position 25465 relative to the genome of Murine hepatitis virus.

[32061] VGAM2293 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2293 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32062] An enzyme complex designated DICER COMPLEX, dices the VGAM2293 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2293 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 76%) nucleotide sequence of VGAM2293 RNA is designated SEQ ID:5004, and is provided hereinbelow with reference to the sequence listing part.

[32063] VGAM2293 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2293 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2293 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN COD-

ING and 3UTR respectively.

[32064] VGAM2293 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2293 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2293 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2293 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2293 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32065] The complementary binding of VGAM2293 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2293 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2293 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2293 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[32066] It is appreciated that VGAM2293 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2293 host target genes. The mRNA of each one of this plurality of VGAM2293 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2293 RNA, herein designated VGAM RNA, and which when bound by VGAM2293 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2293 host target proteins.

[32067] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2293 gene, herein designated VGAM GENE, on one

or more VGAM2293 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32068] It is yet further appreciated that a function of VGAM2293 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2293 include diagnosis, prevention and treatment of viral infection by Murine hepatitis virus. Specific functions, and accordingly utilities, of VGAM2293 correlate with, and may be deduced from, the identity of the host target genes which VGAM2293 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[32069] Nucleotide sequences of the VGAM2293 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2293 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2293 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2293 are further described hereinbelow with reference to Table 1.

[32070] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2293 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[32071] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2294 (VGAM2294) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[32072] VGAM2294 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2294 was detected is de-

scribed hereinabove with reference to Figs. 2-8.

[32073] VGAM2294 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Murine hepatitis virus. VGAM2294 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[32074] VGAM2294 gene, herein designated VGAM GENE, encodes a VGAM2294 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2294 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2294 precursor RNA is designated SEQ ID:2280, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2280 is located at position 22784 relative to the genome of Murine hepatitis virus.

[32075] VGAM2294 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2294 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32076] An enzyme complex designated DICER COMPLEX, dices the VGAM2294 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2294 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2294 RNA is designated SEQ ID:5005, and is provided hereinbelow with reference to the sequence listing part.

[32077] VGAM2294 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2294 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2294 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and

a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32078] VGAM2294 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2294 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2294 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2294 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2294 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both

3UTR and 5UTR regions.

[32079] The complementary binding of VGAM2294 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2294 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2294 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2294 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[32080] It is appreciated that VGAM2294 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2294 host target genes. The mRNA of each one of this plurality of VGAM2294 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2294 RNA, herein designated VGAM RNA, and which when bound by VGAM2294 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2294 host target proteins.

[32081] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM2294 gene, herein designated VGAM GENE, on one or more VGAM2294 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32082] It is yet further appreciated that a function of VGAM2294 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2294 include diagnosis, prevention and treatment of viral infection by Murine hepatitis virus. Specific functions, and accordingly utilities, of VGAM2294 correlate with, and may be deduced from, the identity of the host target genes which VGAM2294 binds and inhibits, and the function of these host target genes, as

elaborated hereinbelow.

[32083] Nucleotide sequences of the VGAM2294 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2294 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2294 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2294 are further described hereinbelow with reference to Table 1.

[32084] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2294 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[32085] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2295 (VGAM2295) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[32086] VGAM2295 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene.

The method by which VGAM2295 was detected is described hereinabove with reference to Figs. 2-8.

[32087] VGAM2295 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia virus. VGAM2295 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[32088] VGAM2295 gene, herein designated VGAM GENE, encodes a VGAM2295 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2295 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2295 precursor RNA is designated SEQ ID:2281, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2281 is located at position 43938 relative to the genome of Ectromelia virus.

[32089] VGAM2295 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2295 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32090] An enzyme complex designated DICER COMPLEX, dices the VGAM2295 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2295 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2295 RNA is designated SEQ ID:5006, and is provided hereinbelow with reference to the sequence listing part.

[32091] VGAM2295 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2295 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2295 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding

gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32092] VGAM2295 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2295 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2295 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2295 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2295 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be lo-

cated in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32093] The complementary binding of VGAM2295 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2295 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2295 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2295 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[32094] It is appreciated that VGAM2295 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2295 host target genes. The mRNA of each one of this plurality of VGAM2295 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2295 RNA, herein designated VGAM RNA, and which when bound by VGAM2295 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2295 host target proteins.

[32095] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM2295 gene, herein designated VGAM GENE, on one or more VGAM2295 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32096] It is yet further appreciated that a function of VGAM2295 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2295 include diagnosis, prevention and treatment of viral infection by Ectromelia virus. Specific functions, and accordingly utilities, of VGAM2295 correlate with, and may be deduced from, the identity of the host target genes which VGAM2295 binds and inhibits,

and the function of these host target genes, as elaborated hereinbelow.

[32097] Nucleotide sequences of the VGAM2295 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2295 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2295 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2295 are further described hereinbelow with reference to Table 1.

[32098] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2295 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[32099] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2296 (VGAM2296) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[32100] VGAM2296 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2296 was detected is described hereinabove with reference to Figs. 2-8.

[32101] VGAM2296 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia virus. VGAM2296 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[32102] VGAM2296 gene, herein designated VGAM GENE, encodes a VGAM2296 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2296 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2296 precursor RNA is designated SEQ ID:2282, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2282 is located at position 27612 relative to the genome of Ectromelia virus.

[32103] VGAM2296 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2296 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32104] An enzyme complex designated DICER COMPLEX, dices the VGAM2296 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2296 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2296 RNA is designated SEQ ID:5007, and is provided hereinbelow with reference to the sequence listing part.

[32105] VGAM2296 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2296 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2296 host target RNA, herein designated VGAM HOST TARGET RNA, comprises

three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32106] VGAM2296 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2296 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2296 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2296 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2296 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an

example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32107] The complementary binding of VGAM2296 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2296 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2296 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2296 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[32108] It is appreciated that VGAM2296 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2296 host target genes. The mRNA of each one of this plurality of VGAM2296 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2296 RNA, herein designated VGAM RNA, and which when bound by VGAM2296 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2296 host target proteins.

[32109] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2296 gene, herein designated VGAM GENE, on one or more VGAM2296 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32110] It is yet further appreciated that a function of VGAM2296 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2296 include diagnosis, prevention and treatment of viral infection by Ectromelia virus. Specific functions, and accordingly utilities, of VGAM2296 correlate with, and may be deduced from, the identity of the

host target genes which VGAM2296 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[32111] Nucleotide sequences of the VGAM2296 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2296 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2296 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2296 are further described hereinbelow with reference to Table 1.

[32112] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2296 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[32113] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2297 (VGAM2297) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[32114] VGAM2297 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2297 was detected is described hereinabove with reference to Figs. 2-8.

[32115] VGAM2297 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia virus. VGAM2297 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[32116] VGAM2297 gene, herein designated VGAM GENE, encodes a VGAM2297 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2297 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2297 precursor RNA is designated SEQ ID:2283, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2283 is located at position 28555 relative to the genome of Ectromelia virus.

[32117] VGAM2297 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2297 folded precursor RNA, herein designated VGAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32118] An enzyme complex designated DICER COMPLEX, dices the VGAM2297 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2297 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2297 RNA is designated SEQ ID:5008, and is provided hereinbelow with reference to the sequence listing part.

[32119] VGAM2297 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2297 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2297 host target RNA,

herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32120] VGAM2297 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2297 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2297 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2297 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2297 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host tar-

get binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32121] The complementary binding of VGAM2297 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2297 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2297 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2297 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[32122] It is appreciated that VGAM2297 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2297 host target genes. The mRNA of each one of this plurality of VGAM2297 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2297 RNA, herein designated VGAM RNA, and which when bound by VGAM2297 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2297 host target proteins.

[32123] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2297 gene, herein designated VGAM GENE, on one or more VGAM2297 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32124] It is yet further appreciated that a function of VGAM2297 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2297 include diagnosis, prevention and treatment of viral infection by Ectromelia virus. Specific functions, and accordingly utilities, of VGAM2297 corre-

late with, and may be deduced from, the identity of the host target genes which VGAM2297 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[32125] Nucleotide sequences of the VGAM2297 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2297 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2297 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2297 are further described hereinbelow with reference to Table 1.

[32126] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2297 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[32127] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2298 (VGAM2298) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the

art.

[32128] VGAM2298 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2298 was detected is described hereinabove with reference to Figs. 2-8.

[32129] VGAM2298 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia virus. VGAM2298 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[32130] VGAM2298 gene, herein designated VGAM GENE, encodes a VGAM2298 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2298 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2298 precursor RNA is designated SEQ ID:2284, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2284 is located at position 32155 relative to the genome of Ectromelia virus.

[32131] VGAM2298 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2298 folded

precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32132] An enzyme complex designated DICER COMPLEX, dices the VGAM2298 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2298 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2298 RNA is designated SEQ ID:5009, and is provided hereinbelow with reference to the sequence listing part.

[32133] VGAM2298 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2298 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM2298 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32134] VGAM2298 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2298 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2298 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2298 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2298 host target RNA, herein designated VGAM HOST TARGET RNA.

It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32135] The complementary binding of VGAM2298 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2298 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2298 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2298 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[32136] It is appreciated that VGAM2298 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2298 host target genes. The mRNA of each one of this plurality of VGAM2298 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2298 RNA, herein designated VGAM RNA, and which when bound by VGAM2298 RNA, herein designated VGAM RNA, causes inhibition of translation of

respective one or more VGAM2298 host target proteins.

[32137] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2298 gene, herein designated VGAM GENE, on one or more VGAM2298 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32138] It is yet further appreciated that a function of VGAM2298 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2298 include diagnosis, prevention and treatment of viral infection by Ectromelia virus. Specific

functions, and accordingly utilities, of VGAM2298 correlate with, and may be deduced from, the identity of the host target genes which VGAM2298 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[32139] Nucleotide sequences of the VGAM2298 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2298 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2298 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2298 are further described hereinbelow with reference to Table 1.

[32140] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2298 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[32141] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2299 (VGAM2299) viral gene, which modulates expression of respective host target genes thereof, the func-

tion and utility of which host target genes is known in the art.

[32142] VGAM2299 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2299 was detected is described hereinabove with reference to Figs. 2-8.

[32143] VGAM2299 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia virus. VGAM2299 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[32144] VGAM2299 gene, herein designated VGAM GENE, encodes a VGAM2299 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2299 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2299 precursor RNA is designated SEQ ID:2285, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2285 is located at position 23346 relative to the genome of Ectromelia virus.

[32145] VGAM2299 precursor RNA, herein designated VGAM PRE-

CURSOR RNA, folds onto itself, forming VGAM2299 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32146] An enzyme complex designated DICER COMPLEX, dices the VGAM2299 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2299 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2299 RNA is designated SEQ ID:5010, and is provided hereinbelow with reference to the sequence listing part.

[32147] VGAM2299 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM2299 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2299 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32148] VGAM2299 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2299 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2299 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2299 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2299 host

target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32149] The complementary binding of VGAM2299 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2299 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2299 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2299 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[32150] It is appreciated that VGAM2299 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2299 host target genes. The mRNA of each one of this plurality of VGAM2299 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2299 RNA, herein designated VGAM RNA, and which when bound by VGAM2299 RNA, herein

designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2299 host target proteins.

[32151] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2299 gene, herein designated VGAM GENE, on one or more VGAM2299 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32152] It is yet further appreciated that a function of VGAM2299 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2299 include diagnosis, prevention and

treatment of viral infection by Ectromelia virus. Specific functions, and accordingly utilities, of VGAM2299 correlate with, and may be deduced from, the identity of the host target genes which VGAM2299 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[32153] Nucleotide sequences of the VGAM2299 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2299 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2299 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2299 are further described hereinbelow with reference to Table 1.

[32154] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2299 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[32155] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2300 (VGAM2300) viral gene, which modulates ex-

pression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[32156] VGAM2300 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2300 was detected is described hereinabove with reference to Figs. 2-8.

[32157] VGAM2300 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia virus. VGAM2300 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[32158] VGAM2300 gene, herein designated VGAM GENE, encodes a VGAM2300 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2300 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2300 precursor RNA is designated SEQ ID:2286, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2286 is located at position 38978 relative to the genome of Ectromelia virus.

[32159] VGAM2300 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2300 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32160] An enzyme complex designated DICER COMPLEX, dices the VGAM2300 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2300 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 58%) nucleotide sequence of VGAM2300 RNA is designated SEQ ID:5011, and is provided hereinbelow with reference to the sequence listing part.

[32161] VGAM2300 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2300 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2300 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32162] VGAM2300 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2300 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2300 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2300 RNA, herein designated VGAM RNA, may have a different number of host target

binding sites in untranslated regions of a VGAM2300 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32163] The complementary binding of VGAM2300 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2300 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2300 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2300 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[32164] It is appreciated that VGAM2300 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2300 host target genes. The mRNA of each one of this plurality of VGAM2300 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2300 RNA, herein designated VGAM

RNA, and which when bound by VGAM2300 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2300 host target proteins.

[32165] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2300 gene, herein designated VGAM GENE, on one or more VGAM2300 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32166] It is yet further appreciated that a function of VGAM2300 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM2300 include diagnosis, prevention and treatment of viral infection by Ectromelia virus. Specific functions, and accordingly utilities, of VGAM2300 correlate with, and may be deduced from, the identity of the host target genes which VGAM2300 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[32167] Nucleotide sequences of the VGAM2300 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2300 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2300 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2300 are further described hereinbelow with reference to Table 1.

[32168] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2300 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[32169] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Mes-

senger 2301 (VGAM2301) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[32170] VGAM2301 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2301 was detected is described hereinabove with reference to Figs. 2-8.

[32171] VGAM2301 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia virus. VGAM2301 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[32172] VGAM2301 gene, herein designated VGAM GENE, encodes a VGAM2301 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2301 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2301 precursor RNA is designated SEQ ID:2287, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2287 is located at position

30387 relative to the genome of Ectromelia virus.

[32173] VGAM2301 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2301 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32174] An enzyme complex designated DICER COMPLEX, dices the VGAM2301 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2301 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2301 RNA is designated SEQ ID:5012, and is provided hereinbelow with reference to the sequence listing part.

[32175] VGAM2301 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2301 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2301 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32176] VGAM2301 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2301 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2301 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2301 RNA, herein designated

VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2301 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32177] The complementary binding of VGAM2301 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2301 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2301 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2301 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[32178] It is appreciated that VGAM2301 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2301 host target genes. The mRNA of each one of this plurality of VGAM2301 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM2301 RNA, herein designated VGAM RNA, and which when bound by VGAM2301 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2301 host target proteins.

[32179] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2301 gene, herein designated VGAM GENE, on one or more VGAM2301 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32180] It is yet further appreciated that a function of VGAM2301 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2301 include diagnosis, prevention and treatment of viral infection by Ectromelia virus. Specific functions, and accordingly utilities, of VGAM2301 correlate with, and may be deduced from, the identity of the host target genes which VGAM2301 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[32181] Nucleotide sequences of the VGAM2301 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2301 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2301 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2301 are further described hereinbelow with reference to Table 1.

[32182] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2301 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[32183] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present

invention, referred to here as Viral Genomic Address Messenger 2302 (VGAM2302) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[32184] VGAM2302 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2302 was detected is described hereinabove with reference to Figs. 2-8.

[32185] VGAM2302 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia virus. VGAM2302 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[32186] VGAM2302 gene, herein designated VGAM GENE, encodes a VGAM2302 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2302 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2302 precursor RNA is designated SEQ ID:2288, and is provided hereinbelow with reference to the sequence listing part. Nu-

cleotide sequence SEQ ID:2288 is located at position 44731 relative to the genome of Ectromelia virus.

[32187] VGAM2302 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2302 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32188] An enzyme complex designated DICER COMPLEX, dices the VGAM2302 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2302 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2302 RNA is designated SEQ ID:5013, and is provided hereinbelow with reference to the sequence

listing part.

[32189] VGAM2302 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2302 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2302 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32190] VGAM2302 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2302 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2302 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not

meant to be limiting VGAM2302 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2302 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32191] The complementary binding of VGAM2302 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2302 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2302 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2302 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[32192] It is appreciated that VGAM2302 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2302 host target genes. The mRNA of each one of this plurality of VGAM2302 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2302 RNA, herein designated VGAM RNA, and which when bound by VGAM2302 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2302 host target proteins.

[32193] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2302 gene, herein designated VGAM GENE, on one or more VGAM2302 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32194] It is yet further appreciated that a function of VGAM2302

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2302 include diagnosis, prevention and treatment of viral infection by Ectromelia virus. Specific functions, and accordingly utilities, of VGAM2302 correlate with, and may be deduced from, the identity of the host target genes which VGAM2302 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[32195] Nucleotide sequences of the VGAM2302 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2302 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2302 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2302 are further described hereinbelow with reference to Table 1.

[32196] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2302 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[32197] Fig. 1 further provides a conceptual description of another

novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2303 (VGAM2303) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[32198] VGAM2303 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2303 was detected is described hereinabove with reference to Figs. 2-8.

[32199] VGAM2303 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia virus. VGAM2303 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[32200] VGAM2303 gene, herein designated VGAM GENE, encodes a VGAM2303 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2303 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2303 precursor RNA is designated SEQ ID:2289, and is provided here-

inbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2289 is located at position 38706 relative to the genome of Ectromelia virus.

[32201] VGAM2303 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2303 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32202] An enzyme complex designated DICER COMPLEX, dices the VGAM2303 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2303 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2303 RNA is designated SEQ ID:5014, and

is provided hereinbelow with reference to the sequence listing part.

[32203] VGAM2303 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2303 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2303 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32204] VGAM2303 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2303 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2303 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites

shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2303 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2303 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32205] The complementary binding of VGAM2303 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2303 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2303 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2303 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[32206] It is appreciated that VGAM2303 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2303 host target genes. The mRNA of each one of this plurality of VGAM2303 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2303 RNA, herein designated VGAM RNA, and which when bound by VGAM2303 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2303 host target proteins.

[32207] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2303 gene, herein designated VGAM GENE, on one or more VGAM2303 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32208] It is yet further appreciated that a function of VGAM2303 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2303 include diagnosis, prevention and treatment of viral infection by Ectromelia virus. Specific functions, and accordingly utilities, of VGAM2303 correlate with, and may be deduced from, the identity of the host target genes which VGAM2303 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[32209] Nucleotide sequences of the VGAM2303 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2303 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2303 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2303 are further described hereinbelow with reference to Table 1.

[32210] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2303 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[32211] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2304 (VGAM2304) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[32212] VGAM2304 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2304 was detected is described hereinabove with reference to Figs. 2-8.

[32213] VGAM2304 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia virus. VGAM2304 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[32214] VGAM2304 gene, herein designated VGAM GENE, encodes a VGAM2304 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2304 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2304 precur-

sor RNA is designated SEQ ID:2290, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2290 is located at position 35690 relative to the genome of Ectromelia virus.

[32215] VGAM2304 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2304 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32216] An enzyme complex designated DICER COMPLEX, dices the VGAM2304 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2304 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 53%) nucleotide se-

quence of VGAM2304 RNA is designated SEQ ID:5015, and is provided hereinbelow with reference to the sequence listing part.

[32217] VGAM2304 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2304 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2304 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32218] VGAM2304 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2304 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2304 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is ap-

preciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2304 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2304 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32219] The complementary binding of VGAM2304 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2304 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2304 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2304 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[32220] It is appreciated that VGAM2304 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2304 host target genes. The mRNA of

each one of this plurality of VGAM2304 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2304 RNA, herein designated VGAM RNA, and which when bound by VGAM2304 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2304 host target proteins.

[32221] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2304 gene, herein designated VGAM GENE, on one or more VGAM2304 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science

294,779 (2001)).

[32222] It is yet further appreciated that a function of VGAM2304 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2304 include diagnosis, prevention and treatment of viral infection by Ectromelia virus. Specific functions, and accordingly utilities, of VGAM2304 correlate with, and may be deduced from, the identity of the host target genes which VGAM2304 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[32223] Nucleotide sequences of the VGAM2304 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2304 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2304 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2304 are further described hereinbelow with reference to Table 1.

[32224] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2304 RNA, herein designated VGAM RNA, are de-

scribed hereinbelow with reference to Table 2.

[32225] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2305 (VGAM2305) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[32226] VGAM2305 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2305 was detected is described hereinabove with reference to Figs. 2-8.

[32227] VGAM2305 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Camelpox virus. VGAM2305 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[32228] VGAM2305 gene, herein designated VGAM GENE, encodes a VGAM2305 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2305 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly

similar to the nucleotide sequence of VGAM2305 precursor RNA is designated SEQ ID:2291, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2291 is located at position 38932 relative to the genome of Camelpox virus.

[32229] VGAM2305 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2305 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32230] An enzyme complex designated DICER COMPLEX, dices the VGAM2305 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2305 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 48%) nucleotide sequence of VGAM2305 RNA is designated SEQ ID:5016, and is provided hereinbelow with reference to the sequence listing part.

[32231] VGAM2305 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2305 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2305 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32232] VGAM2305 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2305 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2305 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I,

BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2305 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2305 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32233] The complementary binding of VGAM2305 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2305 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2305 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2305 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[32234] It is appreciated that VGAM2305 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM2305 host target genes. The mRNA of each one of this plurality of VGAM2305 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2305 RNA, herein designated VGAM RNA, and which when bound by VGAM2305 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2305 host target proteins.

[32235] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2305 gene, herein designated VGAM GENE, on one or more VGAM2305 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32236] It is yet further appreciated that a function of VGAM2305 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2305 include diagnosis, prevention and treatment of viral infection by Camelpox virus. Specific functions, and accordingly utilities, of VGAM2305 correlate with, and may be deduced from, the identity of the host target genes which VGAM2305 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[32237] Nucleotide sequences of the VGAM2305 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2305 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2305 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2305 are further described hereinbelow with reference to Table 1.

[32238] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites

to VGAM2305 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[32239] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2306 (VGAM2306) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[32240] VGAM2306 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2306 was detected is described hereinabove with reference to Figs. 2-8.

[32241] VGAM2306 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia virus. VGAM2306 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[32242] VGAM2306 gene, herein designated VGAM GENE, encodes a VGAM2306 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2306 precursor RNA, herein designated VGAM PRECURSOR RNA, does not en-

code a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2306 precursor RNA is designated SEQ ID:2292, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2292 is located at position 43278 relative to the genome of Ectromelia virus.

[32243] VGAM2306 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2306 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32244] An enzyme complex designated DICER COMPLEX, dices the VGAM2306 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2306 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2306 RNA is designated SEQ ID:5017, and is provided hereinbelow with reference to the sequence listing part.

[32245] VGAM2306 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2306 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2306 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32246] VGAM2306 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2306 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2306 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3

such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2306 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2306 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32247] The complementary binding of VGAM2306 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2306 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2306 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2306 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[32248] It is appreciated that VGAM2306 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2306 host target genes. The mRNA of each one of this plurality of VGAM2306 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2306 RNA, herein designated VGAM RNA, and which when bound by VGAM2306 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2306 host target proteins.

[32249] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2306 gene, herein designated VGAM GENE, on one or more VGAM2306 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32250] It is yet further appreciated that a function of VGAM2306 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2306 include diagnosis, prevention and treatment of viral infection by Ectromelia virus. Specific functions, and accordingly utilities, of VGAM2306 correlate with, and may be deduced from, the identity of the host target genes which VGAM2306 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[32251] Nucleotide sequences of the VGAM2306 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2306 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2306 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2306 are further described hereinbelow with reference to Table 1.

[32252] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the

complementarity of each of these host target binding sites to VGAM2306 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[32253] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2307 (VGAM2307) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[32254] VGAM2307 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2307 was detected is described hereinabove with reference to Figs. 2-8.

[32255] VGAM2307 gene, herein designated VGAM GENE, is a viral gene contained in the genome of lumpy skin disease virus. VGAM2307 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[32256] VGAM2307 gene, herein designated VGAM GENE, encodes a VGAM2307 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2307 precursor RNA,

herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2307 precursor RNA is designated SEQ ID:2293, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2293 is located at position 122989 relative to the genome of lumpy skin disease virus.

[32257] VGAM2307 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2307 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32258] An enzyme complex designated DICER COMPLEX, dices the VGAM2307 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2307 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of VGAM2307 RNA is designated SEQ ID:5018, and is provided hereinbelow with reference to the sequence listing part.

[32259] VGAM2307 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2307 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2307 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32260] VGAM2307 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2307 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2307 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed

sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2307 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2307 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32261] The complementary binding of VGAM2307 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2307 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2307 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2307 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target

protein is therefore outlined by a broken line.

[32262] It is appreciated that VGAM2307 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2307 host target genes. The mRNA of each one of this plurality of VGAM2307 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2307 RNA, herein designated VGAM RNA, and which when bound by VGAM2307 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2307 host target proteins.

[32263] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2307 gene, herein designated VGAM GENE, on one or more VGAM2307 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32264] It is yet further appreciated that a function of VGAM2307 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2307 include diagnosis, prevention and treatment of viral infection by lumpy skin disease virus. Specific functions, and accordingly utilities, of VGAM2307 correlate with, and may be deduced from, the identity of the host target genes which VGAM2307 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[32265] Nucleotide sequences of the VGAM2307 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2307 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2307 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2307 are further described hereinbelow with reference to Table 1.

[32266] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2307 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[32267] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2308 (VGAM2308) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[32268] VGAM2308 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2308 was detected is described hereinabove with reference to Figs. 2-8.

[32269] VGAM2308 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox virus. VGAM2308 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[32270] VGAM2308 gene, herein designated VGAM GENE, encodes a VGAM2308 precursor RNA, herein designated VGAM

PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2308 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2308 precursor RNA is designated SEQ ID:2294, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2294 is located at position 123501 relative to the genome of Goatpox virus.

[32271] VGAM2308 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2308 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32272] An enzyme complex designated DICER COMPLEX, dices the VGAM2308 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2308 RNA, herein designated VGAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2308 RNA is designated SEQ ID:5019, and is provided hereinbelow with reference to the sequence listing part.

[32273] VGAM2308 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2308 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2308 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32274] VGAM2308 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2308 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2308 RNA, herein designated

VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2308 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2308 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32275] The complementary binding of VGAM2308 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2308 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2308 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2308 host target protein, herein desig-

nated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[32276] It is appreciated that VGAM2308 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2308 host target genes. The mRNA of each one of this plurality of VGAM2308 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2308 RNA, herein designated VGAM RNA, and which when bound by VGAM2308 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2308 host target proteins.

[32277] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2308 gene, herein designated VGAM GENE, on one or more VGAM2308 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32278] It is yet further appreciated that a function of VGAM2308 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2308 include diagnosis, prevention and treatment of viral infection by Goatpox virus. Specific functions, and accordingly utilities, of VGAM2308 correlate with, and may be deduced from, the identity of the host target genes which VGAM2308 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[32279] Nucleotide sequences of the VGAM2308 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2308 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2308 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2308 are further described hereinbelow with reference to Table 1.

[32280] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2308 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[32281] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2309 (VGAM2309) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[32282] VGAM2309 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2309 was detected is described hereinabove with reference to Figs. 2-8.

[32283] VGAM2309 gene, herein designated VGAM GENE, is a viral gene contained in the genome of lumpy skin disease virus. VGAM2309 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[32284] VGAM2309 gene, herein designated VGAM GENE, encodes

a VGAM2309 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2309 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2309 precursor RNA is designated SEQ ID:2295, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2295 is located at position 127569 relative to the genome of lumpy skin disease virus.

[32285] VGAM2309 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2309 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32286] An enzyme complex designated DICER COMPLEX, dices the VGAM2309 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, into VGAM2309 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2309 RNA is designated SEQ ID:5020, and is provided hereinbelow with reference to the sequence listing part.

[32287] VGAM2309 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2309 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2309 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32288] VGAM2309 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2309 host target RNA, herein designated VGAM HOST TARGET RNA. This

complementary binding is due to the fact that the nucleotide sequence of VGAM2309 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2309 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2309 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32289] The complementary binding of VGAM2309 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2309 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2309

host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2309 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[32290] It is appreciated that VGAM2309 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2309 host target genes. The mRNA of each one of this plurality of VGAM2309 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2309 RNA, herein designated VGAM RNA, and which when bound by VGAM2309 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2309 host target proteins.

[32291] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2309 gene, herein designated VGAM GENE, on one or more VGAM2309 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32292] It is yet further appreciated that a function of VGAM2309 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2309 include diagnosis, prevention and treatment of viral infection by lumpy skin disease virus. Specific functions, and accordingly utilities, of VGAM2309 correlate with, and may be deduced from, the identity of the host target genes which VGAM2309 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[32293] Nucleotide sequences of the VGAM2309 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2309 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2309 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM2309 are further described hereinbelow with reference to Table 1.

[32294] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2309 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[32295] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2310 (VGAM2310) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[32296] VGAM2310 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2310 was detected is described hereinabove with reference to Figs. 2-8.

[32297] VGAM2310 gene, herein designated VGAM GENE, is a viral gene contained in the genome of lumpy skin disease virus. VGAM2310 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in

the human genome.

[32298] VGAM2310 gene, herein designated VGAM GENE, encodes a VGAM2310 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2310 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2310 precursor RNA is designated SEQ ID:2296, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2296 is located at position 135569 relative to the genome of lumpy skin disease virus.

[32299] VGAM2310 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2310 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32300] An enzyme complex designated DICER COMPLEX, dices the VGAM2310 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2310 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2310 RNA is designated SEQ ID:5021, and is provided hereinbelow with reference to the sequence listing part.

[32301] VGAM2310 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2310 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2310 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32302] VGAM2310 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites

located in untranslated regions of VGAM2310 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2310 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2310 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2310 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32303] The complementary binding of VGAM2310 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2310 host target RNA, herein designated VGAM

HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2310 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2310 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[32304] It is appreciated that VGAM2310 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2310 host target genes. The mRNA of each one of this plurality of VGAM2310 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2310 RNA, herein designated VGAM RNA, and which when bound by VGAM2310 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2310 host target proteins.

[32305] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2310 gene, herein designated VGAM GENE, on one or more VGAM2310 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove

with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32306] It is yet further appreciated that a function of VGAM2310 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2310 include diagnosis, prevention and treatment of viral infection by lumpy skin disease virus. Specific functions, and accordingly utilities, of VGAM2310 correlate with, and may be deduced from, the identity of the host target genes which VGAM2310 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[32307] Nucleotide sequences of the VGAM2310 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2310 RNA, herein designated VGAM RNA, and

a schematic representation of the secondary folding of VGAM2310 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2310 are further described hereinbelow with reference to Table 1.

[32308] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2310 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[32309] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2311 (VGAM2311) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[32310] VGAM2311 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2311 was detected is described hereinabove with reference to Figs. 2-8.

[32311] VGAM2311 gene, herein designated VGAM GENE, is a viral gene contained in the genome of lumpy skin disease

virus. VGAM2311 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[32312] VGAM2311 gene, herein designated VGAM GENE, encodes a VGAM2311 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2311 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2311 precursor RNA is designated SEQ ID:2297, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2297 is located at position 139025 relative to the genome of lumpy skin disease virus.

[32313] VGAM2311 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2311 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32314] An enzyme complex designated DICER COMPLEX, dices the VGAM2311 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2311 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 47%) nucleotide sequence of VGAM2311 RNA is designated SEQ ID:5022, and is provided hereinbelow with reference to the sequence listing part.

[32315] VGAM2311 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2311 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2311 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32316] VGAM2311 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2311 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2311 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2311 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2311 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32317] The complementary binding of VGAM2311 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM2311 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2311 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2311 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[32318] It is appreciated that VGAM2311 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2311 host target genes. The mRNA of each one of this plurality of VGAM2311 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2311 RNA, herein designated VGAM RNA, and which when bound by VGAM2311 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2311 host target proteins.

[32319] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2311 gene, herein designated VGAM GENE, on one or more VGAM2311 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32320] It is yet further appreciated that a function of VGAM2311 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2311 include diagnosis, prevention and treatment of viral infection by lumpy skin disease virus. Specific functions, and accordingly utilities, of VGAM2311 correlate with, and may be deduced from, the identity of the host target genes which VGAM2311 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[32321] Nucleotide sequences of the VGAM2311 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the diced VGAM2311 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2311 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2311 are further described hereinbelow with reference to Table 1.

[32322] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2311 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[32323] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2312 (VGAM2312) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[32324] VGAM2312 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2312 was detected is described hereinabove with reference to Figs. 2-8.

[32325] VGAM2312 gene, herein designated VGAM GENE, is a viral gene contained in the genome of lumpy skin disease virus. VGAM2312 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[32326] VGAM2312 gene, herein designated VGAM GENE, encodes a VGAM2312 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2312 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2312 precursor RNA is designated SEQ ID:2298, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2298 is located at position 2051 relative to the genome of lumpy skin disease virus.

[32327] VGAM2312 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2312 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32328] An enzyme complex designated DICER COMPLEX, dices the VGAM2312 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2312 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 63%) nucleotide sequence of VGAM2312 RNA is designated SEQ ID:5023, and is provided hereinbelow with reference to the sequence listing part.

[32329] VGAM2312 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2312 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2312 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN COD-

ING and 3UTR respectively.

[32330] VGAM2312 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2312 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2312 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2312 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2312 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32331] The complementary binding of VGAM2312 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2312 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2312 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2312 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[32332] It is appreciated that VGAM2312 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2312 host target genes. The mRNA of each one of this plurality of VGAM2312 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2312 RNA, herein designated VGAM RNA, and which when bound by VGAM2312 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2312 host target proteins.

[32333] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2312 gene, herein designated VGAM GENE, on one

or more VGAM2312 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32334] It is yet further appreciated that a function of VGAM2312 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2312 include diagnosis, prevention and treatment of viral infection by lumpy skin disease virus. Specific functions, and accordingly utilities, of VGAM2312 correlate with, and may be deduced from, the identity of the host target genes which VGAM2312 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[32335] Nucleotide sequences of the VGAM2312 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2312 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2312 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2312 are further described hereinbelow with reference to Table 1.

[32336] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2312 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[32337] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2313 (VGAM2313) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[32338] VGAM2313 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2313 was detected is de-

scribed hereinabove with reference to Figs. 2-8.

[32339] VGAM2313 gene, herein designated VGAM GENE, is a viral gene contained in the genome of lumpy skin disease virus. VGAM2313 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[32340] VGAM2313 gene, herein designated VGAM GENE, encodes a VGAM2313 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2313 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2313 precursor RNA is designated SEQ ID:2299, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2299 is located at position 146111 relative to the genome of lumpy skin disease virus.

[32341] VGAM2313 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2313 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32342] An enzyme complex designated DICER COMPLEX, dices the VGAM2313 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2313 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 47%) nucleotide sequence of VGAM2313 RNA is designated SEQ ID:5024, and is provided hereinbelow with reference to the sequence listing part.

[32343] VGAM2313 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2313 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2313 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding

gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32344] VGAM2313 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2313 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2313 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2313 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2313 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be lo-

cated in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32345] The complementary binding of VGAM2313 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2313 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2313 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2313 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[32346] It is appreciated that VGAM2313 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2313 host target genes. The mRNA of each one of this plurality of VGAM2313 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2313 RNA, herein designated VGAM RNA, and which when bound by VGAM2313 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2313 host target proteins.

[32347] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM2313 gene, herein designated VGAM GENE, on one or more VGAM2313 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32348] It is yet further appreciated that a function of VGAM2313 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2313 include diagnosis, prevention and treatment of viral infection by lumpy skin disease virus. Specific functions, and accordingly utilities, of VGAM2313 correlate with, and may be deduced from, the identity of the host target genes which VGAM2313 binds and in-

hibits, and the function of these host target genes, as elaborated hereinbelow.

[32349] Nucleotide sequences of the VGAM2313 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2313 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2313 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2313 are further described hereinbelow with reference to Table 1.

[32350] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2313 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[32351] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2314 (VGAM2314) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[32352] VGAM2314 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2314 was detected is described hereinabove with reference to Figs. 2-8.

[32353] VGAM2314 gene, herein designated VGAM GENE, is a viral gene contained in the genome of lumpy skin disease virus. VGAM2314 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[32354] VGAM2314 gene, herein designated VGAM GENE, encodes a VGAM2314 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2314 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2314 precursor RNA is designated SEQ ID:2300, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2300 is located at position 715 relative to the genome of lumpy skin disease virus.

[32355] VGAM2314 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2314 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32356] An enzyme complex designated DICER COMPLEX, dices the VGAM2314 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2314 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 57%) nucleotide sequence of VGAM2314 RNA is designated SEQ ID:5025, and is provided hereinbelow with reference to the sequence listing part.

[32357] VGAM2314 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2314 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2314 host target RNA, herein designated VGAM HOST TARGET RNA, comprises

three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32358] VGAM2314 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2314 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2314 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2314 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2314 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an

example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32359] The complementary binding of VGAM2314 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2314 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2314 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2314 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[32360] It is appreciated that VGAM2314 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2314 host target genes. The mRNA of each one of this plurality of VGAM2314 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2314 RNA, herein designated VGAM RNA, and which when bound by VGAM2314 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2314 host target proteins.

[32361] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2314 gene, herein designated VGAM GENE, on one or more VGAM2314 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32362] It is yet further appreciated that a function of VGAM2314 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2314 include diagnosis, prevention and treatment of viral infection by lumpy skin disease virus. Specific functions, and accordingly utilities, of VGAM2314 correlate with, and may be deduced from, the identity of

the host target genes which VGAM2314 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[32363] Nucleotide sequences of the VGAM2314 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2314 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2314 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2314 are further described hereinbelow with reference to Table 1.

[32364] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2314 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[32365] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2315 (VGAM2315) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[32366] VGAM2315 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2315 was detected is described hereinabove with reference to Figs. 2-8.

[32367] VGAM2315 gene, herein designated VGAM GENE, is a viral gene contained in the genome of lumpy skin disease virus. VGAM2315 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[32368] VGAM2315 gene, herein designated VGAM GENE, encodes a VGAM2315 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2315 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2315 precursor RNA is designated SEQ ID:2301, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2301 is located at position 128712 relative to the genome of lumpy skin disease virus.

[32369] VGAM2315 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2315 folded

precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32370] An enzyme complex designated DICER COMPLEX, dices the VGAM2315 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2315 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2315 RNA is designated SEQ ID:5026, and is provided hereinbelow with reference to the sequence listing part.

[32371] VGAM2315 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2315 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM2315 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32372] VGAM2315 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2315 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2315 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2315 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2315 host target RNA, herein designated VGAM HOST TARGET RNA.

It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32373] The complementary binding of VGAM2315 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2315 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2315 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2315 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[32374] It is appreciated that VGAM2315 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2315 host target genes. The mRNA of each one of this plurality of VGAM2315 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2315 RNA, herein designated VGAM RNA, and which when bound by VGAM2315 RNA, herein designated VGAM RNA, causes inhibition of translation of

respective one or more VGAM2315 host target proteins.

[32375] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2315 gene, herein designated VGAM GENE, on one or more VGAM2315 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32376] It is yet further appreciated that a function of VGAM2315 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2315 include diagnosis, prevention and treatment of viral infection by lumpy skin disease virus.

Specific functions, and accordingly utilities, of VGAM2315 correlate with, and may be deduced from, the identity of the host target genes which VGAM2315 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[32377] Nucleotide sequences of the VGAM2315 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2315 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2315 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2315 are further described hereinbelow with reference to Table 1.

[32378] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2315 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[32379] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2316 (VGAM2316) viral gene, which modulates expression of respective host target genes thereof, the func-

tion and utility of which host target genes is known in the art.

[32380] VGAM2316 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2316 was detected is described hereinabove with reference to Figs. 2-8.

[32381] VGAM2316 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rana tigrina ranavirus. VGAM2316 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[32382] VGAM2316 gene, herein designated VGAM GENE, encodes a VGAM2316 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2316 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2316 precursor RNA is designated SEQ ID:2302, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2302 is located at position 33473 relative to the genome of Rana tigrina ranavirus.

[32383] VGAM2316 precursor RNA, herein designated VGAM PRE-

CURSOR RNA, folds onto itself, forming VGAM2316 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32384] An enzyme complex designated DICER COMPLEX, dices the VGAM2316 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2316 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2316 RNA is designated SEQ ID:5027, and is provided hereinbelow with reference to the sequence listing part.

[32385] VGAM2316 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM2316 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2316 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32386] VGAM2316 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2316 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2316 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2316 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2316 host

target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32387] The complementary binding of VGAM2316 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2316 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2316 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2316 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[32388] It is appreciated that VGAM2316 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2316 host target genes. The mRNA of each one of this plurality of VGAM2316 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2316 RNA, herein designated VGAM RNA, and which when bound by VGAM2316 RNA, herein

designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2316 host target proteins.

[32389] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2316 gene, herein designated VGAM GENE, on one or more VGAM2316 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32390] It is yet further appreciated that a function of VGAM2316 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2316 include diagnosis, prevention and

treatment of viral infection by Rana tigrina ranavirus. Specific functions, and accordingly utilities, of VGAM2316 correlate with, and may be deduced from, the identity of the host target genes which VGAM2316 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[32391] Nucleotide sequences of the VGAM2316 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2316 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2316 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2316 are further described hereinbelow with reference to Table 1.

[32392] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2316 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[32393] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2317 (VGAM2317) viral gene, which modulates ex-

pression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[32394] VGAM2317 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2317 was detected is described hereinabove with reference to Figs. 2-8.

[32395] VGAM2317 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rana tigrina ranavirus. VGAM2317 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[32396] VGAM2317 gene, herein designated VGAM GENE, encodes a VGAM2317 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2317 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2317 precursor RNA is designated SEQ ID:2303, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2303 is located at position 24685 relative to the genome of Rana tigrina ranavirus.

[32397] VGAM2317 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2317 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32398] An enzyme complex designated DICER COMPLEX, dices the VGAM2317 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2317 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2317 RNA is designated SEQ ID:5028, and is provided hereinbelow with reference to the sequence listing part.

[32399] VGAM2317 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2317 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2317 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32400] VGAM2317 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2317 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2317 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2317 RNA, herein designated VGAM RNA, may have a different number of host target

binding sites in untranslated regions of a VGAM2317 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32401] The complementary binding of VGAM2317 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2317 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2317 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2317 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[32402] It is appreciated that VGAM2317 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2317 host target genes. The mRNA of each one of this plurality of VGAM2317 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2317 RNA, herein designated VGAM

RNA, and which when bound by VGAM2317 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2317 host target proteins.

[32403] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2317 gene, herein designated VGAM GENE, on one or more VGAM2317 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32404] It is yet further appreciated that a function of VGAM2317 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM2317 include diagnosis, prevention and treatment of viral infection by Rana tigrina ranavirus. Specific functions, and accordingly utilities, of VGAM2317 correlate with, and may be deduced from, the identity of the host target genes which VGAM2317 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[32405] Nucleotide sequences of the VGAM2317 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2317 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2317 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2317 are further described hereinbelow with reference to Table 1.

[32406] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2317 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[32407] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Mes-

senger 2318 (VGAM2318) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[32408] VGAM2318 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2318 was detected is described hereinabove with reference to Figs. 2-8.

[32409] VGAM2318 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rana tigrina ranavirus. VGAM2318 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[32410] VGAM2318 gene, herein designated VGAM GENE, encodes a VGAM2318 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2318 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2318 precursor RNA is designated SEQ ID:2304, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2304 is located at position

35010 relative to the genome of Rana tigrina ranavirus.

[32411] VGAM2318 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2318 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32412] An enzyme complex designated DICER COMPLEX, dices the VGAM2318 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2318 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2318 RNA is designated SEQ ID:5029, and is provided hereinbelow with reference to the sequence listing part.

[32413] VGAM2318 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2318 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2318 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32414] VGAM2318 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2318 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2318 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2318 RNA, herein designated

VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2318 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32415] The complementary binding of VGAM2318 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2318 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2318 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2318 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[32416] It is appreciated that VGAM2318 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2318 host target genes. The mRNA of each one of this plurality of VGAM2318 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM2318 RNA, herein designated VGAM RNA, and which when bound by VGAM2318 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2318 host target proteins.

[32417] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2318 gene, herein designated VGAM GENE, on one or more VGAM2318 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32418] It is yet further appreciated that a function of VGAM2318 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2318 include diagnosis, prevention and treatment of viral infection by Rana tigrina ranavirus. Specific functions, and accordingly utilities, of VGAM2318 correlate with, and may be deduced from, the identity of the host target genes which VGAM2318 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[32419] Nucleotide sequences of the VGAM2318 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2318 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2318 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2318 are further described hereinbelow with reference to Table 1.

[32420] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2318 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[32421] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present

invention, referred to here as Viral Genomic Address Messenger 2319 (VGAM2319) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[32422] VGAM2319 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2319 was detected is described hereinabove with reference to Figs. 2-8.

[32423] VGAM2319 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rana tigrina ranavirus. VGAM2319 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[32424] VGAM2319 gene, herein designated VGAM GENE, encodes a VGAM2319 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2319 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2319 precursor RNA is designated SEQ ID:2305, and is provided hereinbelow with reference to the sequence listing part. Nu-

cleotide sequence SEQ ID:2305 is located at position 15762 relative to the genome of Rana tigrina ranavirus.

[32425] VGAM2319 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2319 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32426] An enzyme complex designated DICER COMPLEX, dices the VGAM2319 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2319 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2319 RNA is designated SEQ ID:5030, and is provided hereinbelow with reference to the sequence

listing part.

[32427] VGAM2319 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2319 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2319 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32428] VGAM2319 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2319 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2319 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not

meant to be limiting VGAM2319 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2319 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32429] The complementary binding of VGAM2319 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2319 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2319 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2319 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[32430] It is appreciated that VGAM2319 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2319 host target genes. The mRNA of each one of this plurality of VGAM2319 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2319 RNA, herein designated VGAM RNA, and which when bound by VGAM2319 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2319 host target proteins.

[32431] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2319 gene, herein designated VGAM GENE, on one or more VGAM2319 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32432] It is yet further appreciated that a function of VGAM2319

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2319 include diagnosis, prevention and treatment of viral infection by Rana tigrina ranavirus. Specific functions, and accordingly utilities, of VGAM2319 correlate with, and may be deduced from, the identity of the host target genes which VGAM2319 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[32433] Nucleotide sequences of the VGAM2319 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2319 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2319 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2319 are further described hereinbelow with reference to Table 1.

[32434] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2319 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[32435] Fig. 1 further provides a conceptual description of another

novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2320 (VGAM2320) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[32436] VGAM2320 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2320 was detected is described hereinabove with reference to Figs. 2-8.

[32437] VGAM2320 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rana tigrina ranavirus. VGAM2320 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[32438] VGAM2320 gene, herein designated VGAM GENE, encodes a VGAM2320 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2320 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2320 precursor RNA is designated SEQ ID:2306, and is provided here-

inbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2306 is located at position 28526 relative to the genome of Rana tigrina ranavirus.

[32439] VGAM2320 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2320 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32440] An enzyme complex designated DICER COMPLEX, dices the VGAM2320 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2320 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 48%) nucleotide sequence of VGAM2320 RNA is designated SEQ ID:5031, and

is provided hereinbelow with reference to the sequence listing part.

[32441] VGAM2320 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2320 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2320 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32442] VGAM2320 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2320 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2320 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites

shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2320 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2320 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32443] The complementary binding of VGAM2320 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2320 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2320 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2320 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[32444] It is appreciated that VGAM2320 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2320 host target genes. The mRNA of each one of this plurality of VGAM2320 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2320 RNA, herein designated VGAM RNA, and which when bound by VGAM2320 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2320 host target proteins.

[32445] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2320 gene, herein designated VGAM GENE, on one or more VGAM2320 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32446] It is yet further appreciated that a function of VGAM2320 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2320 include diagnosis, prevention and treatment of viral infection by Rana tigrina ranavirus. Specific functions, and accordingly utilities, of VGAM2320 correlate with, and may be deduced from, the identity of the host target genes which VGAM2320 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[32447] Nucleotide sequences of the VGAM2320 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2320 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2320 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2320 are further described hereinbelow with reference to Table 1.

[32448] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2320 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[32449] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2321 (VGAM2321) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[32450] VGAM2321 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2321 was detected is described hereinabove with reference to Figs. 2-8.

[32451] VGAM2321 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rana tigrina ranavirus. VGAM2321 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[32452] VGAM2321 gene, herein designated VGAM GENE, encodes a VGAM2321 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2321 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2321 precur-

sor RNA is designated SEQ ID:2307, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2307 is located at position 24842 relative to the genome of Rana tigrina ranavirus.

[32453] VGAM2321 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2321 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32454] An enzyme complex designated DICER COMPLEX, dices the VGAM2321 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2321 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide se-

quence of VGAM2321 RNA is designated SEQ ID:5032, and is provided hereinbelow with reference to the sequence listing part.

[32455] VGAM2321 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2321 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2321 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32456] VGAM2321 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2321 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2321 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is ap-

preciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2321 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2321 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32457] The complementary binding of VGAM2321 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2321 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2321 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2321 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[32458] It is appreciated that VGAM2321 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2321 host target genes. The mRNA of

each one of this plurality of VGAM2321 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2321 RNA, herein designated VGAM RNA, and which when bound by VGAM2321 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2321 host target proteins.

[32459] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2321 gene, herein designated VGAM GENE, on one or more VGAM2321 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science

294,779 (2001)).

[32460] It is yet further appreciated that a function of VGAM2321 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2321 include diagnosis, prevention and treatment of viral infection by Rana tigrina ranavirus. Specific functions, and accordingly utilities, of VGAM2321 correlate with, and may be deduced from, the identity of the host target genes which VGAM2321 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[32461] Nucleotide sequences of the VGAM2321 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2321 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2321 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2321 are further described hereinbelow with reference to Table 1.

[32462] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2321 RNA, herein designated VGAM RNA, are de-

scribed hereinbelow with reference to Table 2.

[32463] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2322 (VGAM2322) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[32464] VGAM2322 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2322 was detected is described hereinabove with reference to Figs. 2-8.

[32465] VGAM2322 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rana tigrina ranavirus. VGAM2322 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[32466] VGAM2322 gene, herein designated VGAM GENE, encodes a VGAM2322 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2322 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly

similar to the nucleotide sequence of VGAM2322 precursor RNA is designated SEQ ID:2308, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2308 is located at position 49980 relative to the genome of Rana tigrina ranavirus.

[32467] VGAM2322 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2322 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32468] An enzyme complex designated DICER COMPLEX, dices the VGAM2322 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2322 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2322 RNA is designated SEQ ID:5033, and is provided hereinbelow with reference to the sequence listing part.

[32469] VGAM2322 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2322 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2322 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32470] VGAM2322 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2322 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2322 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I,

BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2322 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2322 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32471] The complementary binding of VGAM2322 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2322 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2322 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2322 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[32472] It is appreciated that VGAM2322 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM2322 host target genes. The mRNA of each one of this plurality of VGAM2322 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2322 RNA, herein designated VGAM RNA, and which when bound by VGAM2322 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2322 host target proteins.

[32473] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2322 gene, herein designated VGAM GENE, on one or more VGAM2322 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32474] It is yet further appreciated that a function of VGAM2322 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2322 include diagnosis, prevention and treatment of viral infection by Rana tigrina ranavirus. Specific functions, and accordingly utilities, of VGAM2322 correlate with, and may be deduced from, the identity of the host target genes which VGAM2322 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[32475] Nucleotide sequences of the VGAM2322 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2322 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2322 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2322 are further described hereinbelow with reference to Table 1.

[32476] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites

to VGAM2322 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[32477] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2323 (VGAM2323) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[32478] VGAM2323 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2323 was detected is described hereinabove with reference to Figs. 2-8.

[32479] VGAM2323 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rana tigrina ranavirus. VGAM2323 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[32480] VGAM2323 gene, herein designated VGAM GENE, encodes a VGAM2323 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2323 precursor RNA, herein designated VGAM PRECURSOR RNA, does not en-

code a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2323 precursor RNA is designated SEQ ID:2309, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2309 is located at position 27691 relative to the genome of Rana tigrina ranavirus.

[32481] VGAM2323 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2323 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32482] An enzyme complex designated DICER COMPLEX, dices the VGAM2323 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2323 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2323 RNA is designated SEQ ID:5034, and is provided hereinbelow with reference to the sequence listing part.

[32483] VGAM2323 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2323 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2323 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32484] VGAM2323 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2323 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2323 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3

such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2323 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2323 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32485] The complementary binding of VGAM2323 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2323 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2323 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2323 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[32486] It is appreciated that VGAM2323 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2323 host target genes. The mRNA of each one of this plurality of VGAM2323 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2323 RNA, herein designated VGAM RNA, and which when bound by VGAM2323 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2323 host target proteins.

[32487] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2323 gene, herein designated VGAM GENE, on one or more VGAM2323 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32488] It is yet further appreciated that a function of VGAM2323 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2323 include diagnosis, prevention and treatment of viral infection by Rana tigrina ranavirus. Specific functions, and accordingly utilities, of VGAM2323 correlate with, and may be deduced from, the identity of the host target genes which VGAM2323 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[32489] Nucleotide sequences of the VGAM2323 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2323 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2323 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2323 are further described hereinbelow with reference to Table 1.

[32490] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the

complementarity of each of these host target binding sites to VGAM2323 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[32491] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2324 (VGAM2324) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[32492] VGAM2324 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2324 was detected is described hereinabove with reference to Figs. 2-8.

[32493] VGAM2324 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rana tigrina ranavirus. VGAM2324 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[32494] VGAM2324 gene, herein designated VGAM GENE, encodes a VGAM2324 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2324 precursor RNA,

herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2324 precursor RNA is designated SEQ ID:2310, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2310 is located at position 26882 relative to the genome of Rana tigrina ranavirus.

[32495] VGAM2324 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2324 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32496] An enzyme complex designated DICER COMPLEX, dices the VGAM2324 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2324 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2324 RNA is designated SEQ ID:5035, and is provided hereinbelow with reference to the sequence listing part.

[32497] VGAM2324 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2324 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2324 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32498] VGAM2324 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2324 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2324 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host

target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2324 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2324 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32499] The complementary binding of VGAM2324 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2324 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2324 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2324 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[32500] It is appreciated that VGAM2324 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2324 host target genes. The mRNA of each one of this plurality of VGAM2324 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2324 RNA, herein designated VGAM RNA, and which when bound by VGAM2324 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2324 host target proteins.

[32501] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2324 gene, herein designated VGAM GENE, on one or more VGAM2324 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32502] It is yet further appreciated that a function of VGAM2324 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2324 include diagnosis, prevention and treatment of viral infection by Rana tigrina ranavirus. Specific functions, and accordingly utilities, of VGAM2324 correlate with, and may be deduced from, the identity of the host target genes which VGAM2324 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[32503] Nucleotide sequences of the VGAM2324 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2324 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2324 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2324 are further described hereinbelow with reference to Table 1.

[32504] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2324 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[32505] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2325 (VGAM2325) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[32506] VGAM2325 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2325 was detected is described hereinabove with reference to Figs. 2-8.

[32507] VGAM2325 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rana tigrina ranavirus. VGAM2325 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[32508] VGAM2325 gene, herein designated VGAM GENE, encodes a VGAM2325 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and un-

like most ordinary genes, VGAM2325 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2325 precursor RNA is designated SEQ ID:2311, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2311 is located at position 28131 relative to the genome of Rana tigrina ranavirus.

[32509] VGAM2325 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2325 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32510] An enzyme complex designated DICER COMPLEX, dices the VGAM2325 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2325 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 55%) nucleotide sequence of VGAM2325 RNA is designated SEQ ID:5036, and is provided hereinbelow with reference to the sequence listing part.

[32511] VGAM2325 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2325 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2325 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32512] VGAM2325 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2325 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2325 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed

sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2325 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2325 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32513] The complementary binding of VGAM2325 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2325 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2325 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2325 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target

protein is therefore outlined by a broken line.

[32514] It is appreciated that VGAM2325 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2325 host target genes. The mRNA of each one of this plurality of VGAM2325 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2325 RNA, herein designated VGAM RNA, and which when bound by VGAM2325 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2325 host target proteins.

[32515] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2325 gene, herein designated VGAM GENE, on one or more VGAM2325 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32516] It is yet further appreciated that a function of VGAM2325 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2325 include diagnosis, prevention and treatment of viral infection by Rana tigrina ranavirus. Specific functions, and accordingly utilities, of VGAM2325 correlate with, and may be deduced from, the identity of the host target genes which VGAM2325 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[32517] Nucleotide sequences of the VGAM2325 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2325 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2325 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2325 are further described hereinbelow with reference to Table 1.

[32518] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2325 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[32519] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2326 (VGAM2326) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[32520] VGAM2326 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2326 was detected is described hereinabove with reference to Figs. 2-8.

[32521] VGAM2326 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rana tigrina ranavirus. VGAM2326 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[32522] VGAM2326 gene, herein designated VGAM GENE, encodes a VGAM2326 precursor RNA, herein designated VGAM

PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2326 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2326 precursor RNA is designated SEQ ID:2312, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2312 is located at position 37660 relative to the genome of Rana tigrina ranavirus.

[32523] VGAM2326 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2326 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32524] An enzyme complex designated DICER COMPLEX, dices the VGAM2326 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2326 RNA, herein designated VGAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2326 RNA is designated SEQ ID:5037, and is provided hereinbelow with reference to the sequence listing part.

[32525] VGAM2326 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2326 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2326 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32526] VGAM2326 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2326 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2326 RNA, herein designated

VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2326 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2326 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32527] The complementary binding of VGAM2326 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2326 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2326 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2326 host target protein, herein desig-

nated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[32528] It is appreciated that VGAM2326 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2326 host target genes. The mRNA of each one of this plurality of VGAM2326 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2326 RNA, herein designated VGAM RNA, and which when bound by VGAM2326 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2326 host target proteins.

[32529] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2326 gene, herein designated VGAM GENE, on one or more VGAM2326 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32530] It is yet further appreciated that a function of VGAM2326 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2326 include diagnosis, prevention and treatment of viral infection by Rana tigrina ranavirus. Specific functions, and accordingly utilities, of VGAM2326 correlate with, and may be deduced from, the identity of the host target genes which VGAM2326 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[32531] Nucleotide sequences of the VGAM2326 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2326 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2326 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2326 are further described hereinbelow with reference to Table 1.

[32532] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2326 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[32533] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2327 (VGAM2327) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[32534] VGAM2327 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2327 was detected is described hereinabove with reference to Figs. 2-8.

[32535] VGAM2327 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rana tigrina ranavirus. VGAM2327 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[32536] VGAM2327 gene, herein designated VGAM GENE, encodes

a VGAM2327 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2327 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2327 precursor RNA is designated SEQ ID:2313, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2313 is located at position 30986 relative to the genome of Rana tigrina ranavirus.

[32537] VGAM2327 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2327 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32538] An enzyme complex designated DICER COMPLEX, dices the VGAM2327 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2327 RNA,

herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 90%) nucleotide sequence of VGAM2327 RNA is designated SEQ ID:5038, and is provided hereinbelow with reference to the sequence listing part.

[32539] VGAM2327 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2327 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2327 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32540] VGAM2327 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2327 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM2327 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2327 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2327 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32541] The complementary binding of VGAM2327 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2327 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2327 host target RNA, herein designated VGAM HOST TARGET

RNA, into VGAM2327 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[32542] It is appreciated that VGAM2327 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2327 host target genes. The mRNA of each one of this plurality of VGAM2327 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2327 RNA, herein designated VGAM RNA, and which when bound by VGAM2327 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2327 host target proteins.

[32543] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2327 gene, herein designated VGAM GENE, on one or more VGAM2327 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32544] It is yet further appreciated that a function of VGAM2327 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2327 include diagnosis, prevention and treatment of viral infection by Rana tigrina ranavirus. Specific functions, and accordingly utilities, of VGAM2327 correlate with, and may be deduced from, the identity of the host target genes which VGAM2327 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[32545] Nucleotide sequences of the VGAM2327 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2327 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2327 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2327 are further

described hereinbelow with reference to Table 1.

[32546] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2327 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[32547] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2328 (VGAM2328) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[32548] VGAM2328 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2328 was detected is described hereinabove with reference to Figs. 2-8.

[32549] VGAM2328 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rana tigrina ranavirus. VGAM2328 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[32550] VGAM2328 gene, herein designated VGAM GENE, encodes a VGAM2328 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2328 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2328 precursor RNA is designated SEQ ID:2314, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2314 is located at position 16752 relative to the genome of Rana tigrina ranavirus.

[32551] VGAM2328 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2328 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32552] An enzyme complex designated DICER COMPLEX, dices the VGAM2328 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, into VGAM2328 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of VGAM2328 RNA is designated SEQ ID:5039, and is provided hereinbelow with reference to the sequence listing part.

[32553] VGAM2328 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2328 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2328 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32554] VGAM2328 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2328 host target RNA, herein designated VGAM HOST TARGET RNA. This

complementary binding is due to the fact that the nucleotide sequence of VGAM2328 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2328 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2328 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32555] The complementary binding of VGAM2328 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2328 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2328

host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2328 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[32556] It is appreciated that VGAM2328 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2328 host target genes. The mRNA of each one of this plurality of VGAM2328 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2328 RNA, herein designated VGAM RNA, and which when bound by VGAM2328 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2328 host target proteins.

[32557] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2328 gene, herein designated VGAM GENE, on one or more VGAM2328 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32558] It is yet further appreciated that a function of VGAM2328 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2328 include diagnosis, prevention and treatment of viral infection by Rana tigrina ranavirus. Specific functions, and accordingly utilities, of VGAM2328 correlate with, and may be deduced from, the identity of the host target genes which VGAM2328 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[32559] Nucleotide sequences of the VGAM2328 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2328 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2328 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM2328 are further described hereinbelow with reference to Table 1.

[32560] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2328 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[32561] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2329 (VGAM2329) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[32562] VGAM2329 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2329 was detected is described hereinabove with reference to Figs. 2-8.

[32563] VGAM2329 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine herpesvirus 2. VGAM2329 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the

human genome.

[32564] VGAM2329 gene, herein designated VGAM GENE, encodes a VGAM2329 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2329 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2329 precursor RNA is designated SEQ ID:2315, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2315 is located at position 39739 relative to the genome of Equine herpesvirus 2.

[32565] VGAM2329 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2329 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32566] An enzyme complex designated DICER COMPLEX, dices

the VGAM2329 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2329 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide sequence of VGAM2329 RNA is designated SEQ ID:5040, and is provided hereinbelow with reference to the sequence listing part.

[32567] VGAM2329 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2329 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2329 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32568] VGAM2329 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2329 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2329 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2329 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2329 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32569] The complementary binding of VGAM2329 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2329 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM2329 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2329 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[32570] It is appreciated that VGAM2329 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2329 host target genes. The mRNA of each one of this plurality of VGAM2329 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2329 RNA, herein designated VGAM RNA, and which when bound by VGAM2329 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2329 host target proteins.

[32571] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2329 gene, herein designated VGAM GENE, on one or more VGAM2329 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32572] It is yet further appreciated that a function of VGAM2329 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2329 include diagnosis, prevention and treatment of viral infection by Equine herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2329 correlate with, and may be deduced from, the identity of the host target genes which VGAM2329 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[32573] Nucleotide sequences of the VGAM2329 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2329 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of

VGAM2329 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2329 are further described hereinbelow with reference to Table 1.

[32574] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2329 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[32575] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2330 (VGAM2330) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[32576] VGAM2330 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2330 was detected is described hereinabove with reference to Figs. 2-8.

[32577] VGAM2330 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine herpesvirus 2. VGAM2330 host target gene, herein designated VGAM

HOST TARGET GENE, is a human gene contained in the human genome.

[32578] VGAM2330 gene, herein designated VGAM GENE, encodes a VGAM2330 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2330 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2330 precursor RNA is designated SEQ ID:2316, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2316 is located at position 1147 relative to the genome of Equine herpesvirus 2.

[32579] VGAM2330 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2330 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32580] An enzyme complex designated DICER COMPLEX, dices the VGAM2330 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2330 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 82%) nucleotide sequence of VGAM2330 RNA is designated SEQ ID:5041, and is provided hereinbelow with reference to the sequence listing part.

[32581] VGAM2330 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2330 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2330 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32582] VGAM2330 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites

located in untranslated regions of VGAM2330 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2330 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2330 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2330 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32583] The complementary binding of VGAM2330 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2330 host target RNA, herein designated VGAM

HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2330 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2330 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[32584] It is appreciated that VGAM2330 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2330 host target genes. The mRNA of each one of this plurality of VGAM2330 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2330 RNA, herein designated VGAM RNA, and which when bound by VGAM2330 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2330 host target proteins.

[32585] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2330 gene, herein designated VGAM GENE, on one or more VGAM2330 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove

with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32586] It is yet further appreciated that a function of VGAM2330 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2330 include diagnosis, prevention and treatment of viral infection by Equine herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2330 correlate with, and may be deduced from, the identity of the host target genes which VGAM2330 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[32587] Nucleotide sequences of the VGAM2330 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2330 RNA, herein designated VGAM RNA, and

a schematic representation of the secondary folding of VGAM2330 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2330 are further described hereinbelow with reference to Table 1.

[32588] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2330 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[32589] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2331 (VGAM2331) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[32590] VGAM2331 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2331 was detected is described hereinabove with reference to Figs. 2-8.

[32591] VGAM2331 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine herpesvirus 2.

VGAM2331 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[32592] VGAM2331 gene, herein designated VGAM GENE, encodes a VGAM2331 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2331 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2331 precursor RNA is designated SEQ ID:2317, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2317 is located at position 42566 relative to the genome of Equine herpesvirus 2.

[32593] VGAM2331 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2331 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[32594] An enzyme complex designated DICER COMPLEX, dices the VGAM2331 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2331 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 50%) nucleotide sequence of VGAM2331 RNA is designated SEQ ID:5042, and is provided hereinbelow with reference to the sequence listing part.

[32595] VGAM2331 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2331 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2331 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32596] VGAM2331 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM2331 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2331 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2331 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2331 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32597] The complementary binding of VGAM2331 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM2331 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2331 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2331 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[32598] It is appreciated that VGAM2331 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2331 host target genes. The mRNA of each one of this plurality of VGAM2331 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2331 RNA, herein designated VGAM RNA, and which when bound by VGAM2331 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2331 host target proteins.

[32599] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2331 gene, herein designated VGAM GENE, on one or more VGAM2331 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32600] It is yet further appreciated that a function of VGAM2331 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2331 include diagnosis, prevention and treatment of viral infection by Equine herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2331 correlate with, and may be deduced from, the identity of the host target genes which VGAM2331 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[32601] Nucleotide sequences of the VGAM2331 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

diced VGAM2331 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2331 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2331 are further described hereinbelow with reference to Table 1.

[32602] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2331 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[32603] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2332 (VGAM2332) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[32604] VGAM2332 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2332 was detected is described hereinabove with reference to Figs. 2-8.

[32605] VGAM2332 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of Equine herpesvirus 2. VGAM2332 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[32606] VGAM2332 gene, herein designated VGAM GENE, encodes a VGAM2332 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2332 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2332 precursor RNA is designated SEQ ID:2318, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2318 is located at position 21991 relative to the genome of Equine herpesvirus 2.

[32607] VGAM2332 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2332 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32608] An enzyme complex designated DICER COMPLEX, dices the VGAM2332 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2332 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2332 RNA is designated SEQ ID:5043, and is provided hereinbelow with reference to the sequence listing part.

[32609] VGAM2332 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2332 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2332 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32610] VGAM2332 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2332 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2332 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2332 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2332 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32611] The complementary binding of VGAM2332 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM2332 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2332 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2332 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[32612] It is appreciated that VGAM2332 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2332 host target genes. The mRNA of each one of this plurality of VGAM2332 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2332 RNA, herein designated VGAM RNA, and which when bound by VGAM2332 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2332 host target proteins.

[32613] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2332 gene, herein designated VGAM GENE, on one or more VGAM2332 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32614] It is yet further appreciated that a function of VGAM2332 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2332 include diagnosis, prevention and treatment of viral infection by Equine herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2332 correlate with, and may be deduced from, the identity of the host target genes which VGAM2332 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[32615] Nucleotide sequences of the VGAM2332 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the diced VGAM2332 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2332 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2332 are further described hereinbelow with reference to Table 1.

[32616] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2332 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[32617] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2333 (VGAM2333) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[32618] VGAM2333 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2333 was detected is described hereinabove with reference to Figs. 2-8.

[32619] VGAM2333 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine herpesvirus 2. VGAM2333 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[32620] VGAM2333 gene, herein designated VGAM GENE, encodes a VGAM2333 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2333 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2333 precursor RNA is designated SEQ ID:2319, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2319 is located at position 36149 relative to the genome of Equine herpesvirus 2.

[32621] VGAM2333 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2333 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32622] An enzyme complex designated DICER COMPLEX, dices the VGAM2333 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2333 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2333 RNA is designated SEQ ID:5044, and is provided hereinbelow with reference to the sequence listing part.

[32623] VGAM2333 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2333 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2333 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN COD-

ING and 3UTR respectively.

[32624] VGAM2333 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2333 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2333 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2333 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2333 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32625] The complementary binding of VGAM2333 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2333 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2333 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2333 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[32626] It is appreciated that VGAM2333 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2333 host target genes. The mRNA of each one of this plurality of VGAM2333 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2333 RNA, herein designated VGAM RNA, and which when bound by VGAM2333 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2333 host target proteins.

[32627] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2333 gene, herein designated VGAM GENE, on one or more VGAM2333 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32628] It is yet further appreciated that a function of VGAM2333 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2333 include diagnosis, prevention and treatment of viral infection by Equine herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2333

correlate with, and may be deduced from, the identity of the host target genes which VGAM2333 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[32629] Nucleotide sequences of the VGAM2333 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2333 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2333 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2333 are further described hereinbelow with reference to Table 1.

[32630] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2333 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[32631] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2334 (VGAM2334) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the

art.

[32632] VGAM2334 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2334 was detected is described hereinabove with reference to Figs. 2-8.

[32633] VGAM2334 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine herpesvirus 2. VGAM2334 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[32634] VGAM2334 gene, herein designated VGAM GENE, encodes a VGAM2334 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2334 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2334 precursor RNA is designated SEQ ID:2320, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2320 is located at position 40967 relative to the genome of Equine herpesvirus 2.

[32635] VGAM2334 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2334 folded

precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32636] An enzyme complex designated DICER COMPLEX, dices the VGAM2334 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2334 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 52%) nucleotide sequence of VGAM2334 RNA is designated SEQ ID:5045, and is provided hereinbelow with reference to the sequence listing part.

[32637] VGAM2334 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2334 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM2334 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32638] VGAM2334 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2334 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2334 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2334 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2334 host target RNA, herein designated VGAM HOST TARGET RNA.

It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32639] The complementary binding of VGAM2334 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2334 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2334 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2334 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[32640] It is appreciated that VGAM2334 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2334 host target genes. The mRNA of each one of this plurality of VGAM2334 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2334 RNA, herein designated VGAM RNA, and which when bound by VGAM2334 RNA, herein designated VGAM RNA, causes inhibition of translation of

respective one or more VGAM2334 host target proteins.

[32641] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2334 gene, herein designated VGAM GENE, on one or more VGAM2334 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32642] It is yet further appreciated that a function of VGAM2334 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2334 include diagnosis, prevention and treatment of viral infection by Equine herpesvirus 2. Spe-

cific functions, and accordingly utilities, of VGAM2334 correlate with, and may be deduced from, the identity of the host target genes which VGAM2334 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[32643] Nucleotide sequences of the VGAM2334 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2334 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2334 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2334 are further described hereinbelow with reference to Table 1.

[32644] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2334 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[32645] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2335 (VGAM2335) viral gene, which modulates expression of respective host target genes thereof, the func-

tion and utility of which host target genes is known in the art.

[32646] VGAM2335 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2335 was detected is described hereinabove with reference to Figs. 2-8.

[32647] VGAM2335 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine herpesvirus 2. VGAM2335 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[32648] VGAM2335 gene, herein designated VGAM GENE, encodes a VGAM2335 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2335 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2335 precursor RNA is designated SEQ ID:2321, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2321 is located at position 42087 relative to the genome of Equine herpesvirus 2.

[32649] VGAM2335 precursor RNA, herein designated VGAM PRE-

CURSOR RNA, folds onto itself, forming VGAM2335 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32650] An enzyme complex designated DICER COMPLEX, dices the VGAM2335 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2335 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 49%) nucleotide sequence of VGAM2335 RNA is designated SEQ ID:5046, and is provided hereinbelow with reference to the sequence listing part.

[32651] VGAM2335 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM2335 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2335 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32652] VGAM2335 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2335 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2335 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2335 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2335 host

target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32653] The complementary binding of VGAM2335 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2335 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2335 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2335 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[32654] It is appreciated that VGAM2335 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2335 host target genes. The mRNA of each one of this plurality of VGAM2335 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2335 RNA, herein designated VGAM RNA, and which when bound by VGAM2335 RNA, herein

designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2335 host target proteins.

[32655] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2335 gene, herein designated VGAM GENE, on one or more VGAM2335 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32656] It is yet further appreciated that a function of VGAM2335 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2335 include diagnosis, prevention and

treatment of viral infection by Equine herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2335 correlate with, and may be deduced from, the identity of the host target genes which VGAM2335 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[32657] Nucleotide sequences of the VGAM2335 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2335 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2335 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2335 are further described hereinbelow with reference to Table 1.

[32658] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2335 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[32659] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2336 (VGAM2336) viral gene, which modulates ex-

pression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[32660] VGAM2336 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2336 was detected is described hereinabove with reference to Figs. 2-8.

[32661] VGAM2336 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine herpesvirus 2. VGAM2336 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[32662] VGAM2336 gene, herein designated VGAM GENE, encodes a VGAM2336 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2336 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2336 precursor RNA is designated SEQ ID:2322, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2322 is located at position 40488 relative to the genome of Equine herpesvirus 2.

[32663] VGAM2336 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2336 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32664] An enzyme complex designated DICER COMPLEX, dices the VGAM2336 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2336 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2336 RNA is designated SEQ ID:5047, and is provided hereinbelow with reference to the sequence listing part.

[32665] VGAM2336 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2336 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2336 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32666] VGAM2336 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2336 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2336 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2336 RNA, herein designated VGAM RNA, may have a different number of host target

binding sites in untranslated regions of a VGAM2336 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32667] The complementary binding of VGAM2336 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2336 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2336 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2336 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[32668] It is appreciated that VGAM2336 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2336 host target genes. The mRNA of each one of this plurality of VGAM2336 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2336 RNA, herein designated VGAM

RNA, and which when bound by VGAM2336 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2336 host target proteins.

[32669] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2336 gene, herein designated VGAM GENE, on one or more VGAM2336 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32670] It is yet further appreciated that a function of VGAM2336 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM2336 include diagnosis, prevention and treatment of viral infection by Equine herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2336 correlate with, and may be deduced from, the identity of the host target genes which VGAM2336 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[32671] Nucleotide sequences of the VGAM2336 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2336 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2336 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2336 are further described hereinbelow with reference to Table 1.

[32672] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2336 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[32673] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Mes-

senger 2337 (VGAM2337) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[32674] VGAM2337 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2337 was detected is described hereinabove with reference to Figs. 2-8.

[32675] VGAM2337 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine herpesvirus 2. VGAM2337 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[32676] VGAM2337 gene, herein designated VGAM GENE, encodes a VGAM2337 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2337 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2337 precursor RNA is designated SEQ ID:2323, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2323 is located at position

42439 relative to the genome of Equine herpesvirus 2.

[32677] VGAM2337 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2337 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32678] An enzyme complex designated DICER COMPLEX, dices the VGAM2337 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2337 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2337 RNA is designated SEQ ID:5048, and is provided hereinbelow with reference to the sequence listing part.

[32679] VGAM2337 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2337 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2337 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32680] VGAM2337 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2337 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2337 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2337 RNA, herein designated

VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2337 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32681] The complementary binding of VGAM2337 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2337 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2337 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2337 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[32682] It is appreciated that VGAM2337 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2337 host target genes. The mRNA of each one of this plurality of VGAM2337 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM2337 RNA, herein designated VGAM RNA, and which when bound by VGAM2337 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2337 host target proteins.

[32683] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2337 gene, herein designated VGAM GENE, on one or more VGAM2337 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32684] It is yet further appreciated that a function of VGAM2337 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2337 include diagnosis, prevention and treatment of viral infection by Equine herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2337 correlate with, and may be deduced from, the identity of the host target genes which VGAM2337 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[32685] Nucleotide sequences of the VGAM2337 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2337 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2337 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2337 are further described hereinbelow with reference to Table 1.

[32686] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2337 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[32687] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present

invention, referred to here as Viral Genomic Address Messenger 2338 (VGAM2338) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[32688] VGAM2338 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2338 was detected is described hereinabove with reference to Figs. 2-8.

[32689] VGAM2338 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine herpesvirus 2. VGAM2338 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[32690] VGAM2338 gene, herein designated VGAM GENE, encodes a VGAM2338 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2338 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2338 precursor RNA is designated SEQ ID:2324, and is provided hereinbelow with reference to the sequence listing part. Nu-

cleotide sequence SEQ ID:2324 is located at position 36402 relative to the genome of Equine herpesvirus 2.

[32691] VGAM2338 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2338 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32692] An enzyme complex designated DICER COMPLEX, dices the VGAM2338 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2338 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2338 RNA is designated SEQ ID:5049, and is provided hereinbelow with reference to the sequence

listing part.

[32693] VGAM2338 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2338 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2338 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32694] VGAM2338 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2338 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2338 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not

meant to be limiting VGAM2338 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2338 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32695] The complementary binding of VGAM2338 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2338 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2338 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2338 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[32696] It is appreciated that VGAM2338 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2338 host target genes. The mRNA of each one of this plurality of VGAM2338 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2338 RNA, herein designated VGAM RNA, and which when bound by VGAM2338 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2338 host target proteins.

[32697] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2338 gene, herein designated VGAM GENE, on one or more VGAM2338 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32698] It is yet further appreciated that a function of VGAM2338

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2338 include diagnosis, prevention and treatment of viral infection by Equine herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2338 correlate with, and may be deduced from, the identity of the host target genes which VGAM2338 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[32699] Nucleotide sequences of the VGAM2338 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2338 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2338 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2338 are further described hereinbelow with reference to Table 1.

[32700] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2338 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[32701] Fig. 1 further provides a conceptual description of another

novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2339 (VGAM2339) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[32702] VGAM2339 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2339 was detected is described hereinabove with reference to Figs. 2-8.

[32703] VGAM2339 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine herpesvirus 2. VGAM2339 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[32704] VGAM2339 gene, herein designated VGAM GENE, encodes a VGAM2339 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2339 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2339 precursor RNA is designated SEQ ID:2325, and is provided here-

inbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2325 is located at position 42978 relative to the genome of Equine herpesvirus 2.

[32705] VGAM2339 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2339 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32706] An enzyme complex designated DICER COMPLEX, dices the VGAM2339 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2339 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 60%) nucleotide sequence of VGAM2339 RNA is designated SEQ ID:5050, and

is provided hereinbelow with reference to the sequence listing part.

[32707] VGAM2339 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2339 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2339 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32708] VGAM2339 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2339 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2339 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites

shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2339 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2339 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32709] The complementary binding of VGAM2339 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2339 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2339 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2339 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[32710] It is appreciated that VGAM2339 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2339 host target genes. The mRNA of each one of this plurality of VGAM2339 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2339 RNA, herein designated VGAM RNA, and which when bound by VGAM2339 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2339 host target proteins.

[32711] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2339 gene, herein designated VGAM GENE, on one or more VGAM2339 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32712] It is yet further appreciated that a function of VGAM2339 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2339 include diagnosis, prevention and treatment of viral infection by Equine herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2339 correlate with, and may be deduced from, the identity of the host target genes which VGAM2339 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[32713] Nucleotide sequences of the VGAM2339 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2339 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2339 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2339 are further described hereinbelow with reference to Table 1.

[32714] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2339 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[32715] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2340 (VGAM2340) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[32716] VGAM2340 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2340 was detected is described hereinabove with reference to Figs. 2-8.

[32717] VGAM2340 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine herpesvirus 2. VGAM2340 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[32718] VGAM2340 gene, herein designated VGAM GENE, encodes a VGAM2340 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2340 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2340 precur-

sor RNA is designated SEQ ID:2326, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2326 is located at position 42263 relative to the genome of Equine herpesvirus 2.

[32719] VGAM2340 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2340 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32720] An enzyme complex designated DICER COMPLEX, dices the VGAM2340 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2340 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide se-

quence of VGAM2340 RNA is designated SEQ ID:5051, and is provided hereinbelow with reference to the sequence listing part.

[32721] VGAM2340 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2340 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2340 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32722] VGAM2340 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2340 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2340 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is ap-

preciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2340 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2340 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32723] The complementary binding of VGAM2340 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2340 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2340 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2340 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[32724] It is appreciated that VGAM2340 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2340 host target genes. The mRNA of

each one of this plurality of VGAM2340 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2340 RNA, herein designated VGAM RNA, and which when bound by VGAM2340 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2340 host target proteins.

[32725] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2340 gene, herein designated VGAM GENE, on one or more VGAM2340 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science

294,779 (2001)).

[32726] It is yet further appreciated that a function of VGAM2340 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2340 include diagnosis, prevention and treatment of viral infection by Equine herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2340 correlate with, and may be deduced from, the identity of the host target genes which VGAM2340 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[32727] Nucleotide sequences of the VGAM2340 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2340 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2340 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2340 are further described hereinbelow with reference to Table 1.

[32728] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2340 RNA, herein designated VGAM RNA, are de-

scribed hereinbelow with reference to Table 2.

[32729] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2341 (VGAM2341) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[32730] VGAM2341 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2341 was detected is described hereinabove with reference to Figs. 2-8.

[32731] VGAM2341 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine herpesvirus 2. VGAM2341 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[32732] VGAM2341 gene, herein designated VGAM GENE, encodes a VGAM2341 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2341 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly

similar to the nucleotide sequence of VGAM2341 precursor RNA is designated SEQ ID:2327, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2327 is located at position 38415 relative to the genome of Equine herpesvirus 2.

[32733] VGAM2341 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2341 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32734] An enzyme complex designated DICER COMPLEX, dices the VGAM2341 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2341 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2341 RNA is designated SEQ ID:5052, and is provided hereinbelow with reference to the sequence listing part.

[32735] VGAM2341 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2341 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2341 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32736] VGAM2341 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2341 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2341 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I,

BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2341 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2341 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32737] The complementary binding of VGAM2341 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2341 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2341 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2341 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[32738] It is appreciated that VGAM2341 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM2341 host target genes. The mRNA of each one of this plurality of VGAM2341 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2341 RNA, herein designated VGAM RNA, and which when bound by VGAM2341 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2341 host target proteins.

[32739] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2341 gene, herein designated VGAM GENE, on one or more VGAM2341 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32740] It is yet further appreciated that a function of VGAM2341 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2341 include diagnosis, prevention and treatment of viral infection by Equine herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2341 correlate with, and may be deduced from, the identity of the host target genes which VGAM2341 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[32741] Nucleotide sequences of the VGAM2341 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2341 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2341 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2341 are further described hereinbelow with reference to Table 1.

[32742] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites

to VGAM2341 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[32743] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2342 (VGAM2342) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[32744] VGAM2342 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2342 was detected is described hereinabove with reference to Figs. 2-8.

[32745] VGAM2342 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine herpesvirus 2. VGAM2342 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[32746] VGAM2342 gene, herein designated VGAM GENE, encodes a VGAM2342 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2342 precursor RNA, herein designated VGAM PRECURSOR RNA, does not en-

code a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2342 precursor RNA is designated SEQ ID:2328, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2328 is located at position 43910 relative to the genome of Equine herpesvirus 2.

[32747] VGAM2342 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2342 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32748] An enzyme complex designated DICER COMPLEX, dices the VGAM2342 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2342 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2342 RNA is designated SEQ ID:5053, and is provided hereinbelow with reference to the sequence listing part.

[32749] VGAM2342 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2342 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2342 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32750] VGAM2342 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2342 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2342 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3

such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2342 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2342 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32751] The complementary binding of VGAM2342 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2342 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2342 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2342 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[32752] It is appreciated that VGAM2342 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2342 host target genes. The mRNA of each one of this plurality of VGAM2342 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2342 RNA, herein designated VGAM RNA, and which when bound by VGAM2342 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2342 host target proteins.

[32753] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2342 gene, herein designated VGAM GENE, on one or more VGAM2342 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32754] It is yet further appreciated that a function of VGAM2342 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2342 include diagnosis, prevention and treatment of viral infection by Equine herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2342 correlate with, and may be deduced from, the identity of the host target genes which VGAM2342 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[32755] Nucleotide sequences of the VGAM2342 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2342 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2342 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2342 are further described hereinbelow with reference to Table 1.

[32756] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the

complementarity of each of these host target binding sites to VGAM2342 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[32757] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2343 (VGAM2343) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[32758] VGAM2343 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2343 was detected is described hereinabove with reference to Figs. 2-8.

[32759] VGAM2343 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine herpesvirus 2. VGAM2343 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[32760] VGAM2343 gene, herein designated VGAM GENE, encodes a VGAM2343 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2343 precursor RNA,

herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2343 precursor RNA is designated SEQ ID:2329, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2329 is located at position 43126 relative to the genome of Equine herpesvirus 2.

[32761] VGAM2343 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2343 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32762] An enzyme complex designated DICER COMPLEX, dices the VGAM2343 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2343 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2343 RNA is designated SEQ ID:5054, and is provided hereinbelow with reference to the sequence listing part.

[32763] VGAM2343 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2343 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2343 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32764] VGAM2343 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2343 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2343 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host

target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2343 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2343 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32765] The complementary binding of VGAM2343 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2343 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2343 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2343 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[32766] It is appreciated that VGAM2343 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2343 host target genes. The mRNA of each one of this plurality of VGAM2343 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2343 RNA, herein designated VGAM RNA, and which when bound by VGAM2343 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2343 host target proteins.

[32767] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2343 gene, herein designated VGAM GENE, on one or more VGAM2343 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32768] It is yet further appreciated that a function of VGAM2343 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2343 include diagnosis, prevention and treatment of viral infection by Equine herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2343 correlate with, and may be deduced from, the identity of the host target genes which VGAM2343 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[32769] Nucleotide sequences of the VGAM2343 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2343 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2343 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2343 are further described hereinbelow with reference to Table 1.

[32770] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2343 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[32771] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2344 (VGAM2344) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[32772] VGAM2344 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2344 was detected is described hereinabove with reference to Figs. 2-8.

[32773] VGAM2344 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine herpesvirus 2. VGAM2344 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[32774] VGAM2344 gene, herein designated VGAM GENE, encodes a VGAM2344 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and un-

like most ordinary genes, VGAM2344 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2344 precursor RNA is designated SEQ ID:2330, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2330 is located at position 38540 relative to the genome of Equine herpesvirus 2.

[32775] VGAM2344 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2344 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32776] An enzyme complex designated DICER COMPLEX, dices the VGAM2344 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2344 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 92%) nucleotide sequence of VGAM2344 RNA is designated SEQ ID:5055, and is provided hereinbelow with reference to the sequence listing part.

[32777] VGAM2344 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2344 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2344 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32778] VGAM2344 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2344 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2344 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed

sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2344 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2344 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32779] The complementary binding of VGAM2344 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2344 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2344 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2344 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target

protein is therefore outlined by a broken line.

[32780] It is appreciated that VGAM2344 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2344 host target genes. The mRNA of each one of this plurality of VGAM2344 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2344 RNA, herein designated VGAM RNA, and which when bound by VGAM2344 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2344 host target proteins.

[32781] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2344 gene, herein designated VGAM GENE, on one or more VGAM2344 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32782] It is yet further appreciated that a function of VGAM2344 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2344 include diagnosis, prevention and treatment of viral infection by Equine herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2344 correlate with, and may be deduced from, the identity of the host target genes which VGAM2344 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[32783] Nucleotide sequences of the VGAM2344 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2344 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2344 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2344 are further described hereinbelow with reference to Table 1.

[32784] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2344 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[32785] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2345 (VGAM2345) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[32786] VGAM2345 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2345 was detected is described hereinabove with reference to Figs. 2-8.

[32787] VGAM2345 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine herpesvirus 2. VGAM2345 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[32788] VGAM2345 gene, herein designated VGAM GENE, encodes a VGAM2345 precursor RNA, herein designated VGAM

PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2345 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2345 precursor RNA is designated SEQ ID:2331, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2331 is located at position 41319 relative to the genome of Equine herpesvirus 2.

[32789] VGAM2345 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2345 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32790] An enzyme complex designated DICER COMPLEX, dices the VGAM2345 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2345 RNA, herein designated VGAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2345 RNA is designated SEQ ID:5056, and is provided hereinbelow with reference to the sequence listing part.

[32791] VGAM2345 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2345 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2345 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32792] VGAM2345 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2345 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2345 RNA, herein designated

VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2345 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2345 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32793] The complementary binding of VGAM2345 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2345 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2345 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2345 host target protein, herein desig-

nated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[32794] It is appreciated that VGAM2345 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2345 host target genes. The mRNA of each one of this plurality of VGAM2345 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2345 RNA, herein designated VGAM RNA, and which when bound by VGAM2345 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2345 host target proteins.

[32795] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2345 gene, herein designated VGAM GENE, on one or more VGAM2345 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32796] It is yet further appreciated that a function of VGAM2345 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2345 include diagnosis, prevention and treatment of viral infection by Equine herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2345 correlate with, and may be deduced from, the identity of the host target genes which VGAM2345 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[32797] Nucleotide sequences of the VGAM2345 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2345 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2345 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2345 are further described hereinbelow with reference to Table 1.

[32798] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2345 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[32799] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2346 (VGAM2346) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[32800] VGAM2346 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2346 was detected is described hereinabove with reference to Figs. 2-8.

[32801] VGAM2346 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine herpesvirus 2. VGAM2346 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[32802] VGAM2346 gene, herein designated VGAM GENE, encodes

a VGAM2346 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2346 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2346 precursor RNA is designated SEQ ID:2332, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2332 is located at position 38013 relative to the genome of Equine herpesvirus 2.

[32803] VGAM2346 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2346 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32804] An enzyme complex designated DICER COMPLEX, dices the VGAM2346 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2346 RNA,

herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2346 RNA is designated SEQ ID:5057, and is provided hereinbelow with reference to the sequence listing part.

[32805] VGAM2346 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2346 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2346 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32806] VGAM2346 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2346 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM2346 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2346 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2346 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32807] The complementary binding of VGAM2346 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2346 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2346 host target RNA, herein designated VGAM HOST TARGET

RNA, into VGAM2346 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[32808] It is appreciated that VGAM2346 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2346 host target genes. The mRNA of each one of this plurality of VGAM2346 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2346 RNA, herein designated VGAM RNA, and which when bound by VGAM2346 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2346 host target proteins.

[32809] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2346 gene, herein designated VGAM GENE, on one or more VGAM2346 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32810] It is yet further appreciated that a function of VGAM2346 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2346 include diagnosis, prevention and treatment of viral infection by Equine herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2346 correlate with, and may be deduced from, the identity of the host target genes which VGAM2346 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[32811] Nucleotide sequences of the VGAM2346 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2346 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2346 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2346 are further

described hereinbelow with reference to Table 1.

[32812] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2346 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[32813] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2347 (VGAM2347) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[32814] VGAM2347 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2347 was detected is described hereinabove with reference to Figs. 2-8.

[32815] VGAM2347 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine herpesvirus 2. VGAM2347 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[32816] VGAM2347 gene, herein designated VGAM GENE, encodes a VGAM2347 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2347 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2347 precursor RNA is designated SEQ ID:2333, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2333 is located at position 44095 relative to the genome of Equine herpesvirus 2.

[32817] VGAM2347 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2347 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32818] An enzyme complex designated DICER COMPLEX, dices the VGAM2347 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, into VGAM2347 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 65%) nucleotide sequence of VGAM2347 RNA is designated SEQ ID:5058, and is provided hereinbelow with reference to the sequence listing part.

[32819] VGAM2347 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2347 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2347 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32820] VGAM2347 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2347 host target RNA, herein designated VGAM HOST TARGET RNA. This

complementary binding is due to the fact that the nucleotide sequence of VGAM2347 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2347 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2347 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32821] The complementary binding of VGAM2347 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2347 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2347

host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2347 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[32822] It is appreciated that VGAM2347 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2347 host target genes. The mRNA of each one of this plurality of VGAM2347 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2347 RNA, herein designated VGAM RNA, and which when bound by VGAM2347 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2347 host target proteins.

[32823] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2347 gene, herein designated VGAM GENE, on one or more VGAM2347 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32824] It is yet further appreciated that a function of VGAM2347 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2347 include diagnosis, prevention and treatment of viral infection by Equine herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2347 correlate with, and may be deduced from, the identity of the host target genes which VGAM2347 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[32825] Nucleotide sequences of the VGAM2347 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2347 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2347 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM2347 are further described hereinbelow with reference to Table 1.

[32826] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2347 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[32827] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2348 (VGAM2348) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[32828] VGAM2348 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2348 was detected is described hereinabove with reference to Figs. 2-8.

[32829] VGAM2348 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine herpesvirus 2. VGAM2348 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the

human genome.

[32830] VGAM2348 gene, herein designated VGAM GENE, encodes a VGAM2348 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2348 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2348 precursor RNA is designated SEQ ID:2334, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2334 is located at position 16485 relative to the genome of Equine herpesvirus 2.

[32831] VGAM2348 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2348 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32832] An enzyme complex designated DICER COMPLEX, dices

the VGAM2348 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2348 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 59%) nucleotide sequence of VGAM2348 RNA is designated SEQ ID:5059, and is provided hereinbelow with reference to the sequence listing part.

[32833] VGAM2348 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2348 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2348 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32834] VGAM2348 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2348 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2348 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2348 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2348 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32835] The complementary binding of VGAM2348 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2348 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM2348 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2348 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[32836] It is appreciated that VGAM2348 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2348 host target genes. The mRNA of each one of this plurality of VGAM2348 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2348 RNA, herein designated VGAM RNA, and which when bound by VGAM2348 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2348 host target proteins.

[32837] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2348 gene, herein designated VGAM GENE, on one or more VGAM2348 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32838] It is yet further appreciated that a function of VGAM2348 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2348 include diagnosis, prevention and treatment of viral infection by Equine herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2348 correlate with, and may be deduced from, the identity of the host target genes which VGAM2348 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[32839] Nucleotide sequences of the VGAM2348 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2348 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of

VGAM2348 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2348 are further described hereinbelow with reference to Table 1.

[32840] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2348 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[32841] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2349 (VGAM2349) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[32842] VGAM2349 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2349 was detected is described hereinabove with reference to Figs. 2-8.

[32843] VGAM2349 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine herpesvirus 2. VGAM2349 host target gene, herein designated VGAM

HOST TARGET GENE, is a human gene contained in the human genome.

[32844] VGAM2349 gene, herein designated VGAM GENE, encodes a VGAM2349 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2349 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2349 precursor RNA is designated SEQ ID:2335, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2335 is located at position 19286 relative to the genome of Equine herpesvirus 2.

[32845] VGAM2349 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2349 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32846] An enzyme complex designated DICER COMPLEX, dices the VGAM2349 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2349 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 49%) nucleotide sequence of VGAM2349 RNA is designated SEQ ID:5060, and is provided hereinbelow with reference to the sequence listing part.

[32847] VGAM2349 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2349 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2349 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32848] VGAM2349 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites

located in untranslated regions of VGAM2349 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2349 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2349 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32849] The complementary binding of VGAM2349 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2349 host target RNA, herein designated VGAM

HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2349 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2349 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[32850] It is appreciated that VGAM2349 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2349 host target genes. The mRNA of each one of this plurality of VGAM2349 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2349 RNA, herein designated VGAM RNA, and which when bound by VGAM2349 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2349 host target proteins.

[32851] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2349 gene, herein designated VGAM GENE, on one or more VGAM2349 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove

with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32852] It is yet further appreciated that a function of VGAM2349 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2349 include diagnosis, prevention and treatment of viral infection by Equine herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2349 correlate with, and may be deduced from, the identity of the host target genes which VGAM2349 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[32853] Nucleotide sequences of the VGAM2349 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2349 RNA, herein designated VGAM RNA, and

a schematic representation of the secondary folding of VGAM2349 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2349 are further described hereinbelow with reference to Table 1.

[32854] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2349 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[32855] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2350 (VGAM2350) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[32856] VGAM2350 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2350 was detected is described hereinabove with reference to Figs. 2-8.

[32857] VGAM2350 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine herpesvirus 2.

VGAM2350 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[32858] VGAM2350 gene, herein designated VGAM GENE, encodes a VGAM2350 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2350 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2350 precursor RNA is designated SEQ ID:2336, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2336 is located at position 13649 relative to the genome of Equine herpesvirus 2.

[32859] VGAM2350 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2350 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[32860] An enzyme complex designated DICER COMPLEX, dices the VGAM2350 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2350 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2350 RNA is designated SEQ ID:5061, and is provided hereinbelow with reference to the sequence listing part.

[32861] VGAM2350 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2350 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2350 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32862] VGAM2350 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM2350 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2350 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2350 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2350 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32863] The complementary binding of VGAM2350 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM2350 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2350 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2350 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[32864] It is appreciated that VGAM2350 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2350 host target genes. The mRNA of each one of this plurality of VGAM2350 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2350 RNA, herein designated VGAM RNA, and which when bound by VGAM2350 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2350 host target proteins.

[32865] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2350 gene, herein designated VGAM GENE, on one or more VGAM2350 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32866] It is yet further appreciated that a function of VGAM2350 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2350 include diagnosis, prevention and treatment of viral infection by Equine herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2350 correlate with, and may be deduced from, the identity of the host target genes which VGAM2350 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[32867] Nucleotide sequences of the VGAM2350 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

diced VGAM2350 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2350 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2350 are further described hereinbelow with reference to Table 1.

[32868] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2350 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[32869] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2351 (VGAM2351) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[32870] VGAM2351 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2351 was detected is described hereinabove with reference to Figs. 2-8.

[32871] VGAM2351 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of Equine herpesvirus 2. VGAM2351 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[32872] VGAM2351 gene, herein designated VGAM GENE, encodes a VGAM2351 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2351 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2351 precursor RNA is designated SEQ ID:2337, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2337 is located at position 28694 relative to the genome of Equine herpesvirus 2.

[32873] VGAM2351 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2351 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32874] An enzyme complex designated DICER COMPLEX, dices the VGAM2351 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2351 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 49%) nucleotide sequence of VGAM2351 RNA is designated SEQ ID:5062, and is provided hereinbelow with reference to the sequence listing part.

[32875] VGAM2351 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2351 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2351 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32876] VGAM2351 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2351 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2351 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2351 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2351 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32877] The complementary binding of VGAM2351 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM2351 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2351 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2351 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[32878] It is appreciated that VGAM2351 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2351 host target genes. The mRNA of each one of this plurality of VGAM2351 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2351 RNA, herein designated VGAM RNA, and which when bound by VGAM2351 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2351 host target proteins.

[32879] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2351 gene, herein designated VGAM GENE, on one or more VGAM2351 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32880] It is yet further appreciated that a function of VGAM2351 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2351 include diagnosis, prevention and treatment of viral infection by Equine herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2351 correlate with, and may be deduced from, the identity of the host target genes which VGAM2351 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[32881] Nucleotide sequences of the VGAM2351 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the diced VGAM2351 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2351 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2351 are further described hereinbelow with reference to Table 1.

[32882] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2351 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[32883] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2352 (VGAM2352) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[32884] VGAM2352 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2352 was detected is described hereinabove with reference to Figs. 2-8.

[32885] VGAM2352 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine herpesvirus 2. VGAM2352 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[32886] VGAM2352 gene, herein designated VGAM GENE, encodes a VGAM2352 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2352 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2352 precursor RNA is designated SEQ ID:2338, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2338 is located at position 8029 relative to the genome of Equine herpesvirus 2.

[32887] VGAM2352 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2352 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32888] An enzyme complex designated DICER COMPLEX, dices the VGAM2352 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2352 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 50%) nucleotide sequence of VGAM2352 RNA is designated SEQ ID:5063, and is provided hereinbelow with reference to the sequence listing part.

[32889] VGAM2352 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2352 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2352 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN COD-

ING and 3UTR respectively.

[32890] VGAM2352 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2352 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2352 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2352 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2352 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32891] The complementary binding of VGAM2352 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2352 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2352 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2352 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[32892] It is appreciated that VGAM2352 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2352 host target genes. The mRNA of each one of this plurality of VGAM2352 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2352 RNA, herein designated VGAM RNA, and which when bound by VGAM2352 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2352 host target proteins.

[32893] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2352 gene, herein designated VGAM GENE, on one

or more VGAM2352 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32894] It is yet further appreciated that a function of VGAM2352 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2352 include diagnosis, prevention and treatment of viral infection by Equine herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2352 correlate with, and may be deduced from, the identity of the host target genes which VGAM2352 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[32895] Nucleotide sequences of the VGAM2352 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2352 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2352 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2352 are further described hereinbelow with reference to Table 1.

[32896] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2352 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[32897] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2353 (VGAM2353) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[32898] VGAM2353 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2353 was detected is de-

scribed hereinabove with reference to Figs. 2-8.

[32899] VGAM2353 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine herpesvirus 2. VGAM2353 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[32900] VGAM2353 gene, herein designated VGAM GENE, encodes a VGAM2353 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2353 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2353 precursor RNA is designated SEQ ID:2339, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2339 is located at position 15043 relative to the genome of Equine herpesvirus 2.

[32901] VGAM2353 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2353 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32902] An enzyme complex designated DICER COMPLEX, dices the VGAM2353 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2353 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 68%) nucleotide sequence of VGAM2353 RNA is designated SEQ ID:5064, and is provided hereinbelow with reference to the sequence listing part.

[32903] VGAM2353 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2353 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2353 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and

a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32904] VGAM2353 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2353 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2353 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2353 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both

3UTR and 5UTR regions.

[32905] The complementary binding of VGAM2353 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2353 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2353 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2353 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[32906] It is appreciated that VGAM2353 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2353 host target genes. The mRNA of each one of this plurality of VGAM2353 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2353 RNA, herein designated VGAM RNA, and which when bound by VGAM2353 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2353 host target proteins.

[32907] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM2353 gene, herein designated VGAM GENE, on one or more VGAM2353 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32908] It is yet further appreciated that a function of VGAM2353 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of viral infection by Equine herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2353 correlate with, and may be deduced from, the identity of the host target genes which VGAM2353 binds and inhibits, and the function of these host target genes, as

elaborated hereinbelow.

[32909] Nucleotide sequences of the VGAM2353 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2353 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2353 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2353 are further described hereinbelow with reference to Table 1.

[32910] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2353 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[32911] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2354 (VGAM2354) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[32912] VGAM2354 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene.

The method by which VGAM2354 was detected is described hereinabove with reference to Figs. 2-8.

[32913] VGAM2354 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine herpesvirus 2. VGAM2354 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[32914] VGAM2354 gene, herein designated VGAM GENE, encodes a VGAM2354 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2354 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2354 precursor RNA is designated SEQ ID:2340, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2340 is located at position 18623 relative to the genome of Equine herpesvirus 2.

[32915] VGAM2354 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2354 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32916] An enzyme complex designated DICER COMPLEX, dices the VGAM2354 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2354 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 63%) nucleotide sequence of VGAM2354 RNA is designated SEQ ID:5065, and is provided hereinbelow with reference to the sequence listing part.

[32917] VGAM2354 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2354 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2354 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding

gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32918] VGAM2354 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2354 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2354 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2354 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2354 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be lo-

cated in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32919] The complementary binding of VGAM2354 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2354 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2354 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2354 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[32920] It is appreciated that VGAM2354 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2354 host target genes. The mRNA of each one of this plurality of VGAM2354 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2354 RNA, herein designated VGAM RNA, and which when bound by VGAM2354 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2354 host target proteins.

[32921] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM2354 gene, herein designated VGAM GENE, on one or more VGAM2354 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32922] It is yet further appreciated that a function of VGAM2354 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2354 include diagnosis, prevention and treatment of viral infection by Equine herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2354 correlate with, and may be deduced from, the identity of the host target genes which VGAM2354 binds and in-

hibits, and the function of these host target genes, as elaborated hereinbelow.

[32923] Nucleotide sequences of the VGAM2354 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2354 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2354 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2354 are further described hereinbelow with reference to Table 1.

[32924] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2354 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[32925] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2355 (VGAM2355) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[32926] VGAM2355 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2355 was detected is described hereinabove with reference to Figs. 2-8.

[32927] VGAM2355 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine herpesvirus 2. VGAM2355 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[32928] VGAM2355 gene, herein designated VGAM GENE, encodes a VGAM2355 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2355 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2355 precursor RNA is designated SEQ ID:2341, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2341 is located at position 39033 relative to the genome of Equine herpesvirus 2.

[32929] VGAM2355 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2355 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32930] An enzyme complex designated DICER COMPLEX, dices the VGAM2355 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2355 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2355 RNA is designated SEQ ID:5066, and is provided hereinbelow with reference to the sequence listing part.

[32931] VGAM2355 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2355 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2355 host target RNA, herein designated VGAM HOST TARGET RNA, comprises

three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32932] VGAM2355 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2355 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2355 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2355 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2355 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an

example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32933] The complementary binding of VGAM2355 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2355 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2355 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2355 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[32934] It is appreciated that VGAM2355 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2355 host target genes. The mRNA of each one of this plurality of VGAM2355 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2355 RNA, herein designated VGAM RNA, and which when bound by VGAM2355 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2355 host target proteins.

[32935] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2355 gene, herein designated VGAM GENE, on one or more VGAM2355 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32936] It is yet further appreciated that a function of VGAM2355 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2355 include diagnosis, prevention and treatment of viral infection by Equine herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2355 correlate with, and may be deduced from, the identity of

the host target genes which VGAM2355 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[32937] Nucleotide sequences of the VGAM2355 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2355 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2355 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2355 are further described hereinbelow with reference to Table 1.

[32938] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2355 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[32939] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2356 (VGAM2356) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[32940] VGAM2356 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2356 was detected is described hereinabove with reference to Figs. 2-8.

[32941] VGAM2356 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine herpesvirus 2. VGAM2356 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[32942] VGAM2356 gene, herein designated VGAM GENE, encodes a VGAM2356 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2356 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2356 precursor RNA is designated SEQ ID:2342, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2342 is located at position 38873 relative to the genome of Equine herpesvirus 2.

[32943] VGAM2356 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2356 folded precursor RNA, herein designated VGAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32944] An enzyme complex designated DICER COMPLEX, dices the VGAM2356 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2356 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2356 RNA is designated SEQ ID:5067, and is provided hereinbelow with reference to the sequence listing part.

[32945] VGAM2356 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2356 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2356 host target RNA,

herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32946] VGAM2356 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2356 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2356 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2356 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2356 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host tar-

get binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32947] The complementary binding of VGAM2356 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2356 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2356 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2356 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[32948] It is appreciated that VGAM2356 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2356 host target genes. The mRNA of each one of this plurality of VGAM2356 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2356 RNA, herein designated VGAM RNA, and which when bound by VGAM2356 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2356 host target proteins.

[32949] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2356 gene, herein designated VGAM GENE, on one or more VGAM2356 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32950] It is yet further appreciated that a function of VGAM2356 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2356 include diagnosis, prevention and treatment of viral infection by Equine herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2356

correlate with, and may be deduced from, the identity of the host target genes which VGAM2356 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[32951] Nucleotide sequences of the VGAM2356 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2356 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2356 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2356 are further described hereinbelow with reference to Table 1.

[32952] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2356 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[32953] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2357 (VGAM2357) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the

art.

[32954] VGAM2357 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2357 was detected is described hereinabove with reference to Figs. 2-8.

[32955] VGAM2357 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine herpesvirus 2. VGAM2357 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[32956] VGAM2357 gene, herein designated VGAM GENE, encodes a VGAM2357 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2357 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2357 precursor RNA is designated SEQ ID:2343, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2343 is located at position 32894 relative to the genome of Equine herpesvirus 2.

[32957] VGAM2357 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2357 folded

precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32958] An enzyme complex designated DICER COMPLEX, dices the VGAM2357 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2357 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2357 RNA is designated SEQ ID:5068, and is provided hereinbelow with reference to the sequence listing part.

[32959] VGAM2357 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2357 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM2357 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32960] VGAM2357 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2357 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2357 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2357 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2357 host target RNA, herein designated VGAM HOST TARGET RNA.

It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32961] The complementary binding of VGAM2357 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2357 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2357 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2357 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[32962] It is appreciated that VGAM2357 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2357 host target genes. The mRNA of each one of this plurality of VGAM2357 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2357 RNA, herein designated VGAM RNA, and which when bound by VGAM2357 RNA, herein designated VGAM RNA, causes inhibition of translation of

respective one or more VGAM2357 host target proteins.

[32963] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2357 gene, herein designated VGAM GENE, on one or more VGAM2357 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32964] It is yet further appreciated that a function of VGAM2357 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2357 include diagnosis, prevention and treatment of viral infection by Equine herpesvirus 2. Spe-

cific functions, and accordingly utilities, of VGAM2357 correlate with, and may be deduced from, the identity of the host target genes which VGAM2357 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[32965] Nucleotide sequences of the VGAM2357 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2357 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2357 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2357 are further described hereinbelow with reference to Table 1.

[32966] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2357 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[32967] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2358 (VGAM2358) viral gene, which modulates expression of respective host target genes thereof, the func-

tion and utility of which host target genes is known in the art.

[32968] VGAM2358 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2358 was detected is described hereinabove with reference to Figs. 2-8.

[32969] VGAM2358 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine herpesvirus 2. VGAM2358 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[32970] VGAM2358 gene, herein designated VGAM GENE, encodes a VGAM2358 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2358 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2358 precursor RNA is designated SEQ ID:2344, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2344 is located at position 44667 relative to the genome of Equine herpesvirus 2.

[32971] VGAM2358 precursor RNA, herein designated VGAM PRE-

CURSOR RNA, folds onto itself, forming VGAM2358 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32972] An enzyme complex designated DICER COMPLEX, dices the VGAM2358 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2358 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2358 RNA is designated SEQ ID:5069, and is provided hereinbelow with reference to the sequence listing part.

[32973] VGAM2358 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM2358 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2358 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32974] VGAM2358 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2358 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2358 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2358 host

target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32975] The complementary binding of VGAM2358 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2358 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2358 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2358 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[32976] It is appreciated that VGAM2358 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2358 host target genes. The mRNA of each one of this plurality of VGAM2358 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2358 RNA, herein designated VGAM RNA, and which when bound by VGAM2358 RNA, herein

designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2358 host target proteins.

[32977] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2358 gene, herein designated VGAM GENE, on one or more VGAM2358 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32978] It is yet further appreciated that a function of VGAM2358 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2358 include diagnosis, prevention and

treatment of viral infection by Equine herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2358 correlate with, and may be deduced from, the identity of the host target genes which VGAM2358 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[32979] Nucleotide sequences of the VGAM2358 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2358 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2358 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2358 are further described hereinbelow with reference to Table 1.

[32980] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2358 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[32981] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2359 (VGAM2359) viral gene, which modulates ex-

pression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[32982] VGAM2359 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2359 was detected is described hereinabove with reference to Figs. 2-8.

[32983] VGAM2359 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine herpesvirus 2. VGAM2359 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[32984] VGAM2359 gene, herein designated VGAM GENE, encodes a VGAM2359 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2359 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2359 precursor RNA is designated SEQ ID:2345, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2345 is located at position 34353 relative to the genome of Equine herpesvirus 2.

[32985] VGAM2359 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2359 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32986] An enzyme complex designated DICER COMPLEX, dices the VGAM2359 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2359 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 57%) nucleotide sequence of VGAM2359 RNA is designated SEQ ID:5070, and is provided hereinbelow with reference to the sequence listing part.

[32987] VGAM2359 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2359 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2359 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32988] VGAM2359 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2359 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2359 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2359 RNA, herein designated VGAM RNA, may have a different number of host target

binding sites in untranslated regions of a VGAM2359 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32989] The complementary binding of VGAM2359 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2359 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2359 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2359 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[32990] It is appreciated that VGAM2359 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2359 host target genes. The mRNA of each one of this plurality of VGAM2359 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2359 RNA, herein designated VGAM

RNA, and which when bound by VGAM2359 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2359 host target proteins.

[32991] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2359 gene, herein designated VGAM GENE, on one or more VGAM2359 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32992] It is yet further appreciated that a function of VGAM2359 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM2359 include diagnosis, prevention and treatment of viral infection by Equine herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2359 correlate with, and may be deduced from, the identity of the host target genes which VGAM2359 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[32993] Nucleotide sequences of the VGAM2359 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2359 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2359 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2359 are further described hereinbelow with reference to Table 1.

[32994] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2359 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[32995] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Mes-

senger 2360 (VGAM2360) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[32996] VGAM2360 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2360 was detected is described hereinabove with reference to Figs. 2-8.

[32997] VGAM2360 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine herpesvirus 2. VGAM2360 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[32998] VGAM2360 gene, herein designated VGAM GENE, encodes a VGAM2360 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2360 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2360 precursor RNA is designated SEQ ID:2346, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2346 is located at position

40669 relative to the genome of Equine herpesvirus 2.

[32999] VGAM2360 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2360 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33000] An enzyme complex designated DICER COMPLEX, dices the VGAM2360 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2360 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2360 RNA is designated SEQ ID:5071, and is provided hereinbelow with reference to the sequence listing part.

[33001] VGAM2360 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2360 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2360 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33002] VGAM2360 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2360 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2360 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2360 RNA, herein designated

VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2360 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33003] The complementary binding of VGAM2360 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2360 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2360 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2360 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[33004] It is appreciated that VGAM2360 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2360 host target genes. The mRNA of each one of this plurality of VGAM2360 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM2360 RNA, herein designated VGAM RNA, and which when bound by VGAM2360 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2360 host target proteins.

[33005] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2360 gene, herein designated VGAM GENE, on one or more VGAM2360 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33006] It is yet further appreciated that a function of VGAM2360 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2360 include diagnosis, prevention and treatment of viral infection by Equine herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2360 correlate with, and may be deduced from, the identity of the host target genes which VGAM2360 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[33007] Nucleotide sequences of the VGAM2360 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2360 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2360 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2360 are further described hereinbelow with reference to Table 1.

[33008] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2360 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[33009] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present

invention, referred to here as Viral Genomic Address Messenger 2361 (VGAM2361) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[33010] VGAM2361 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2361 was detected is described hereinabove with reference to Figs. 2-8.

[33011] VGAM2361 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine herpesvirus 2. VGAM2361 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[33012] VGAM2361 gene, herein designated VGAM GENE, encodes a VGAM2361 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2361 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2361 precursor RNA is designated SEQ ID:2347, and is provided hereinbelow with reference to the sequence listing part. Nu-

cleotide sequence SEQ ID:2347 is located at position 23557 relative to the genome of Equine herpesvirus 2.

[33013] VGAM2361 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2361 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33014] An enzyme complex designated DICER COMPLEX, dices the VGAM2361 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2361 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 51%) nucleotide sequence of VGAM2361 RNA is designated SEQ ID:5072, and is provided hereinbelow with reference to the sequence

listing part.

[33015] VGAM2361 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2361 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2361 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33016] VGAM2361 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2361 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2361 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not

meant to be limiting VGAM2361 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2361 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33017] The complementary binding of VGAM2361 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2361 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2361 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2361 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[33018] It is appreciated that VGAM2361 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2361 host target genes. The mRNA of each one of this plurality of VGAM2361 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2361 RNA, herein designated VGAM RNA, and which when bound by VGAM2361 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2361 host target proteins.

[33019] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2361 gene, herein designated VGAM GENE, on one or more VGAM2361 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33020] It is yet further appreciated that a function of VGAM2361

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2361 include diagnosis, prevention and treatment of viral infection by Equine herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2361 correlate with, and may be deduced from, the identity of the host target genes which VGAM2361 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[33021] Nucleotide sequences of the VGAM2361 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2361 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2361 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2361 are further described hereinbelow with reference to Table 1.

[33022] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2361 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[33023] Fig. 1 further provides a conceptual description of another

novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2362 (VGAM2362) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[33024] VGAM2362 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2362 was detected is described hereinabove with reference to Figs. 2-8.

[33025] VGAM2362 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine herpesvirus 2. VGAM2362 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[33026] VGAM2362 gene, herein designated VGAM GENE, encodes a VGAM2362 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2362 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2362 precursor RNA is designated SEQ ID:2348, and is provided here-

inbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2348 is located at position 25075 relative to the genome of Equine herpesvirus 2.

[33027] VGAM2362 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2362 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33028] An enzyme complex designated DICER COMPLEX, dices the VGAM2362 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2362 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2362 RNA is designated SEQ ID:5073, and

is provided hereinbelow with reference to the sequence listing part.

[33029] VGAM2362 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2362 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2362 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33030] VGAM2362 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2362 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2362 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites

shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2362 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2362 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33031] The complementary binding of VGAM2362 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2362 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2362 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2362 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[33032] It is appreciated that VGAM2362 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2362 host target genes. The mRNA of each one of this plurality of VGAM2362 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2362 RNA, herein designated VGAM RNA, and which when bound by VGAM2362 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2362 host target proteins.

[33033] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2362 gene, herein designated VGAM GENE, on one or more VGAM2362 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33034] It is yet further appreciated that a function of VGAM2362 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2362 include diagnosis, prevention and treatment of viral infection by Equine herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2362 correlate with, and may be deduced from, the identity of the host target genes which VGAM2362 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[33035] Nucleotide sequences of the VGAM2362 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2362 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2362 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2362 are further described hereinbelow with reference to Table 1.

[33036] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2362 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[33037] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2363 (VGAM2363) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[33038] VGAM2363 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2363 was detected is described hereinabove with reference to Figs. 2-8.

[33039] VGAM2363 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine herpesvirus 2. VGAM2363 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[33040] VGAM2363 gene, herein designated VGAM GENE, encodes a VGAM2363 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2363 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2363 precur-

sor RNA is designated SEQ ID:2349, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2349 is located at position 40183 relative to the genome of Equine herpesvirus 2.

[33041] VGAM2363 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2363 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33042] An enzyme complex designated DICER COMPLEX, dices the VGAM2363 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2363 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide se-

quence of VGAM2363 RNA is designated SEQ ID:5074, and is provided hereinbelow with reference to the sequence listing part.

[33043] VGAM2363 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2363 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2363 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33044] VGAM2363 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2363 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2363 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is ap-

preciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2363 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2363 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33045] The complementary binding of VGAM2363 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2363 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2363 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2363 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[33046] It is appreciated that VGAM2363 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2363 host target genes. The mRNA of

each one of this plurality of VGAM2363 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2363 RNA, herein designated VGAM RNA, and which when bound by VGAM2363 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2363 host target proteins.

[33047] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2363 gene, herein designated VGAM GENE, on one or more VGAM2363 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science

294,779 (2001)).

[33048] It is yet further appreciated that a function of VGAM2363 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2363 include diagnosis, prevention and treatment of viral infection by Equine herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2363 correlate with, and may be deduced from, the identity of the host target genes which VGAM2363 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[33049] Nucleotide sequences of the VGAM2363 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2363 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2363 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2363 are further described hereinbelow with reference to Table 1.

[33050] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2363 RNA, herein designated VGAM RNA, are de-

scribed hereinbelow with reference to Table 2.

[33051] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2364 (VGAM2364) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[33052] VGAM2364 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2364 was detected is described hereinabove with reference to Figs. 2-8.

[33053] VGAM2364 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine herpesvirus 2. VGAM2364 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[33054] VGAM2364 gene, herein designated VGAM GENE, encodes a VGAM2364 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2364 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly

similar to the nucleotide sequence of VGAM2364 precursor RNA is designated SEQ ID:2350, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2350 is located at position 23189 relative to the genome of Equine herpesvirus 2.

[33055] VGAM2364 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2364 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33056] An enzyme complex designated DICER COMPLEX, dices the VGAM2364 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2364 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 64%) nucleotide sequence of VGAM2364 RNA is designated SEQ ID:5075, and is provided hereinbelow with reference to the sequence listing part.

[33057] VGAM2364 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2364 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2364 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33058] VGAM2364 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2364 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2364 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I,

BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2364 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2364 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33059] The complementary binding of VGAM2364 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2364 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2364 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2364 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[33060] It is appreciated that VGAM2364 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM2364 host target genes. The mRNA of each one of this plurality of VGAM2364 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2364 RNA, herein designated VGAM RNA, and which when bound by VGAM2364 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2364 host target proteins.

[33061] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2364 gene, herein designated VGAM GENE, on one or more VGAM2364 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33062] It is yet further appreciated that a function of VGAM2364 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2364 include diagnosis, prevention and treatment of viral infection by Equine herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2364 correlate with, and may be deduced from, the identity of the host target genes which VGAM2364 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[33063] Nucleotide sequences of the VGAM2364 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2364 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2364 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2364 are further described hereinbelow with reference to Table 1.

[33064] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites

to VGAM2364 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[33065] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2365 (VGAM2365) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[33066] VGAM2365 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2365 was detected is described hereinabove with reference to Figs. 2-8.

[33067] VGAM2365 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rat cytomegalovirus. VGAM2365 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[33068] VGAM2365 gene, herein designated VGAM GENE, encodes a VGAM2365 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2365 precursor RNA, herein designated VGAM PRECURSOR RNA, does not en-

code a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2365 precursor RNA is designated SEQ ID:2351, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2351 is located at position 185947 relative to the genome of Rat cytomegalovirus.

[33069] VGAM2365 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2365 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33070] An enzyme complex designated DICER COMPLEX, dices the VGAM2365 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2365 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2365 RNA is designated SEQ ID:5076, and is provided hereinbelow with reference to the sequence listing part.

[33071] VGAM2365 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2365 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2365 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33072] VGAM2365 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2365 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2365 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3

such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2365 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2365 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33073] The complementary binding of VGAM2365 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2365 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2365 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2365 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[33074] It is appreciated that VGAM2365 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2365 host target genes. The mRNA of each one of this plurality of VGAM2365 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2365 RNA, herein designated VGAM RNA, and which when bound by VGAM2365 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2365 host target proteins.

[33075] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2365 gene, herein designated VGAM GENE, on one or more VGAM2365 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33076] It is yet further appreciated that a function of VGAM2365 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2365 include diagnosis, prevention and treatment of viral infection by Rat cytomegalovirus. Specific functions, and accordingly utilities, of VGAM2365 correlate with, and may be deduced from, the identity of the host target genes which VGAM2365 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[33077] Nucleotide sequences of the VGAM2365 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2365 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2365 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2365 are further described hereinbelow with reference to Table 1.

[33078] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the

complementarity of each of these host target binding sites to VGAM2365 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[33079] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2366 (VGAM2366) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[33080] VGAM2366 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2366 was detected is described hereinabove with reference to Figs. 2-8.

[33081] VGAM2366 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rat cytomegalovirus. VGAM2366 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[33082] VGAM2366 gene, herein designated VGAM GENE, encodes a VGAM2366 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2366 precursor RNA,

herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2366 precursor RNA is designated SEQ ID:2352, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2352 is located at position 183326 relative to the genome of Rat cytomegalovirus.

[33083] VGAM2366 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2366 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33084] An enzyme complex designated DICER COMPLEX, dices the VGAM2366 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2366 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2366 RNA is designated SEQ ID:5077, and is provided hereinbelow with reference to the sequence listing part.

[33085] VGAM2366 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2366 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2366 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33086] VGAM2366 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2366 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2366 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host

target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2366 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2366 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33087] The complementary binding of VGAM2366 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2366 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2366 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2366 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[33088] It is appreciated that VGAM2366 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2366 host target genes. The mRNA of each one of this plurality of VGAM2366 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2366 RNA, herein designated VGAM RNA, and which when bound by VGAM2366 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2366 host target proteins.

[33089] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2366 gene, herein designated VGAM GENE, on one or more VGAM2366 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33090] It is yet further appreciated that a function of VGAM2366 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2366 include diagnosis, prevention and treatment of viral infection by Rat cytomegalovirus. Specific functions, and accordingly utilities, of VGAM2366 correlate with, and may be deduced from, the identity of the host target genes which VGAM2366 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[33091] Nucleotide sequences of the VGAM2366 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2366 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2366 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2366 are further described hereinbelow with reference to Table 1.

[33092] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2366 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[33093] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2367 (VGAM2367) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[33094] VGAM2367 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2367 was detected is described hereinabove with reference to Figs. 2-8.

[33095] VGAM2367 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rat cytomegalovirus. VGAM2367 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[33096] VGAM2367 gene, herein designated VGAM GENE, encodes a VGAM2367 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and un-

like most ordinary genes, VGAM2367 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2367 precursor RNA is designated SEQ ID:2353, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2353 is located at position 207957 relative to the genome of Rat cytomegalovirus.

[33097] VGAM2367 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2367 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33098] An enzyme complex designated DICER COMPLEX, dices the VGAM2367 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2367 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2367 RNA is designated SEQ ID:5078, and is provided hereinbelow with reference to the sequence listing part.

[33099] VGAM2367 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2367 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2367 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33100] VGAM2367 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2367 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2367 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed

sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2367 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2367 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33101] The complementary binding of VGAM2367 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2367 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2367 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2367 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target

protein is therefore outlined by a broken line.

[33102] It is appreciated that VGAM2367 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2367 host target genes. The mRNA of each one of this plurality of VGAM2367 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2367 RNA, herein designated VGAM RNA, and which when bound by VGAM2367 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2367 host target proteins.

[33103] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2367 gene, herein designated VGAM GENE, on one or more VGAM2367 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33104] It is yet further appreciated that a function of VGAM2367 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2367 include diagnosis, prevention and treatment of viral infection by Rat cytomegalovirus. Specific functions, and accordingly utilities, of VGAM2367 correlate with, and may be deduced from, the identity of the host target genes which VGAM2367 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[33105] Nucleotide sequences of the VGAM2367 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2367 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2367 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2367 are further described hereinbelow with reference to Table 1.

[33106] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2367 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[33107] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2368 (VGAM2368) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[33108] VGAM2368 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2368 was detected is described hereinabove with reference to Figs. 2-8.

[33109] VGAM2368 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rat cytomegalovirus. VGAM2368 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[33110] VGAM2368 gene, herein designated VGAM GENE, encodes a VGAM2368 precursor RNA, herein designated VGAM

PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2368 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2368 precursor RNA is designated SEQ ID:2354, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2354 is located at position 223088 relative to the genome of Rat cytomegalovirus.

[33111] VGAM2368 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2368 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33112] An enzyme complex designated DICER COMPLEX, dices the VGAM2368 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2368 RNA, herein designated VGAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2368 RNA is designated SEQ ID:5079, and is provided hereinbelow with reference to the sequence listing part.

[33113] VGAM2368 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2368 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2368 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33114] VGAM2368 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2368 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2368 RNA, herein designated

VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2368 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2368 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33115] The complementary binding of VGAM2368 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2368 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2368 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2368 host target protein, herein desig-

nated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[33116] It is appreciated that VGAM2368 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2368 host target genes. The mRNA of each one of this plurality of VGAM2368 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2368 RNA, herein designated VGAM RNA, and which when bound by VGAM2368 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2368 host target proteins.

[33117] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2368 gene, herein designated VGAM GENE, on one or more VGAM2368 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33118] It is yet further appreciated that a function of VGAM2368 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2368 include diagnosis, prevention and treatment of viral infection by Rat cytomegalovirus. Specific functions, and accordingly utilities, of VGAM2368 correlate with, and may be deduced from, the identity of the host target genes which VGAM2368 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[33119] Nucleotide sequences of the VGAM2368 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2368 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2368 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2368 are further described hereinbelow with reference to Table 1.

[33120] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2368 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[33121] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2369 (VGAM2369) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[33122] VGAM2369 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2369 was detected is described hereinabove with reference to Figs. 2-8.

[33123] VGAM2369 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rat cytomegalovirus. VGAM2369 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[33124] VGAM2369 gene, herein designated VGAM GENE, encodes

a VGAM2369 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2369 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2369 precursor RNA is designated SEQ ID:2355, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2355 is located at position 208920 relative to the genome of Rat cytomegalovirus.

[33125] VGAM2369 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2369 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33126] An enzyme complex designated DICER COMPLEX, dices the VGAM2369 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2369 RNA,

herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 48%) nucleotide sequence of VGAM2369 RNA is designated SEQ ID:5080, and is provided hereinbelow with reference to the sequence listing part.

[33127] VGAM2369 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2369 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2369 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33128] VGAM2369 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2369 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM2369 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2369 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2369 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33129] The complementary binding of VGAM2369 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2369 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2369 host target RNA, herein designated VGAM HOST TARGET

RNA, into VGAM2369 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[33130] It is appreciated that VGAM2369 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2369 host target genes. The mRNA of each one of this plurality of VGAM2369 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2369 RNA, herein designated VGAM RNA, and which when bound by VGAM2369 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2369 host target proteins.

[33131] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2369 gene, herein designated VGAM GENE, on one or more VGAM2369 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33132] It is yet further appreciated that a function of VGAM2369 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2369 include diagnosis, prevention and treatment of viral infection by Rat cytomegalovirus. Specific functions, and accordingly utilities, of VGAM2369 correlate with, and may be deduced from, the identity of the host target genes which VGAM2369 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[33133] Nucleotide sequences of the VGAM2369 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2369 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2369 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2369 are further

described hereinbelow with reference to Table 1.

[33134] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2369 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[33135] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2370 (VGAM2370) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[33136] VGAM2370 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2370 was detected is described hereinabove with reference to Figs. 2-8.

[33137] VGAM2370 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rat cytomegalovirus. VGAM2370 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[33138] VGAM2370 gene, herein designated VGAM GENE, encodes a VGAM2370 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2370 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2370 precursor RNA is designated SEQ ID:2356, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2356 is located at position 217655 relative to the genome of Rat cytomegalovirus.

[33139] VGAM2370 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2370 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33140] An enzyme complex designated DICER COMPLEX, dices the VGAM2370 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, into VGAM2370 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2370 RNA is designated SEQ ID:5081, and is provided hereinbelow with reference to the sequence listing part.

[33141] VGAM2370 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2370 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2370 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33142] VGAM2370 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2370 host target RNA, herein designated VGAM HOST TARGET RNA. This

complementary binding is due to the fact that the nucleotide sequence of VGAM2370 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2370 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2370 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33143] The complementary binding of VGAM2370 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2370 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2370

host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2370 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[33144] It is appreciated that VGAM2370 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2370 host target genes. The mRNA of each one of this plurality of VGAM2370 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2370 RNA, herein designated VGAM RNA, and which when bound by VGAM2370 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2370 host target proteins.

[33145] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2370 gene, herein designated VGAM GENE, on one or more VGAM2370 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33146] It is yet further appreciated that a function of VGAM2370 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2370 include diagnosis, prevention and treatment of viral infection by Rat cytomegalovirus. Specific functions, and accordingly utilities, of VGAM2370 correlate with, and may be deduced from, the identity of the host target genes which VGAM2370 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[33147] Nucleotide sequences of the VGAM2370 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2370 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2370 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM2370 are further described hereinbelow with reference to Table 1.

[33148] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2370 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[33149] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2371 (VGAM2371) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[33150] VGAM2371 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2371 was detected is described hereinabove with reference to Figs. 2-8.

[33151] VGAM2371 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rat cytomegalovirus. VGAM2371 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the

human genome.

[33152] VGAM2371 gene, herein designated VGAM GENE, encodes a VGAM2371 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2371 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2371 precursor RNA is designated SEQ ID:2357, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2357 is located at position 183987 relative to the genome of Rat cytomegalovirus.

[33153] VGAM2371 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2371 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33154] An enzyme complex designated DICER COMPLEX, dices

the VGAM2371 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2371 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 60%) nucleotide sequence of VGAM2371 RNA is designated SEQ ID:5082, and is provided hereinbelow with reference to the sequence listing part.

[33155] VGAM2371 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2371 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2371 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33156] VGAM2371 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2371 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2371 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2371 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2371 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33157] The complementary binding of VGAM2371 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2371 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM2371 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2371 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[33158] It is appreciated that VGAM2371 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2371 host target genes. The mRNA of each one of this plurality of VGAM2371 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2371 RNA, herein designated VGAM RNA, and which when bound by VGAM2371 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2371 host target proteins.

[33159] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2371 gene, herein designated VGAM GENE, on one or more VGAM2371 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33160] It is yet further appreciated that a function of VGAM2371 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2371 include diagnosis, prevention and treatment of viral infection by Rat cytomegalovirus. Specific functions, and accordingly utilities, of VGAM2371 correlate with, and may be deduced from, the identity of the host target genes which VGAM2371 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[33161] Nucleotide sequences of the VGAM2371 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2371 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of

VGAM2371 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2371 are further described hereinbelow with reference to Table 1.

[33162] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2371 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[33163] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2372 (VGAM2372) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[33164] VGAM2372 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2372 was detected is described hereinabove with reference to Figs. 2-8.

[33165] VGAM2372 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rat cytomegalovirus. VGAM2372 host target gene, herein designated VGAM

HOST TARGET GENE, is a human gene contained in the human genome.

[33166] VGAM2372 gene, herein designated VGAM GENE, encodes a VGAM2372 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2372 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2372 precursor RNA is designated SEQ ID:2358, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2358 is located at position 208652 relative to the genome of Rat cytomegalovirus.

[33167] VGAM2372 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2372 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33168] An enzyme complex designated DICER COMPLEX, dices the VGAM2372 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2372 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 51%) nucleotide sequence of VGAM2372 RNA is designated SEQ ID:5083, and is provided hereinbelow with reference to the sequence listing part.

[33169] VGAM2372 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2372 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2372 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33170] VGAM2372 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites

located in untranslated regions of VGAM2372 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2372 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2372 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2372 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33171] The complementary binding of VGAM2372 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2372 host target RNA, herein designated VGAM

HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2372 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2372 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[33172] It is appreciated that VGAM2372 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2372 host target genes. The mRNA of each one of this plurality of VGAM2372 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2372 RNA, herein designated VGAM RNA, and which when bound by VGAM2372 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2372 host target proteins.

[33173] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2372 gene, herein designated VGAM GENE, on one or more VGAM2372 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove

with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33174] It is yet further appreciated that a function of VGAM2372 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2372 include diagnosis, prevention and treatment of viral infection by Rat cytomegalovirus. Specific functions, and accordingly utilities, of VGAM2372 correlate with, and may be deduced from, the identity of the host target genes which VGAM2372 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[33175] Nucleotide sequences of the VGAM2372 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2372 RNA, herein designated VGAM RNA, and

a schematic representation of the secondary folding of VGAM2372 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2372 are further described hereinbelow with reference to Table 1.

[33176] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2372 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[33177] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2373 (VGAM2373) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[33178] VGAM2373 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2373 was detected is described hereinabove with reference to Figs. 2-8.

[33179] VGAM2373 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rat cytomegalovirus.

VGAM2373 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[33180] VGAM2373 gene, herein designated VGAM GENE, encodes a VGAM2373 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2373 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2373 precursor RNA is designated SEQ ID:2359, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2359 is located at position 222910 relative to the genome of Rat cytomegalovirus.

[33181] VGAM2373 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2373 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[33182] An enzyme complex designated DICER COMPLEX, dices the VGAM2373 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2373 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2373 RNA is designated SEQ ID:5084, and is provided hereinbelow with reference to the sequence listing part.

[33183] VGAM2373 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2373 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2373 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33184] VGAM2373 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM2373 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2373 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2373 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2373 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33185] The complementary binding of VGAM2373 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM2373 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2373 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2373 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[33186] It is appreciated that VGAM2373 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2373 host target genes. The mRNA of each one of this plurality of VGAM2373 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2373 RNA, herein designated VGAM RNA, and which when bound by VGAM2373 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2373 host target proteins.

[33187] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2373 gene, herein designated VGAM GENE, on one or more VGAM2373 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33188] It is yet further appreciated that a function of VGAM2373 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2373 include diagnosis, prevention and treatment of viral infection by Rat cytomegalovirus. Specific functions, and accordingly utilities, of VGAM2373 correlate with, and may be deduced from, the identity of the host target genes which VGAM2373 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[33189] Nucleotide sequences of the VGAM2373 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

diced VGAM2373 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2373 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2373 are further described hereinbelow with reference to Table 1.

[33190] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2373 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[33191] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2374 (VGAM2374) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[33192] VGAM2374 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2374 was detected is described hereinabove with reference to Figs. 2-8.

[33193] VGAM2374 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of Rat cytomegalovirus. VGAM2374 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[33194] VGAM2374 gene, herein designated VGAM GENE, encodes a VGAM2374 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2374 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2374 precursor RNA is designated SEQ ID:2360, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2360 is located at position 203878 relative to the genome of Rat cytomegalovirus.

[33195] VGAM2374 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2374 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33196] An enzyme complex designated DICER COMPLEX, dices the VGAM2374 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2374 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 61%) nucleotide sequence of VGAM2374 RNA is designated SEQ ID:5085, and is provided hereinbelow with reference to the sequence listing part.

[33197] VGAM2374 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2374 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2374 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33198] VGAM2374 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2374 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2374 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2374 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2374 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33199] The complementary binding of VGAM2374 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM2374 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2374 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2374 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[33200] It is appreciated that VGAM2374 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2374 host target genes. The mRNA of each one of this plurality of VGAM2374 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2374 RNA, herein designated VGAM RNA, and which when bound by VGAM2374 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2374 host target proteins.

[33201] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2374 gene, herein designated VGAM GENE, on one or more VGAM2374 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33202] It is yet further appreciated that a function of VGAM2374 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2374 include diagnosis, prevention and treatment of viral infection by Rat cytomegalovirus. Specific functions, and accordingly utilities, of VGAM2374 correlate with, and may be deduced from, the identity of the host target genes which VGAM2374 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[33203] Nucleotide sequences of the VGAM2374 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the diced VGAM2374 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2374 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2374 are further described hereinbelow with reference to Table 1.

[33204] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2374 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[33205] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2375 (VGAM2375) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[33206] VGAM2375 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2375 was detected is described hereinabove with reference to Figs. 2-8.

[33207] VGAM2375 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rat cytomegalovirus. VGAM2375 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[33208] VGAM2375 gene, herein designated VGAM GENE, encodes a VGAM2375 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2375 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2375 precursor RNA is designated SEQ ID:2361, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2361 is located at position 217137 relative to the genome of Rat cytomegalovirus.

[33209] VGAM2375 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2375 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33210] An enzyme complex designated DICER COMPLEX, dices the VGAM2375 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2375 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2375 RNA is designated SEQ ID:5086, and is provided hereinbelow with reference to the sequence listing part.

[33211] VGAM2375 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2375 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2375 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN COD-

ING and 3UTR respectively.

[33212] VGAM2375 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2375 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2375 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2375 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2375 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33213] The complementary binding of VGAM2375 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2375 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2375 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2375 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[33214] It is appreciated that VGAM2375 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2375 host target genes. The mRNA of each one of this plurality of VGAM2375 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2375 RNA, herein designated VGAM RNA, and which when bound by VGAM2375 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2375 host target proteins.

[33215] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2375 gene, herein designated VGAM GENE, on one

or more VGAM2375 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33216] It is yet further appreciated that a function of VGAM2375 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2375 include diagnosis, prevention and treatment of viral infection by Rat cytomegalovirus. Specific functions, and accordingly utilities, of VGAM2375 correlate with, and may be deduced from, the identity of the host target genes which VGAM2375 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[33217] Nucleotide sequences of the VGAM2375 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2375 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2375 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2375 are further described hereinbelow with reference to Table 1.

[33218] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2375 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[33219] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2376 (VGAM2376) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[33220] VGAM2376 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2376 was detected is de-

scribed hereinabove with reference to Figs. 2-8.

[33221] VGAM2376 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rat cytomegalovirus. VGAM2376 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[33222] VGAM2376 gene, herein designated VGAM GENE, encodes a VGAM2376 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2376 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2376 precursor RNA is designated SEQ ID:2362, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2362 is located at position 188783 relative to the genome of Rat cytomegalovirus.

[33223] VGAM2376 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2376 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33224] An enzyme complex designated DICER COMPLEX, dices the VGAM2376 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2376 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2376 RNA is designated SEQ ID:5087, and is provided hereinbelow with reference to the sequence listing part.

[33225] VGAM2376 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2376 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2376 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and

a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33226] VGAM2376 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2376 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2376 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2376 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2376 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both

3UTR and 5UTR regions.

[33227] The complementary binding of VGAM2376 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2376 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2376 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2376 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[33228] It is appreciated that VGAM2376 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2376 host target genes. The mRNA of each one of this plurality of VGAM2376 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2376 RNA, herein designated VGAM RNA, and which when bound by VGAM2376 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2376 host target proteins.

[33229] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM2376 gene, herein designated VGAM GENE, on one or more VGAM2376 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33230] It is yet further appreciated that a function of VGAM2376 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2376 include diagnosis, prevention and treatment of viral infection by Rat cytomegalovirus. Specific functions, and accordingly utilities, of VGAM2376 correlate with, and may be deduced from, the identity of the host target genes which VGAM2376 binds and inhibits, and the function of these host target genes, as

elaborated hereinbelow.

[33231] Nucleotide sequences of the VGAM2376 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2376 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2376 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2376 are further described hereinbelow with reference to Table 1.

[33232] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2376 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[33233] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2377 (VGAM2377) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[33234] VGAM2377 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene.

The method by which VGAM2377 was detected is described hereinabove with reference to Figs. 2-8.

[33235] VGAM2377 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rat cytomegalovirus. VGAM2377 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[33236] VGAM2377 gene, herein designated VGAM GENE, encodes a VGAM2377 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2377 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2377 precursor RNA is designated SEQ ID:2363, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2363 is located at position 197566 relative to the genome of Rat cytomegalovirus.

[33237] VGAM2377 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2377 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33238] An enzyme complex designated DICER COMPLEX, dices the VGAM2377 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2377 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 50%) nucleotide sequence of VGAM2377 RNA is designated SEQ ID:5088, and is provided hereinbelow with reference to the sequence listing part.

[33239] VGAM2377 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2377 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2377 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding

gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33240] VGAM2377 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2377 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2377 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2377 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2377 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be lo-

cated in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33241] The complementary binding of VGAM2377 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2377 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2377 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2377 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[33242] It is appreciated that VGAM2377 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2377 host target genes. The mRNA of each one of this plurality of VGAM2377 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2377 RNA, herein designated VGAM RNA, and which when bound by VGAM2377 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2377 host target proteins.

[33243] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM2377 gene, herein designated VGAM GENE, on one or more VGAM2377 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33244] It is yet further appreciated that a function of VGAM2377 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2377 include diagnosis, prevention and treatment of viral infection by Rat cytomegalovirus. Specific functions, and accordingly utilities, of VGAM2377 correlate with, and may be deduced from, the identity of the host target genes which VGAM2377 binds and in-

hibits, and the function of these host target genes, as elaborated hereinbelow.

[33245] Nucleotide sequences of the VGAM2377 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2377 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2377 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2377 are further described hereinbelow with reference to Table 1.

[33246] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2377 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[33247] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2378 (VGAM2378) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[33248] VGAM2378 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2378 was detected is described hereinabove with reference to Figs. 2-8.

[33249] VGAM2378 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rat cytomegalovirus. VGAM2378 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[33250] VGAM2378 gene, herein designated VGAM GENE, encodes a VGAM2378 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2378 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2378 precursor RNA is designated SEQ ID:2364, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2364 is located at position 219131 relative to the genome of Rat cytomegalovirus.

[33251] VGAM2378 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2378 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33252] An enzyme complex designated DICER COMPLEX, dices the VGAM2378 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2378 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 59%) nucleotide sequence of VGAM2378 RNA is designated SEQ ID:5089, and is provided hereinbelow with reference to the sequence listing part.

[33253] VGAM2378 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2378 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2378 host target RNA, herein designated VGAM HOST TARGET RNA, comprises

three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33254] VGAM2378 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2378 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2378 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2378 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2378 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an

example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33255] The complementary binding of VGAM2378 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2378 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2378 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2378 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[33256] It is appreciated that VGAM2378 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2378 host target genes. The mRNA of each one of this plurality of VGAM2378 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2378 RNA, herein designated VGAM RNA, and which when bound by VGAM2378 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2378 host target proteins.

[33257] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2378 gene, herein designated VGAM GENE, on one or more VGAM2378 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33258] It is yet further appreciated that a function of VGAM2378 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2378 include diagnosis, prevention and treatment of viral infection by Rat cytomegalovirus. Specific functions, and accordingly utilities, of VGAM2378 correlate with, and may be deduced from, the identity of

the host target genes which VGAM2378 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[33259] Nucleotide sequences of the VGAM2378 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2378 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2378 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2378 are further described hereinbelow with reference to Table 1.

[33260] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2378 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[33261] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2379 (VGAM2379) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[33262] VGAM2379 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2379 was detected is described hereinabove with reference to Figs. 2-8.

[33263] VGAM2379 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rat cytomegalovirus. VGAM2379 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[33264] VGAM2379 gene, herein designated VGAM GENE, encodes a VGAM2379 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2379 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2379 precursor RNA is designated SEQ ID:2365, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2365 is located at position 212075 relative to the genome of Rat cytomegalovirus.

[33265] VGAM2379 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2379 folded precursor RNA, herein designated VGAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33266] An enzyme complex designated DICER COMPLEX, dices the VGAM2379 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2379 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 84%) nucleotide sequence of VGAM2379 RNA is designated SEQ ID:5090, and is provided hereinbelow with reference to the sequence listing part.

[33267] VGAM2379 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2379 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2379 host target RNA,

herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33268] VGAM2379 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2379 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2379 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2379 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2379 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host tar-

get binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33269] The complementary binding of VGAM2379 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2379 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2379 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2379 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[33270] It is appreciated that VGAM2379 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2379 host target genes. The mRNA of each one of this plurality of VGAM2379 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2379 RNA, herein designated VGAM RNA, and which when bound by VGAM2379 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2379 host target proteins.

[33271] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2379 gene, herein designated VGAM GENE, on one or more VGAM2379 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33272] It is yet further appreciated that a function of VGAM2379 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2379 include diagnosis, prevention and treatment of viral infection by Rat cytomegalovirus. Specific functions, and accordingly utilities, of VGAM2379

correlate with, and may be deduced from, the identity of the host target genes which VGAM2379 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[33273] Nucleotide sequences of the VGAM2379 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2379 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2379 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2379 are further described hereinbelow with reference to Table 1.

[33274] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2379 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[33275] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2380 (VGAM2380) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the

art.

[33276] VGAM2380 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2380 was detected is described hereinabove with reference to Figs. 2-8.

[33277] VGAM2380 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human herpesvirus 4. VGAM2380 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[33278] VGAM2380 gene, herein designated VGAM GENE, encodes a VGAM2380 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2380 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2380 precursor RNA is designated SEQ ID:2366, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2366 is located at position 7588 relative to the genome of Human herpesvirus 4.

[33279] VGAM2380 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2380 folded

precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33280] An enzyme complex designated DICER COMPLEX, dices the VGAM2380 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2380 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 91%) nucleotide sequence of VGAM2380 RNA is designated SEQ ID:5091, and is provided hereinbelow with reference to the sequence listing part.

[33281] VGAM2380 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2380 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM2380 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33282] VGAM2380 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2380 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2380 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2380 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2380 host target RNA, herein designated VGAM HOST TARGET RNA.

It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33283] The complementary binding of VGAM2380 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2380 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2380 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2380 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[33284] It is appreciated that VGAM2380 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2380 host target genes. The mRNA of each one of this plurality of VGAM2380 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2380 RNA, herein designated VGAM RNA, and which when bound by VGAM2380 RNA, herein designated VGAM RNA, causes inhibition of translation of

respective one or more VGAM2380 host target proteins.

[33285] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2380 gene, herein designated VGAM GENE, on one or more VGAM2380 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33286] It is yet further appreciated that a function of VGAM2380 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2380 include diagnosis, prevention and treatment of viral infection by Human herpesvirus 4. Spe-

cific functions, and accordingly utilities, of VGAM2380 correlate with, and may be deduced from, the identity of the host target genes which VGAM2380 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[33287] Nucleotide sequences of the VGAM2380 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2380 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2380 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2380 are further described hereinbelow with reference to Table 1.

[33288] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2380 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[33289] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2381 (VGAM2381) viral gene, which modulates expression of respective host target genes thereof, the func-

tion and utility of which host target genes is known in the art.

[33290] VGAM2381 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2381 was detected is described hereinabove with reference to Figs. 2-8.

[33291] VGAM2381 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human herpesvirus 4. VGAM2381 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[33292] VGAM2381 gene, herein designated VGAM GENE, encodes a VGAM2381 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2381 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2381 precursor RNA is designated SEQ ID:2367, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2367 is located at position 48597 relative to the genome of Human herpesvirus 4.

[33293] VGAM2381 precursor RNA, herein designated VGAM PRE-

CURSOR RNA, folds onto itself, forming VGAM2381 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33294] An enzyme complex designated DICER COMPLEX, dices the VGAM2381 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2381 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 69%) nucleotide sequence of VGAM2381 RNA is designated SEQ ID:5092, and is provided hereinbelow with reference to the sequence listing part.

[33295] VGAM2381 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM2381 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2381 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33296] VGAM2381 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2381 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2381 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2381 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2381 host

target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33297] The complementary binding of VGAM2381 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2381 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2381 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2381 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[33298] It is appreciated that VGAM2381 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2381 host target genes. The mRNA of each one of this plurality of VGAM2381 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2381 RNA, herein designated VGAM RNA, and which when bound by VGAM2381 RNA, herein

designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2381 host target proteins.

[33299] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2381 gene, herein designated VGAM GENE, on one or more VGAM2381 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33300] It is yet further appreciated that a function of VGAM2381 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2381 include diagnosis, prevention and

treatment of viral infection by Human herpesvirus 4. Specific functions, and accordingly utilities, of VGAM2381 correlate with, and may be deduced from, the identity of the host target genes which VGAM2381 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[33301] Nucleotide sequences of the VGAM2381 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2381 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2381 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2381 are further described hereinbelow with reference to Table 1.

[33302] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2381 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[33303] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2382 (VGAM2382) viral gene, which modulates ex-

pression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[33304] VGAM2382 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2382 was detected is described hereinabove with reference to Figs. 2-8.

[33305] VGAM2382 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human herpesvirus 4. VGAM2382 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[33306] VGAM2382 gene, herein designated VGAM GENE, encodes a VGAM2382 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2382 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2382 precursor RNA is designated SEQ ID:2368, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2368 is located at position 54739 relative to the genome of Human herpesvirus 4.

[33307] VGAM2382 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2382 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33308] An enzyme complex designated DICER COMPLEX, dices the VGAM2382 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2382 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 55%) nucleotide sequence of VGAM2382 RNA is designated SEQ ID:5093, and is provided hereinbelow with reference to the sequence listing part.

[33309] VGAM2382 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2382 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2382 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33310] VGAM2382 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2382 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2382 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2382 RNA, herein designated VGAM RNA, may have a different number of host target

binding sites in untranslated regions of a VGAM2382 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33311] The complementary binding of VGAM2382 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2382 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2382 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2382 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[33312] It is appreciated that VGAM2382 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2382 host target genes. The mRNA of each one of this plurality of VGAM2382 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2382 RNA, herein designated VGAM

RNA, and which when bound by VGAM2382 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2382 host target proteins.

[33313] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2382 gene, herein designated VGAM GENE, on one or more VGAM2382 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33314] It is yet further appreciated that a function of VGAM2382 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM2382 include diagnosis, prevention and treatment of viral infection by Human herpesvirus 4. Specific functions, and accordingly utilities, of VGAM2382 correlate with, and may be deduced from, the identity of the host target genes which VGAM2382 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[33315] Nucleotide sequences of the VGAM2382 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2382 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2382 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2382 are further described hereinbelow with reference to Table 1.

[33316] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2382 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[33317] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Mes-

senger 2383 (VGAM2383) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[33318] VGAM2383 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2383 was detected is described hereinabove with reference to Figs. 2-8.

[33319] VGAM2383 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human herpesvirus 4. VGAM2383 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[33320] VGAM2383 gene, herein designated VGAM GENE, encodes a VGAM2383 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2383 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2383 precursor RNA is designated SEQ ID:2369, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2369 is located at position

53736 relative to the genome of Human herpesvirus 4.

[33321] VGAM2383 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2383 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33322] An enzyme complex designated DICER COMPLEX, dices the VGAM2383 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2383 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 48%) nucleotide sequence of VGAM2383 RNA is designated SEQ ID:5094, and is provided hereinbelow with reference to the sequence listing part.

[33323] VGAM2383 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2383 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2383 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33324] VGAM2383 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2383 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2383 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2383 RNA, herein designated

VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2383 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33325] The complementary binding of VGAM2383 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2383 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2383 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2383 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[33326] It is appreciated that VGAM2383 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2383 host target genes. The mRNA of each one of this plurality of VGAM2383 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM2383 RNA, herein designated VGAM RNA, and which when bound by VGAM2383 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2383 host target proteins.

[33327] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2383 gene, herein designated VGAM GENE, on one or more VGAM2383 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33328] It is yet further appreciated that a function of VGAM2383 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2383 include diagnosis, prevention and treatment of viral infection by Human herpesvirus 4. Specific functions, and accordingly utilities, of VGAM2383 correlate with, and may be deduced from, the identity of the host target genes which VGAM2383 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[33329] Nucleotide sequences of the VGAM2383 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2383 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2383 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2383 are further described hereinbelow with reference to Table 1.

[33330] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2383 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[33331] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present

invention, referred to here as Viral Genomic Address Messenger 2384 (VGAM2384) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[33332] VGAM2384 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2384 was detected is described hereinabove with reference to Figs. 2-8.

[33333] VGAM2384 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human herpesvirus 4. VGAM2384 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[33334] VGAM2384 gene, herein designated VGAM GENE, encodes a VGAM2384 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2384 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2384 precursor RNA is designated SEQ ID:2370, and is provided hereinbelow with reference to the sequence listing part. Nu-

cleotide sequence SEQ ID:2370 is located at position 5198 relative to the genome of Human herpesvirus 4.

[33335] VGAM2384 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2384 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33336] An enzyme complex designated DICER COMPLEX, dices the VGAM2384 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2384 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2384 RNA is designated SEQ ID:5095, and is provided hereinbelow with reference to the sequence

listing part.

[33337] VGAM2384 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2384 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2384 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33338] VGAM2384 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2384 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2384 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not

meant to be limiting VGAM2384 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2384 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33339] The complementary binding of VGAM2384 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2384 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2384 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2384 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[33340] It is appreciated that VGAM2384 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2384 host target genes. The mRNA of each one of this plurality of VGAM2384 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2384 RNA, herein designated VGAM RNA, and which when bound by VGAM2384 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2384 host target proteins.

[33341] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2384 gene, herein designated VGAM GENE, on one or more VGAM2384 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33342] It is yet further appreciated that a function of VGAM2384

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2384 include diagnosis, prevention and treatment of viral infection by Human herpesvirus 4. Specific functions, and accordingly utilities, of VGAM2384 correlate with, and may be deduced from, the identity of the host target genes which VGAM2384 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[33343] Nucleotide sequences of the VGAM2384 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2384 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2384 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2384 are further described hereinbelow with reference to Table 1.

[33344] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2384 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[33345] Fig. 1 further provides a conceptual description of another

novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2385 (VGAM2385) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[33346] VGAM2385 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2385 was detected is described hereinabove with reference to Figs. 2-8.

[33347] VGAM2385 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human herpesvirus 4. VGAM2385 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[33348] VGAM2385 gene, herein designated VGAM GENE, encodes a VGAM2385 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2385 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2385 precursor RNA is designated SEQ ID:2371, and is provided here-

inbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2371 is located at position 7899 relative to the genome of Human herpesvirus 4.

[33349] VGAM2385 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2385 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33350] An enzyme complex designated DICER COMPLEX, dices the VGAM2385 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2385 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 90%) nucleotide sequence of VGAM2385 RNA is designated SEQ ID:5096, and

is provided hereinbelow with reference to the sequence listing part.

[33351] VGAM2385 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2385 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2385 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33352] VGAM2385 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2385 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2385 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites

shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2385 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2385 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33353] The complementary binding of VGAM2385 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2385 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2385 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2385 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[33354] It is appreciated that VGAM2385 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2385 host target genes. The mRNA of each one of this plurality of VGAM2385 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2385 RNA, herein designated VGAM RNA, and which when bound by VGAM2385 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2385 host target proteins.

[33355] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2385 gene, herein designated VGAM GENE, on one or more VGAM2385 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33356] It is yet further appreciated that a function of VGAM2385 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2385 include diagnosis, prevention and treatment of viral infection by Human herpesvirus 4. Specific functions, and accordingly utilities, of VGAM2385 correlate with, and may be deduced from, the identity of the host target genes which VGAM2385 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[33357] Nucleotide sequences of the VGAM2385 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2385 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2385 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2385 are further described hereinbelow with reference to Table 1.

[33358] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2385 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[33359] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2386 (VGAM2386) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[33360] VGAM2386 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2386 was detected is described hereinabove with reference to Figs. 2-8.

[33361] VGAM2386 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human herpesvirus 4. VGAM2386 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[33362] VGAM2386 gene, herein designated VGAM GENE, encodes a VGAM2386 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2386 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2386 precur-

sor RNA is designated SEQ ID:2372, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2372 is located at position 6848 relative to the genome of Human herpesvirus 4.

[33363] VGAM2386 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2386 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33364] An enzyme complex designated DICER COMPLEX, dices the VGAM2386 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2386 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide se-

quence of VGAM2386 RNA is designated SEQ ID:5097, and is provided hereinbelow with reference to the sequence listing part.

[33365] VGAM2386 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2386 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2386 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33366] VGAM2386 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2386 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2386 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is ap-

preciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2386 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2386 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33367] The complementary binding of VGAM2386 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2386 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2386 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2386 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[33368] It is appreciated that VGAM2386 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2386 host target genes. The mRNA of

each one of this plurality of VGAM2386 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2386 RNA, herein designated VGAM RNA, and which when bound by VGAM2386 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2386 host target proteins.

[33369] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2386 gene, herein designated VGAM GENE, on one or more VGAM2386 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science

294,779 (2001)).

[33370] It is yet further appreciated that a function of VGAM2386 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2386 include diagnosis, prevention and treatment of viral infection by Human herpesvirus 4. Specific functions, and accordingly utilities, of VGAM2386 correlate with, and may be deduced from, the identity of the host target genes which VGAM2386 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[33371] Nucleotide sequences of the VGAM2386 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2386 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2386 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2386 are further described hereinbelow with reference to Table 1.

[33372] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2386 RNA, herein designated VGAM RNA, are de-

scribed hereinbelow with reference to Table 2.

[33373] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2387 (VGAM2387) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[33374] VGAM2387 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2387 was detected is described hereinabove with reference to Figs. 2-8.

[33375] VGAM2387 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human herpesvirus 4. VGAM2387 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[33376] VGAM2387 gene, herein designated VGAM GENE, encodes a VGAM2387 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2387 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly

similar to the nucleotide sequence of VGAM2387 precursor RNA is designated SEQ ID:2373, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2373 is located at position 7029 relative to the genome of Human herpesvirus 4.

[33377] VGAM2387 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2387 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33378] An enzyme complex designated DICER COMPLEX, dices the VGAM2387 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2387 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2387 RNA is designated SEQ ID:5098, and is provided hereinbelow with reference to the sequence listing part.

[33379] VGAM2387 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2387 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2387 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33380] VGAM2387 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2387 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2387 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I,

BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2387 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2387 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33381] The complementary binding of VGAM2387 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2387 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2387 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2387 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[33382] It is appreciated that VGAM2387 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM2387 host target genes. The mRNA of each one of this plurality of VGAM2387 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2387 RNA, herein designated VGAM RNA, and which when bound by VGAM2387 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2387 host target proteins.

[33383] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2387 gene, herein designated VGAM GENE, on one or more VGAM2387 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33384] It is yet further appreciated that a function of VGAM2387 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2387 include diagnosis, prevention and treatment of viral infection by Human herpesvirus 4. Specific functions, and accordingly utilities, of VGAM2387 correlate with, and may be deduced from, the identity of the host target genes which VGAM2387 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[33385] Nucleotide sequences of the VGAM2387 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2387 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2387 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2387 are further described hereinbelow with reference to Table 1.

[33386] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites

to VGAM2387 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[33387] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2388 (VGAM2388) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[33388] VGAM2388 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2388 was detected is described hereinabove with reference to Figs. 2-8.

[33389] VGAM2388 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human herpesvirus 4. VGAM2388 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[33390] VGAM2388 gene, herein designated VGAM GENE, encodes a VGAM2388 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2388 precursor RNA, herein designated VGAM PRECURSOR RNA, does not en-

code a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2388 precursor RNA is designated SEQ ID:2374, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2374 is located at position 55246 relative to the genome of Human herpesvirus 4.

[33391] VGAM2388 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2388 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33392] An enzyme complex designated DICER COMPLEX, dices the VGAM2388 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2388 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2388 RNA is designated SEQ ID:5099, and is provided hereinbelow with reference to the sequence listing part.

[33393] VGAM2388 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2388 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2388 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33394] VGAM2388 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2388 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2388 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3

such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2388 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2388 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33395] The complementary binding of VGAM2388 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2388 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2388 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2388 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[33396] It is appreciated that VGAM2388 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2388 host target genes. The mRNA of each one of this plurality of VGAM2388 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2388 RNA, herein designated VGAM RNA, and which when bound by VGAM2388 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2388 host target proteins.

[33397] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2388 gene, herein designated VGAM GENE, on one or more VGAM2388 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33398] It is yet further appreciated that a function of VGAM2388 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2388 include diagnosis, prevention and treatment of viral infection by Human herpesvirus 4. Specific functions, and accordingly utilities, of VGAM2388 correlate with, and may be deduced from, the identity of the host target genes which VGAM2388 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[33399] Nucleotide sequences of the VGAM2388 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2388 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2388 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2388 are further described hereinbelow with reference to Table 1.

[33400] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the

complementarity of each of these host target binding sites to VGAM2388 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[33401] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2389 (VGAM2389) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[33402] VGAM2389 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2389 was detected is described hereinabove with reference to Figs. 2-8.

[33403] VGAM2389 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox virus.
VGAM2389 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[33404] VGAM2389 gene, herein designated VGAM GENE, encodes a VGAM2389 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2389 precursor RNA,

herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2389 precursor RNA is designated SEQ ID:2375, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2375 is located at position 19516 relative to the genome of Goatpox virus.

[33405] VGAM2389 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2389 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33406] An enzyme complex designated DICER COMPLEX, dices the VGAM2389 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2389 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2389 RNA is designated SEQ ID:5100, and is provided hereinbelow with reference to the sequence listing part.

[33407] VGAM2389 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2389 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2389 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33408] VGAM2389 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2389 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2389 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host

target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2389 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2389 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33409] The complementary binding of VGAM2389 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2389 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2389 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2389 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[33410] It is appreciated that VGAM2389 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2389 host target genes. The mRNA of each one of this plurality of VGAM2389 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2389 RNA, herein designated VGAM RNA, and which when bound by VGAM2389 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2389 host target proteins.

[33411] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2389 gene, herein designated VGAM GENE, on one or more VGAM2389 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33412] It is yet further appreciated that a function of VGAM2389 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2389 include diagnosis, prevention and treatment of viral infection by Goatpox virus. Specific functions, and accordingly utilities, of VGAM2389 correlate with, and may be deduced from, the identity of the host target genes which VGAM2389 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[33413] Nucleotide sequences of the VGAM2389 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2389 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2389 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2389 are further described hereinbelow with reference to Table 1.

[33414] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2389 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[33415] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2390 (VGAM2390) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[33416] VGAM2390 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2390 was detected is described hereinabove with reference to Figs. 2-8.

[33417] VGAM2390 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox virus. VGAM2390 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[33418] VGAM2390 gene, herein designated VGAM GENE, encodes a VGAM2390 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and un-

like most ordinary genes, VGAM2390 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2390 precursor RNA is designated SEQ ID:2376, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2376 is located at position 85371 relative to the genome of Goatpox virus.

[33419] VGAM2390 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2390 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33420] An enzyme complex designated DICER COMPLEX, dices the VGAM2390 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2390 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2390 RNA is designated SEQ ID:5101, and is provided hereinbelow with reference to the sequence listing part.

[33421] VGAM2390 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2390 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2390 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33422] VGAM2390 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2390 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2390 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed

sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2390 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2390 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33423] The complementary binding of VGAM2390 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2390 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2390 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2390 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target

protein is therefore outlined by a broken line.

[33424] It is appreciated that VGAM2390 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2390 host target genes. The mRNA of each one of this plurality of VGAM2390 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2390 RNA, herein designated VGAM RNA, and which when bound by VGAM2390 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2390 host target proteins.

[33425] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2390 gene, herein designated VGAM GENE, on one or more VGAM2390 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33426] It is yet further appreciated that a function of VGAM2390 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2390 include diagnosis, prevention and treatment of viral infection by Goatpox virus. Specific functions, and accordingly utilities, of VGAM2390 correlate with, and may be deduced from, the identity of the host target genes which VGAM2390 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[33427] Nucleotide sequences of the VGAM2390 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2390 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2390 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2390 are further described hereinbelow with reference to Table 1.

[33428] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2390 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[33429] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2391 (VGAM2391) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[33430] VGAM2391 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2391 was detected is described hereinabove with reference to Figs. 2-8.

[33431] VGAM2391 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox virus.
VGAM2391 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[33432] VGAM2391 gene, herein designated VGAM GENE, encodes a VGAM2391 precursor RNA, herein designated VGAM

PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2391 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2391 precursor RNA is designated SEQ ID:2377, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2377 is located at position 22657 relative to the genome of Goatpox virus.

[33433] VGAM2391 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2391 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33434] An enzyme complex designated DICER COMPLEX, dices the VGAM2391 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2391 RNA, herein designated VGAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 71%) nucleotide sequence of VGAM2391 RNA is designated SEQ ID:5102, and is provided hereinbelow with reference to the sequence listing part.

[33435] VGAM2391 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2391 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2391 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33436] VGAM2391 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2391 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2391 RNA, herein designated

VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2391 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2391 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33437] The complementary binding of VGAM2391 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2391 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2391 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2391 host target protein, herein desig-

nated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[33438] It is appreciated that VGAM2391 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2391 host target genes. The mRNA of each one of this plurality of VGAM2391 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2391 RNA, herein designated VGAM RNA, and which when bound by VGAM2391 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2391 host target proteins.

[33439] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2391 gene, herein designated VGAM GENE, on one or more VGAM2391 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33440] It is yet further appreciated that a function of VGAM2391 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2391 include diagnosis, prevention and treatment of viral infection by Goatpox virus. Specific functions, and accordingly utilities, of VGAM2391 correlate with, and may be deduced from, the identity of the host target genes which VGAM2391 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[33441] Nucleotide sequences of the VGAM2391 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2391 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2391 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2391 are further described hereinbelow with reference to Table 1.

[33442] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2391 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[33443] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2392 (VGAM2392) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[33444] VGAM2392 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2392 was detected is described hereinabove with reference to Figs. 2-8.

[33445] VGAM2392 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox virus.
VGAM2392 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[33446] VGAM2392 gene, herein designated VGAM GENE, encodes

a VGAM2392 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2392 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2392 precursor RNA is designated SEQ ID:2378, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2378 is located at position 9075 relative to the genome of Goatpox virus.

[33447] VGAM2392 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2392 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33448] An enzyme complex designated DICER COMPLEX, dices the VGAM2392 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2392 RNA,

herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 63%) nucleotide sequence of VGAM2392 RNA is designated SEQ ID:5103, and is provided hereinbelow with reference to the sequence listing part.

[33449] VGAM2392 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2392 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2392 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33450] VGAM2392 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2392 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM2392 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2392 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2392 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33451] The complementary binding of VGAM2392 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2392 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2392 host target RNA, herein designated VGAM HOST TARGET

RNA, into VGAM2392 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[33452] It is appreciated that VGAM2392 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2392 host target genes. The mRNA of each one of this plurality of VGAM2392 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2392 RNA, herein designated VGAM RNA, and which when bound by VGAM2392 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2392 host target proteins.

[33453] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2392 gene, herein designated VGAM GENE, on one or more VGAM2392 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33454] It is yet further appreciated that a function of VGAM2392 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2392 include diagnosis, prevention and treatment of viral infection by Goatpox virus. Specific functions, and accordingly utilities, of VGAM2392 correlate with, and may be deduced from, the identity of the host target genes which VGAM2392 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[33455] Nucleotide sequences of the VGAM2392 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2392 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2392 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2392 are further

described hereinbelow with reference to Table 1.

[33456] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2392 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[33457] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2393 (VGAM2393) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[33458] VGAM2393 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2393 was detected is described hereinabove with reference to Figs. 2-8.

[33459] VGAM2393 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox virus.
VGAM2393 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[33460] VGAM2393 gene, herein designated VGAM GENE, encodes a VGAM2393 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2393 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2393 precursor RNA is designated SEQ ID:2379, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2379 is located at position 35069 relative to the genome of Goatpox virus.

[33461] VGAM2393 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2393 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33462] An enzyme complex designated DICER COMPLEX, dices the VGAM2393 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, into VGAM2393 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 53%) nucleotide sequence of VGAM2393 RNA is designated SEQ ID:5104, and is provided hereinbelow with reference to the sequence listing part.

[33463] VGAM2393 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2393 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2393 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33464] VGAM2393 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2393 host target RNA, herein designated VGAM HOST TARGET RNA. This

complementary binding is due to the fact that the nucleotide sequence of VGAM2393 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2393 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2393 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33465] The complementary binding of VGAM2393 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2393 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2393

host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2393 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[33466] It is appreciated that VGAM2393 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2393 host target genes. The mRNA of each one of this plurality of VGAM2393 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2393 RNA, herein designated VGAM RNA, and which when bound by VGAM2393 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2393 host target proteins.

[33467] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2393 gene, herein designated VGAM GENE, on one or more VGAM2393 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33468] It is yet further appreciated that a function of VGAM2393 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2393 include diagnosis, prevention and treatment of viral infection by Goatpox virus. Specific functions, and accordingly utilities, of VGAM2393 correlate with, and may be deduced from, the identity of the host target genes which VGAM2393 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[33469] Nucleotide sequences of the VGAM2393 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2393 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2393 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM2393 are further described hereinbelow with reference to Table 1.

[33470] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2393 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[33471] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2394 (VGAM2394) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[33472] VGAM2394 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2394 was detected is described hereinabove with reference to Figs. 2-8.

[33473] VGAM2394 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox virus. VGAM2394 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the

human genome.

[33474] VGAM2394 gene, herein designated VGAM GENE, encodes a VGAM2394 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2394 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2394 precursor RNA is designated SEQ ID:2380, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2380 is located at position 149142 relative to the genome of Goatpox virus.

[33475] VGAM2394 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2394 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33476] An enzyme complex designated DICER COMPLEX, dices

the VGAM2394 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2394 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2394 RNA is designated SEQ ID:5105, and is provided hereinbelow with reference to the sequence listing part.

[33477] VGAM2394 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2394 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2394 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33478] VGAM2394 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2394 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2394 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2394 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2394 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33479] The complementary binding of VGAM2394 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2394 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM2394 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2394 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[33480] It is appreciated that VGAM2394 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2394 host target genes. The mRNA of each one of this plurality of VGAM2394 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2394 RNA, herein designated VGAM RNA, and which when bound by VGAM2394 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2394 host target proteins.

[33481] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2394 gene, herein designated VGAM GENE, on one or more VGAM2394 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33482] It is yet further appreciated that a function of VGAM2394 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2394 include diagnosis, prevention and treatment of viral infection by Goatpox virus. Specific functions, and accordingly utilities, of VGAM2394 correlate with, and may be deduced from, the identity of the host target genes which VGAM2394 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[33483] Nucleotide sequences of the VGAM2394 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2394 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of

VGAM2394 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2394 are further described hereinbelow with reference to Table 1.

[33484] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2394 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[33485] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2395 (VGAM2395) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[33486] VGAM2395 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2395 was detected is described hereinabove with reference to Figs. 2-8.

[33487] VGAM2395 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox virus. VGAM2395 host target gene, herein designated VGAM

HOST TARGET GENE, is a human gene contained in the human genome.

[33488] VGAM2395 gene, herein designated VGAM GENE, encodes a VGAM2395 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2395 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2395 precursor RNA is designated SEQ ID:2381, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2381 is located at position 120551 relative to the genome of Goatpox virus.

[33489] VGAM2395 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2395 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33490] An enzyme complex designated DICER COMPLEX, dices the VGAM2395 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2395 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 48%) nucleotide sequence of VGAM2395 RNA is designated SEQ ID:5106, and is provided hereinbelow with reference to the sequence listing part.

[33491] VGAM2395 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2395 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2395 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33492] VGAM2395 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites

located in untranslated regions of VGAM2395 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2395 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2395 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2395 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33493] The complementary binding of VGAM2395 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2395 host target RNA, herein designated VGAM

HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2395 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2395 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[33494] It is appreciated that VGAM2395 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2395 host target genes. The mRNA of each one of this plurality of VGAM2395 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2395 RNA, herein designated VGAM RNA, and which when bound by VGAM2395 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2395 host target proteins.

[33495] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2395 gene, herein designated VGAM GENE, on one or more VGAM2395 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove

with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33496] It is yet further appreciated that a function of VGAM2395 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2395 include diagnosis, prevention and treatment of viral infection by Goatpox virus. Specific functions, and accordingly utilities, of VGAM2395 correlate with, and may be deduced from, the identity of the host target genes which VGAM2395 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[33497] Nucleotide sequences of the VGAM2395 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2395 RNA, herein designated VGAM RNA, and

a schematic representation of the secondary folding of VGAM2395 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2395 are further described hereinbelow with reference to Table 1.

[33498] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2395 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[33499] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2396 (VGAM2396) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[33500] VGAM2396 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2396 was detected is described hereinabove with reference to Figs. 2-8.

[33501] VGAM2396 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox virus.

VGAM2396 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[33502] VGAM2396 gene, herein designated VGAM GENE, encodes a VGAM2396 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2396 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2396 precursor RNA is designated SEQ ID:2382, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2382 is located at position 93517 relative to the genome of Goatpox virus.

[33503] VGAM2396 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2396 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[33504] An enzyme complex designated DICER COMPLEX, dices the VGAM2396 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2396 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2396 RNA is designated SEQ ID:5107, and is provided hereinbelow with reference to the sequence listing part.

[33505] VGAM2396 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2396 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2396 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33506] VGAM2396 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM2396 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2396 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2396 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2396 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33507] The complementary binding of VGAM2396 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM2396 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2396 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2396 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[33508] It is appreciated that VGAM2396 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2396 host target genes. The mRNA of each one of this plurality of VGAM2396 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2396 RNA, herein designated VGAM RNA, and which when bound by VGAM2396 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2396 host target proteins.

[33509] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2396 gene, herein designated VGAM GENE, on one or more VGAM2396 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33510] It is yet further appreciated that a function of VGAM2396 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2396 include diagnosis, prevention and treatment of viral infection by Goatpox virus. Specific functions, and accordingly utilities, of VGAM2396 correlate with, and may be deduced from, the identity of the host target genes which VGAM2396 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[33511] Nucleotide sequences of the VGAM2396 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

diced VGAM2396 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2396 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2396 are further described hereinbelow with reference to Table 1.

[33512] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2396 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[33513] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2397 (VGAM2397) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[33514] VGAM2397 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2397 was detected is described hereinabove with reference to Figs. 2-8.

[33515] VGAM2397 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of Goatpox virus. VGAM2397 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[33516] VGAM2397 gene, herein designated VGAM GENE, encodes a VGAM2397 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2397 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2397 precursor RNA is designated SEQ ID:2383, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2383 is located at position 149485 relative to the genome of Goatpox virus.

[33517] VGAM2397 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2397 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33518] An enzyme complex designated DICER COMPLEX, dices the VGAM2397 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2397 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2397 RNA is designated SEQ ID:5108, and is provided hereinbelow with reference to the sequence listing part.

[33519] VGAM2397 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2397 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2397 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33520] VGAM2397 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2397 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2397 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2397 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2397 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33521] The complementary binding of VGAM2397 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM2397 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2397 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2397 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[33522] It is appreciated that VGAM2397 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2397 host target genes. The mRNA of each one of this plurality of VGAM2397 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2397 RNA, herein designated VGAM RNA, and which when bound by VGAM2397 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2397 host target proteins.

[33523] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2397 gene, herein designated VGAM GENE, on one or more VGAM2397 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33524] It is yet further appreciated that a function of VGAM2397 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2397 include diagnosis, prevention and treatment of viral infection by Goatpox virus. Specific functions, and accordingly utilities, of VGAM2397 correlate with, and may be deduced from, the identity of the host target genes which VGAM2397 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[33525] Nucleotide sequences of the VGAM2397 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the diced VGAM2397 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2397 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2397 are further described hereinbelow with reference to Table 1.

[33526] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2397 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[33527] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2398 (VGAM2398) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[33528] VGAM2398 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2398 was detected is described hereinabove with reference to Figs. 2-8.

[33529] VGAM2398 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox virus. VGAM2398 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[33530] VGAM2398 gene, herein designated VGAM GENE, encodes a VGAM2398 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2398 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2398 precursor RNA is designated SEQ ID:2384, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2384 is located at position 101040 relative to the genome of Goatpox virus.

[33531] VGAM2398 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2398 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33532] An enzyme complex designated DICER COMPLEX, dices the VGAM2398 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2398 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2398 RNA is designated SEQ ID:5109, and is provided hereinbelow with reference to the sequence listing part.

[33533] VGAM2398 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2398 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2398 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN COD-

ING and 3UTR respectively.

[33534] VGAM2398 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2398 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2398 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2398 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2398 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33535] The complementary binding of VGAM2398 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2398 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2398 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2398 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[33536] It is appreciated that VGAM2398 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2398 host target genes. The mRNA of each one of this plurality of VGAM2398 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2398 RNA, herein designated VGAM RNA, and which when bound by VGAM2398 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2398 host target proteins.

[33537] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2398 gene, herein designated VGAM GENE, on one

or more VGAM2398 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33538] It is yet further appreciated that a function of VGAM2398 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2398 include diagnosis, prevention and treatment of viral infection by Goatpox virus. Specific functions, and accordingly utilities, of VGAM2398 correlate with, and may be deduced from, the identity of the host target genes which VGAM2398 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[33539] Nucleotide sequences of the VGAM2398 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2398 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2398 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2398 are further described hereinbelow with reference to Table 1.

[33540] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2398 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[33541] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2399 (VGAM2399) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[33542] VGAM2399 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2399 was detected is de-

scribed hereinabove with reference to Figs. 2-8.

[33543] VGAM2399 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox virus. VGAM2399 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[33544] VGAM2399 gene, herein designated VGAM GENE, encodes a VGAM2399 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2399 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2399 precursor RNA is designated SEQ ID:2385, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2385 is located at position 23504 relative to the genome of Goatpox virus.

[33545] VGAM2399 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2399 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33546] An enzyme complex designated DICER COMPLEX, dices the VGAM2399 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2399 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2399 RNA is designated SEQ ID:5110, and is provided hereinbelow with reference to the sequence listing part.

[33547] VGAM2399 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2399 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2399 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and

a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33548] VGAM2399 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2399 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2399 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2399 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2399 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both

3UTR and 5UTR regions.

[33549] The complementary binding of VGAM2399 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2399 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2399 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2399 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[33550] It is appreciated that VGAM2399 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2399 host target genes. The mRNA of each one of this plurality of VGAM2399 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2399 RNA, herein designated VGAM RNA, and which when bound by VGAM2399 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2399 host target proteins.

[33551] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM2399 gene, herein designated VGAM GENE, on one or more VGAM2399 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33552] It is yet further appreciated that a function of VGAM2399 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2399 include diagnosis, prevention and treatment of viral infection by Goatpox virus. Specific functions, and accordingly utilities, of VGAM2399 correlate with, and may be deduced from, the identity of the host target genes which VGAM2399 binds and inhibits, and the function of these host target genes, as elaborated

hereinbelow.

[33553] Nucleotide sequences of the VGAM2399 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2399 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2399 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2399 are further described hereinbelow with reference to Table 1.

[33554] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2399 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[33555] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2400 (VGAM2400) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[33556] VGAM2400 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene.

The method by which VGAM2400 was detected is described hereinabove with reference to Figs. 2-8.

[33557] VGAM2400 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox virus. VGAM2400 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[33558] VGAM2400 gene, herein designated VGAM GENE, encodes a VGAM2400 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2400 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2400 precursor RNA is designated SEQ ID:2386, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2386 is located at position 89837 relative to the genome of Goatpox virus.

[33559] VGAM2400 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2400 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33560] An enzyme complex designated DICER COMPLEX, dices the VGAM2400 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2400 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2400 RNA is designated SEQ ID:5111, and is provided hereinbelow with reference to the sequence listing part.

[33561] VGAM2400 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2400 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2400 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding

gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33562] VGAM2400 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2400 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2400 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2400 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2400 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be lo-

cated in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33563] The complementary binding of VGAM2400 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2400 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2400 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2400 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[33564] It is appreciated that VGAM2400 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2400 host target genes. The mRNA of each one of this plurality of VGAM2400 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2400 RNA, herein designated VGAM RNA, and which when bound by VGAM2400 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2400 host target proteins.

[33565] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM2400 gene, herein designated VGAM GENE, on one or more VGAM2400 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33566] It is yet further appreciated that a function of VGAM2400 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2400 include diagnosis, prevention and treatment of viral infection by Goatpox virus. Specific functions, and accordingly utilities, of VGAM2400 correlate with, and may be deduced from, the identity of the host target genes which VGAM2400 binds and inhibits,

and the function of these host target genes, as elaborated hereinbelow.

[33567] Nucleotide sequences of the VGAM2400 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2400 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2400 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2400 are further described hereinbelow with reference to Table 1.

[33568] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2400 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[33569] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2401 (VGAM2401) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[33570] VGAM2401 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2401 was detected is described hereinabove with reference to Figs. 2-8.

[33571] VGAM2401 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox virus. VGAM2401 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[33572] VGAM2401 gene, herein designated VGAM GENE, encodes a VGAM2401 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2401 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2401 precursor RNA is designated SEQ ID:2387, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2387 is located at position 109414 relative to the genome of Goatpox virus.

[33573] VGAM2401 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2401 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33574] An enzyme complex designated DICER COMPLEX, dices the VGAM2401 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2401 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 53%) nucleotide sequence of VGAM2401 RNA is designated SEQ ID:5112, and is provided hereinbelow with reference to the sequence listing part.

[33575] VGAM2401 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2401 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2401 host target RNA, herein designated VGAM HOST TARGET RNA, comprises

three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33576] VGAM2401 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2401 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2401 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2401 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2401 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an

example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33577] The complementary binding of VGAM2401 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2401 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2401 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2401 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[33578] It is appreciated that VGAM2401 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2401 host target genes. The mRNA of each one of this plurality of VGAM2401 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2401 RNA, herein designated VGAM RNA, and which when bound by VGAM2401 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2401 host target proteins.

[33579] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2401 gene, herein designated VGAM GENE, on one or more VGAM2401 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33580] It is yet further appreciated that a function of VGAM2401 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2401 include diagnosis, prevention and treatment of viral infection by Goatpox virus. Specific functions, and accordingly utilities, of VGAM2401 correlate with, and may be deduced from, the identity of the

host target genes which VGAM2401 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[33581] Nucleotide sequences of the VGAM2401 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2401 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2401 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2401 are further described hereinbelow with reference to Table 1.

[33582] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2401 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[33583] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2402 (VGAM2402) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[33584] VGAM2402 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2402 was detected is described hereinabove with reference to Figs. 2-8.

[33585] VGAM2402 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox virus. VGAM2402 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[33586] VGAM2402 gene, herein designated VGAM GENE, encodes a VGAM2402 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2402 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2402 precursor RNA is designated SEQ ID:2388, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2388 is located at position 702 relative to the genome of Goatpox virus.

[33587] VGAM2402 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2402 folded precursor RNA, herein designated VGAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33588] An enzyme complex designated DICER COMPLEX, dices the VGAM2402 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2402 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2402 RNA is designated SEQ ID:5113, and is provided hereinbelow with reference to the sequence listing part.

[33589] VGAM2402 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2402 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2402 host target RNA,

herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33590] VGAM2402 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2402 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2402 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2402 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2402 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host tar-

get binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33591] The complementary binding of VGAM2402 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2402 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2402 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2402 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[33592] It is appreciated that VGAM2402 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2402 host target genes. The mRNA of each one of this plurality of VGAM2402 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2402 RNA, herein designated VGAM RNA, and which when bound by VGAM2402 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2402 host target proteins.

[33593] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2402 gene, herein designated VGAM GENE, on one or more VGAM2402 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33594] It is yet further appreciated that a function of VGAM2402 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2402 include diagnosis, prevention and treatment of viral infection by Goatpox virus. Specific functions, and accordingly utilities, of VGAM2402 corre-

late with, and may be deduced from, the identity of the host target genes which VGAM2402 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[33595] Nucleotide sequences of the VGAM2402 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2402 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2402 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2402 are further described hereinbelow with reference to Table 1.

[33596] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2402 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[33597] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2403 (VGAM2403) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the

art.

[33598] VGAM2403 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2403 was detected is described hereinabove with reference to Figs. 2-8.

[33599] VGAM2403 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox virus. VGAM2403 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[33600] VGAM2403 gene, herein designated VGAM GENE, encodes a VGAM2403 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2403 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2403 precursor RNA is designated SEQ ID:2389, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2389 is located at position 52365 relative to the genome of Goatpox virus.

[33601] VGAM2403 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2403 folded

precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33602] An enzyme complex designated DICER COMPLEX, dices the VGAM2403 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2403 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 85%) nucleotide sequence of VGAM2403 RNA is designated SEQ ID:5114, and is provided hereinbelow with reference to the sequence listing part.

[33603] VGAM2403 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2403 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM2403 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33604] VGAM2403 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2403 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2403 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2403 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2403 host target RNA, herein designated VGAM HOST TARGET RNA.

It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33605] The complementary binding of VGAM2403 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2403 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2403 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2403 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[33606] It is appreciated that VGAM2403 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2403 host target genes. The mRNA of each one of this plurality of VGAM2403 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2403 RNA, herein designated VGAM RNA, and which when bound by VGAM2403 RNA, herein designated VGAM RNA, causes inhibition of translation of

respective one or more VGAM2403 host target proteins.

[33607] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2403 gene, herein designated VGAM GENE, on one or more VGAM2403 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33608] It is yet further appreciated that a function of VGAM2403 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2403 include diagnosis, prevention and treatment of viral infection by Goatpox virus. Specific

functions, and accordingly utilities, of VGAM2403 correlate with, and may be deduced from, the identity of the host target genes which VGAM2403 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[33609] Nucleotide sequences of the VGAM2403 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2403 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2403 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2403 are further described hereinbelow with reference to Table 1.

[33610] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2403 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[33611] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2404 (VGAM2404) viral gene, which modulates expression of respective host target genes thereof, the func-

tion and utility of which host target genes is known in the art.

[33612] VGAM2404 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2404 was detected is described hereinabove with reference to Figs. 2-8.

[33613] VGAM2404 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox virus. VGAM2404 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[33614] VGAM2404 gene, herein designated VGAM GENE, encodes a VGAM2404 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2404 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2404 precursor RNA is designated SEQ ID:2390, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2390 is located at position 65726 relative to the genome of Goatpox virus.

[33615] VGAM2404 precursor RNA, herein designated VGAM PRE-

CURSOR RNA, folds onto itself, forming VGAM2404 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33616] An enzyme complex designated DICER COMPLEX, dices the VGAM2404 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2404 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 52%) nucleotide sequence of VGAM2404 RNA is designated SEQ ID:5115, and is provided hereinbelow with reference to the sequence listing part.

[33617] VGAM2404 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM2404 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2404 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33618] VGAM2404 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2404 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2404 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2404 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2404 host

target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33619] The complementary binding of VGAM2404 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2404 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2404 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2404 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[33620] It is appreciated that VGAM2404 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2404 host target genes. The mRNA of each one of this plurality of VGAM2404 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2404 RNA, herein designated VGAM RNA, and which when bound by VGAM2404 RNA, herein

designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2404 host target proteins.

[33621] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2404 gene, herein designated VGAM GENE, on one or more VGAM2404 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33622] It is yet further appreciated that a function of VGAM2404 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2404 include diagnosis, prevention and

treatment of viral infection by Goatpox virus. Specific functions, and accordingly utilities, of VGAM2404 correlate with, and may be deduced from, the identity of the host target genes which VGAM2404 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[33623] Nucleotide sequences of the VGAM2404 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2404 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2404 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2404 are further described hereinbelow with reference to Table 1.

[33624] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2404 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[33625] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2405 (VGAM2405) viral gene, which modulates ex-

pression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[33626] VGAM2405 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2405 was detected is described hereinabove with reference to Figs. 2-8.

[33627] VGAM2405 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox virus. VGAM2405 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[33628] VGAM2405 gene, herein designated VGAM GENE, encodes a VGAM2405 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2405 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2405 precursor RNA is designated SEQ ID:2391, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2391 is located at position 127713 relative to the genome of Goatpox virus.

[33629] VGAM2405 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2405 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33630] An enzyme complex designated DICER COMPLEX, dices the VGAM2405 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2405 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2405 RNA is designated SEQ ID:5116, and is provided hereinbelow with reference to the sequence listing part.

[33631] VGAM2405 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2405 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2405 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33632] VGAM2405 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2405 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2405 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2405 RNA, herein designated VGAM RNA, may have a different number of host target

binding sites in untranslated regions of a VGAM2405 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33633] The complementary binding of VGAM2405 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2405 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2405 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2405 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[33634] It is appreciated that VGAM2405 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2405 host target genes. The mRNA of each one of this plurality of VGAM2405 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2405 RNA, herein designated VGAM

RNA, and which when bound by VGAM2405 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2405 host target proteins.

[33635] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2405 gene, herein designated VGAM GENE, on one or more VGAM2405 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33636] It is yet further appreciated that a function of VGAM2405 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM2405 include diagnosis, prevention and treatment of viral infection by Goatpox virus. Specific functions, and accordingly utilities, of VGAM2405 correlate with, and may be deduced from, the identity of the host target genes which VGAM2405 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[33637] Nucleotide sequences of the VGAM2405 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2405 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2405 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2405 are further described hereinbelow with reference to Table 1.

[33638] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2405 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[33639] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Mes-

senger 2406 (VGAM2406) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[33640] VGAM2406 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2406 was detected is described hereinabove with reference to Figs. 2-8.

[33641] VGAM2406 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox virus. VGAM2406 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[33642] VGAM2406 gene, herein designated VGAM GENE, encodes a VGAM2406 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2406 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2406 precursor RNA is designated SEQ ID:2392, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2392 is located at position

118549 relative to the genome of Goatpox virus.

[33643] VGAM2406 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2406 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33644] An enzyme complex designated DICER COMPLEX, dices the VGAM2406 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2406 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 66%) nucleotide sequence of VGAM2406 RNA is designated SEQ ID:5117, and is provided hereinbelow with reference to the sequence listing part.

[33645] VGAM2406 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2406 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2406 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33646] VGAM2406 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2406 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2406 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2406 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2406 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33647] The complementary binding of VGAM2406 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM2406 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2406 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2406 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[33648] It is appreciated that VGAM2406 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2406 host target genes. The mRNA of each one of this plurality of VGAM2406 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2406 RNA, herein designated VGAM RNA, and which when bound by VGAM2406 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2406 host target proteins.

[33649] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2406 gene, herein designated VGAM GENE, on one or more VGAM2406 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33650] It is yet further appreciated that a function of VGAM2406 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2406 include diagnosis, prevention and treatment of viral infection by Goatpox virus. Specific functions, and accordingly utilities, of VGAM2406 correlate with, and may be deduced from, the identity of the host target genes which VGAM2406 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[33651] Nucleotide sequences of the VGAM2406 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the diced VGAM2406 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2406 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2406 are further described hereinbelow with reference to Table 1.

[33652] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2406 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[33653] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2407 (VGAM2407) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[33654] VGAM2407 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2407 was detected is described hereinabove with reference to Figs. 2-8.

[33655] VGAM2407 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox virus. VGAM2407 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[33656] VGAM2407 gene, herein designated VGAM GENE, encodes a VGAM2407 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2407 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2407 precursor RNA is designated SEQ ID:2393, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2393 is located at position 111620 relative to the genome of Goatpox virus.

[33657] VGAM2407 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2407 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33658] An enzyme complex designated DICER COMPLEX, dices the VGAM2407 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2407 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2407 RNA is designated SEQ ID:5118, and is provided hereinbelow with reference to the sequence listing part.

[33659] VGAM2407 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2407 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2407 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN COD-

ING and 3UTR respectively.

[33660] VGAM2407 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2407 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2407 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2407 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2407 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33661] The complementary binding of VGAM2407 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2407 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2407 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2407 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[33662] It is appreciated that VGAM2407 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2407 host target genes. The mRNA of each one of this plurality of VGAM2407 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2407 RNA, herein designated VGAM RNA, and which when bound by VGAM2407 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2407 host target proteins.

[33663] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2407 gene, herein designated VGAM GENE, on one

or more VGAM2407 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33664] It is yet further appreciated that a function of VGAM2407 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2407 include diagnosis, prevention and treatment of viral infection by Goatpox virus. Specific functions, and accordingly utilities, of VGAM2407 correlate with, and may be deduced from, the identity of the host target genes which VGAM2407 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[33665] Nucleotide sequences of the VGAM2407 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2407 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2407 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2407 are further described hereinbelow with reference to Table 1.

[33666] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2407 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[33667] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2408 (VGAM2408) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[33668] VGAM2408 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2408 was detected is de-

scribed hereinabove with reference to Figs. 2-8.

[33669] VGAM2408 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox virus. VGAM2408 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[33670] VGAM2408 gene, herein designated VGAM GENE, encodes a VGAM2408 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2408 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2408 precursor RNA is designated SEQ ID:2394, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2394 is located at position 36819 relative to the genome of Goatpox virus.

[33671] VGAM2408 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2408 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33672] An enzyme complex designated DICER COMPLEX, dices the VGAM2408 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2408 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 47%) nucleotide sequence of VGAM2408 RNA is designated SEQ ID:5119, and is provided hereinbelow with reference to the sequence listing part.

[33673] VGAM2408 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2408 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2408 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and

a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33674] VGAM2408 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2408 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2408 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2408 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2408 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both

3UTR and 5UTR regions.

[33675] The complementary binding of VGAM2408 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2408 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2408 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2408 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[33676] It is appreciated that VGAM2408 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2408 host target genes. The mRNA of each one of this plurality of VGAM2408 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2408 RNA, herein designated VGAM RNA, and which when bound by VGAM2408 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2408 host target proteins.

[33677] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM2408 gene, herein designated VGAM GENE, on one or more VGAM2408 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33678] It is yet further appreciated that a function of VGAM2408 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2408 include diagnosis, prevention and treatment of viral infection by Goatpox virus. Specific functions, and accordingly utilities, of VGAM2408 correlate with, and may be deduced from, the identity of the host target genes which VGAM2408 binds and inhibits, and the function of these host target genes, as elaborated

hereinbelow.

[33679] Nucleotide sequences of the VGAM2408 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2408 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2408 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2408 are further described hereinbelow with reference to Table 1.

[33680] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2408 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[33681] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2409 (VGAM2409) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[33682] VGAM2409 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene.

The method by which VGAM2409 was detected is described hereinabove with reference to Figs. 2-8.

[33683] VGAM2409 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox virus. VGAM2409 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[33684] VGAM2409 gene, herein designated VGAM GENE, encodes a VGAM2409 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2409 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2409 precursor RNA is designated SEQ ID:2395, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2395 is located at position 109177 relative to the genome of Goatpox virus.

[33685] VGAM2409 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2409 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33686] An enzyme complex designated DICER COMPLEX, dices the VGAM2409 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2409 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 55%) nucleotide sequence of VGAM2409 RNA is designated SEQ ID:5120, and is provided hereinbelow with reference to the sequence listing part.

[33687] VGAM2409 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2409 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2409 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding

gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33688] VGAM2409 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2409 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2409 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2409 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2409 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be lo-

cated in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33689] The complementary binding of VGAM2409 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2409 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2409 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2409 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[33690] It is appreciated that VGAM2409 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2409 host target genes. The mRNA of each one of this plurality of VGAM2409 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2409 RNA, herein designated VGAM RNA, and which when bound by VGAM2409 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2409 host target proteins.

[33691] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM2409 gene, herein designated VGAM GENE, on one or more VGAM2409 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33692] It is yet further appreciated that a function of VGAM2409 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2409 include diagnosis, prevention and treatment of viral infection by Goatpox virus. Specific functions, and accordingly utilities, of VGAM2409 correlate with, and may be deduced from, the identity of the host target genes which VGAM2409 binds and inhibits,

and the function of these host target genes, as elaborated hereinbelow.

[33693] Nucleotide sequences of the VGAM2409 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2409 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2409 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2409 are further described hereinbelow with reference to Table 1.

[33694] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2409 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[33695] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2410 (VGAM2410) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[33696] VGAM2410 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2410 was detected is described hereinabove with reference to Figs. 2-8.

[33697] VGAM2410 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox virus. VGAM2410 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[33698] VGAM2410 gene, herein designated VGAM GENE, encodes a VGAM2410 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2410 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2410 precursor RNA is designated SEQ ID:2396, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2396 is located at position 118894 relative to the genome of Goatpox virus.

[33699] VGAM2410 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2410 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33700] An enzyme complex designated DICER COMPLEX, dices the VGAM2410 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2410 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2410 RNA is designated SEQ ID:5121, and is provided hereinbelow with reference to the sequence listing part.

[33701] VGAM2410 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2410 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2410 host target RNA, herein designated VGAM HOST TARGET RNA, comprises

three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33702] VGAM2410 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2410 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2410 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2410 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2410 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an

example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33703] The complementary binding of VGAM2410 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2410 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2410 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2410 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[33704] It is appreciated that VGAM2410 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2410 host target genes. The mRNA of each one of this plurality of VGAM2410 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2410 RNA, herein designated VGAM RNA, and which when bound by VGAM2410 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2410 host target proteins.

[33705] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2410 gene, herein designated VGAM GENE, on one or more VGAM2410 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33706] It is yet further appreciated that a function of VGAM2410 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2410 include diagnosis, prevention and treatment of viral infection by Goatpox virus. Specific functions, and accordingly utilities, of VGAM2410 correlate with, and may be deduced from, the identity of the

host target genes which VGAM2410 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[33707] Nucleotide sequences of the VGAM2410 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2410 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2410 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2410 are further described hereinbelow with reference to Table 1.

[33708] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2410 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[33709] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2411 (VGAM2411) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[33710] VGAM2411 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2411 was detected is described hereinabove with reference to Figs. 2-8.

[33711] VGAM2411 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox virus. VGAM2411 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[33712] VGAM2411 gene, herein designated VGAM GENE, encodes a VGAM2411 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2411 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2411 precursor RNA is designated SEQ ID:2397, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2397 is located at position 74764 relative to the genome of Goatpox virus.

[33713] VGAM2411 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2411 folded precursor RNA, herein designated VGAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33714] An enzyme complex designated DICER COMPLEX, dices the VGAM2411 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2411 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 48%) nucleotide sequence of VGAM2411 RNA is designated SEQ ID:5122, and is provided hereinbelow with reference to the sequence listing part.

[33715] VGAM2411 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2411 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2411 host target RNA,

herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33716] VGAM2411 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2411 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2411 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2411 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2411 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host tar-

get binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33717] The complementary binding of VGAM2411 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2411 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2411 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2411 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[33718] It is appreciated that VGAM2411 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2411 host target genes. The mRNA of each one of this plurality of VGAM2411 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2411 RNA, herein designated VGAM RNA, and which when bound by VGAM2411 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2411 host target proteins.

[33719] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2411 gene, herein designated VGAM GENE, on one or more VGAM2411 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33720] It is yet further appreciated that a function of VGAM2411 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2411 include diagnosis, prevention and treatment of viral infection by Goatpox virus. Specific functions, and accordingly utilities, of VGAM2411 corre-

late with, and may be deduced from, the identity of the host target genes which VGAM2411 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[33721] Nucleotide sequences of the VGAM2411 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2411 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2411 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2411 are further described hereinbelow with reference to Table 1.

[33722] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2411 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[33723] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2412 (VGAM2412) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the

art.

[33724] VGAM2412 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2412 was detected is described hereinabove with reference to Figs. 2-8.

[33725] VGAM2412 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox virus. VGAM2412 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[33726] VGAM2412 gene, herein designated VGAM GENE, encodes a VGAM2412 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2412 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2412 precursor RNA is designated SEQ ID:2398, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2398 is located at position 52802 relative to the genome of Goatpox virus.

[33727] VGAM2412 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2412 folded

precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33728] An enzyme complex designated DICER COMPLEX, dices the VGAM2412 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2412 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 67%) nucleotide sequence of VGAM2412 RNA is designated SEQ ID:5123, and is provided hereinbelow with reference to the sequence listing part.

[33729] VGAM2412 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2412 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM2412 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33730] VGAM2412 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2412 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2412 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2412 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2412 host target RNA, herein designated VGAM HOST TARGET RNA.

It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33731] The complementary binding of VGAM2412 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2412 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2412 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2412 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[33732] It is appreciated that VGAM2412 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2412 host target genes. The mRNA of each one of this plurality of VGAM2412 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2412 RNA, herein designated VGAM RNA, and which when bound by VGAM2412 RNA, herein designated VGAM RNA, causes inhibition of translation of

respective one or more VGAM2412 host target proteins.

[33733] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2412 gene, herein designated VGAM GENE, on one or more VGAM2412 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33734] It is yet further appreciated that a function of VGAM2412 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2412 include diagnosis, prevention and treatment of viral infection by Goatpox virus. Specific

functions, and accordingly utilities, of VGAM2412 correlate with, and may be deduced from, the identity of the host target genes which VGAM2412 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[33735] Nucleotide sequences of the VGAM2412 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2412 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2412 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2412 are further described hereinbelow with reference to Table 1.

[33736] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2412 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[33737] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2413 (VGAM2413) viral gene, which modulates expression of respective host target genes thereof, the func-

tion and utility of which host target genes is known in the art.

[33738] VGAM2413 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2413 was detected is described hereinabove with reference to Figs. 2-8.

[33739] VGAM2413 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox virus. VGAM2413 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[33740] VGAM2413 gene, herein designated VGAM GENE, encodes a VGAM2413 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2413 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2413 precursor RNA is designated SEQ ID:2399, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2399 is located at position 77043 relative to the genome of Goatpox virus.

[33741] VGAM2413 precursor RNA, herein designated VGAM PRE-

CURSOR RNA, folds onto itself, forming VGAM2413 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33742] An enzyme complex designated DICER COMPLEX, dices the VGAM2413 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2413 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2413 RNA is designated SEQ ID:5124, and is provided hereinbelow with reference to the sequence listing part.

[33743] VGAM2413 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM2413 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2413 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33744] VGAM2413 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2413 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2413 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2413 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2413 host

target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33745] The complementary binding of VGAM2413 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2413 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2413 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2413 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[33746] It is appreciated that VGAM2413 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2413 host target genes. The mRNA of each one of this plurality of VGAM2413 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2413 RNA, herein designated VGAM RNA, and which when bound by VGAM2413 RNA, herein

designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2413 host target proteins.

[33747] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2413 gene, herein designated VGAM GENE, on one or more VGAM2413 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33748] It is yet further appreciated that a function of VGAM2413 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2413 include diagnosis, prevention and

treatment of viral infection by Goatpox virus. Specific functions, and accordingly utilities, of VGAM2413 correlate with, and may be deduced from, the identity of the host target genes which VGAM2413 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[33749] Nucleotide sequences of the VGAM2413 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2413 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2413 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2413 are further described hereinbelow with reference to Table 1.

[33750] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2413 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[33751] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2414 (VGAM2414) viral gene, which modulates ex-

pression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[33752] VGAM2414 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2414 was detected is described hereinabove with reference to Figs. 2-8.

[33753] VGAM2414 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox virus. VGAM2414 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[33754] VGAM2414 gene, herein designated VGAM GENE, encodes a VGAM2414 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2414 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2414 precursor RNA is designated SEQ ID:2400, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2400 is located at position 57820 relative to the genome of Goatpox virus.

[33755] VGAM2414 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2414 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33756] An enzyme complex designated DICER COMPLEX, dices the VGAM2414 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2414 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2414 RNA is designated SEQ ID:5125, and is provided hereinbelow with reference to the sequence listing part.

[33757] VGAM2414 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2414 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2414 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33758] VGAM2414 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2414 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2414 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2414 RNA, herein designated VGAM RNA, may have a different number of host target

binding sites in untranslated regions of a VGAM2414 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33759] The complementary binding of VGAM2414 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2414 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2414 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2414 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[33760] It is appreciated that VGAM2414 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2414 host target genes. The mRNA of each one of this plurality of VGAM2414 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2414 RNA, herein designated VGAM

RNA, and which when bound by VGAM2414 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2414 host target proteins.

[33761] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2414 gene, herein designated VGAM GENE, on one or more VGAM2414 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33762] It is yet further appreciated that a function of VGAM2414 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM2414 include diagnosis, prevention and treatment of viral infection by Goatpox virus. Specific functions, and accordingly utilities, of VGAM2414 correlate with, and may be deduced from, the identity of the host target genes which VGAM2414 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[33763] Nucleotide sequences of the VGAM2414 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2414 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2414 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2414 are further described hereinbelow with reference to Table 1.

[33764] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2414 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[33765]

[33766] Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present inven-

tion, referred to here as Viral Genomic Address Messenger 2415 (VGAM2415) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[33767] VGAM2415 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2415 was detected is described hereinabove with reference to Figs. 2-8.

[33768] VGAM2415 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox virus. VGAM2415 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[33769] VGAM2415 gene, herein designated VGAM GENE, encodes a VGAM2415 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2415 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2415 precursor RNA is designated SEQ ID:2401, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2401 is located at position

96068 relative to the genome of Goatpox virus.

[33770] VGAM2415 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2415 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33771] An enzyme complex designated DICER COMPLEX, dices the VGAM2415 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2415 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2415 RNA is designated SEQ ID:5126, and is provided hereinbelow with reference to the sequence listing part.

[33772] VGAM2415 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2415 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2415 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33773] VGAM2415 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2415 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2415 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2415 RNA, herein designated

VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2415 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33774] The complementary binding of VGAM2415 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2415 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2415 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2415 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[33775] It is appreciated that VGAM2415 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2415 host target genes. The mRNA of each one of this plurality of VGAM2415 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM2415 RNA, herein designated VGAM RNA, and which when bound by VGAM2415 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2415 host target proteins.

[33776] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2415 gene, herein designated VGAM GENE, on one or more VGAM2415 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33777] It is yet further appreciated that a function of VGAM2415 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2415 include diagnosis, prevention and treatment of viral infection by Goatpox virus. Specific functions, and accordingly utilities, of VGAM2415 correlate with, and may be deduced from, the identity of the host target genes which VGAM2415 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[33778] Nucleotide sequences of the VGAM2415 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2415 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2415 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2415 are further described hereinbelow with reference to Table 1.

[33779] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2415 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[33780] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present

invention, referred to here as Viral Genomic Address Messenger 2416 (VGAM2416) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[33781] VGAM2416 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2416 was detected is described hereinabove with reference to Figs. 2-8.

[33782] VGAM2416 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox virus. VGAM2416 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[33783] VGAM2416 gene, herein designated VGAM GENE, encodes a VGAM2416 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2416 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2416 precursor RNA is designated SEQ ID:2402, and is provided hereinbelow with reference to the sequence listing part. Nu-

cleotide sequence SEQ ID:2402 is located at position 126030 relative to the genome of Goatpox virus.

[33784] VGAM2416 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2416 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33785] An enzyme complex designated DICER COMPLEX, dices the VGAM2416 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2416 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2416 RNA is designated SEQ ID:5127, and is provided hereinbelow with reference to the sequence

listing part.

[33786] VGAM2416 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2416 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2416 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33787] VGAM2416 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2416 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2416 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not

meant to be limiting VGAM2416 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2416 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33788] The complementary binding of VGAM2416 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2416 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2416 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2416 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[33789] It is appreciated that VGAM2416 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2416 host target genes. The mRNA of each one of this plurality of VGAM2416 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2416 RNA, herein designated VGAM RNA, and which when bound by VGAM2416 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2416 host target proteins.

[33790] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2416 gene, herein designated VGAM GENE, on one or more VGAM2416 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33791] It is yet further appreciated that a function of VGAM2416

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2416 include diagnosis, prevention and treatment of viral infection by Goatpox virus. Specific functions, and accordingly utilities, of VGAM2416 correlate with, and may be deduced from, the identity of the host target genes which VGAM2416 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[33792] Nucleotide sequences of the VGAM2416 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2416 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2416 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2416 are further described hereinbelow with reference to Table 1.

[33793] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2416 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[33794] Fig. 1 further provides a conceptual description of another

novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2417 (VGAM2417) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[33795] VGAM2417 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2417 was detected is described hereinabove with reference to Figs. 2-8.

[33796] VGAM2417 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox virus. VGAM2417 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[33797] VGAM2417 gene, herein designated VGAM GENE, encodes a VGAM2417 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2417 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2417 precursor RNA is designated SEQ ID:2403, and is provided here-

inbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2403 is located at position 96899 relative to the genome of Goatpox virus.

[33798] VGAM2417 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2417 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33799] An enzyme complex designated DICER COMPLEX, dices the VGAM2417 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2417 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2417 RNA is designated SEQ ID:5128, and

is provided hereinbelow with reference to the sequence listing part.

[33800] VGAM2417 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2417 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2417 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33801] VGAM2417 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2417 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2417 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites

shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2417 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2417 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33802] The complementary binding of VGAM2417 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2417 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2417 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2417 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[33803] It is appreciated that VGAM2417 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2417 host target genes. The mRNA of each one of this plurality of VGAM2417 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2417 RNA, herein designated VGAM RNA, and which when bound by VGAM2417 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2417 host target proteins.

[33804] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2417 gene, herein designated VGAM GENE, on one or more VGAM2417 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33805] It is yet further appreciated that a function of VGAM2417 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2417 include diagnosis, prevention and treatment of viral infection by Goatpox virus. Specific functions, and accordingly utilities, of VGAM2417 correlate with, and may be deduced from, the identity of the host target genes which VGAM2417 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[33806] Nucleotide sequences of the VGAM2417 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2417 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2417 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2417 are further described hereinbelow with reference to Table 1.

[33807] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2417 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[33808] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2418 (VGAM2418) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[33809] VGAM2418 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2418 was detected is described hereinabove with reference to Figs. 2-8.

[33810] VGAM2418 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox virus. VGAM2418 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[33811] VGAM2418 gene, herein designated VGAM GENE, encodes a VGAM2418 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2418 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2418 precur-

sor RNA is designated SEQ ID:2404, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2404 is located at position 117185 relative to the genome of Goatpox virus.

[33812] VGAM2418 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2418 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33813] An enzyme complex designated DICER COMPLEX, dices the VGAM2418 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2418 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide se-

quence of VGAM2418 RNA is designated SEQ ID:5129, and is provided hereinbelow with reference to the sequence listing part.

[33814] VGAM2418 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2418 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2418 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33815] VGAM2418 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2418 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2418 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is ap-

preciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2418 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2418 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33816] The complementary binding of VGAM2418 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2418 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2418 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2418 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[33817] It is appreciated that VGAM2418 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2418 host target genes. The mRNA of

each one of this plurality of VGAM2418 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2418 RNA, herein designated VGAM RNA, and which when bound by VGAM2418 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2418 host target proteins.

[33818] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2418 gene, herein designated VGAM GENE, on one or more VGAM2418 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science

294,779 (2001)).

[33819] It is yet further appreciated that a function of VGAM2418 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2418 include diagnosis, prevention and treatment of viral infection by Goatpox virus. Specific functions, and accordingly utilities, of VGAM2418 correlate with, and may be deduced from, the identity of the host target genes which VGAM2418 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[33820] Nucleotide sequences of the VGAM2418 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2418 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2418 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2418 are further described hereinbelow with reference to Table 1.

[33821] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2418 RNA, herein designated VGAM RNA, are de-

scribed hereinbelow with reference to Table 2.

[33822] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2419 (VGAM2419) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[33823] VGAM2419 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2419 was detected is described hereinabove with reference to Figs. 2-8.

[33824] VGAM2419 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox virus.
VGAM2419 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[33825] VGAM2419 gene, herein designated VGAM GENE, encodes a VGAM2419 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2419 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly

similar to the nucleotide sequence of VGAM2419 precursor RNA is designated SEQ ID:2405, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2405 is located at position 104440 relative to the genome of Goatpox virus.

[33826] VGAM2419 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2419 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33827] An enzyme complex designated DICER COMPLEX, dices the VGAM2419 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2419 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2419 RNA is designated SEQ ID:5130, and is provided hereinbelow with reference to the sequence listing part.

[33828] VGAM2419 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2419 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2419 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33829] VGAM2419 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2419 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2419 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I,

BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2419 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2419 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33830] The complementary binding of VGAM2419 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2419 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2419 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2419 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[33831] It is appreciated that VGAM2419 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM2419 host target genes. The mRNA of each one of this plurality of VGAM2419 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2419 RNA, herein designated VGAM RNA, and which when bound by VGAM2419 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2419 host target proteins.

[33832] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2419 gene, herein designated VGAM GENE, on one or more VGAM2419 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33833] It is yet further appreciated that a function of VGAM2419 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2419 include diagnosis, prevention and treatment of viral infection by Goatpox virus. Specific functions, and accordingly utilities, of VGAM2419 correlate with, and may be deduced from, the identity of the host target genes which VGAM2419 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[33834] Nucleotide sequences of the VGAM2419 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2419 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2419 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2419 are further described hereinbelow with reference to Table 1.

[33835] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites

to VGAM2419 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[33836] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2420 (VGAM2420) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[33837] VGAM2420 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2420 was detected is described hereinabove with reference to Figs. 2-8.

[33838] VGAM2420 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox virus. VGAM2420 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[33839] VGAM2420 gene, herein designated VGAM GENE, encodes a VGAM2420 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2420 precursor RNA, herein designated VGAM PRECURSOR RNA, does not en-

code a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2420 precursor RNA is designated SEQ ID:2406, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2406 is located at position 138753 relative to the genome of Goatpox virus.

[33840] VGAM2420 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2420 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33841] An enzyme complex designated DICER COMPLEX, dices the VGAM2420 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2420 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2420 RNA is designated SEQ ID:5131, and is provided hereinbelow with reference to the sequence listing part.

[33842] VGAM2420 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2420 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2420 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33843] VGAM2420 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2420 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2420 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3

such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2420 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2420 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33844] The complementary binding of VGAM2420 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2420 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2420 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2420 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[33845] It is appreciated that VGAM2420 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2420 host target genes. The mRNA of each one of this plurality of VGAM2420 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2420 RNA, herein designated VGAM RNA, and which when bound by VGAM2420 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2420 host target proteins.

[33846] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2420 gene, herein designated VGAM GENE, on one or more VGAM2420 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33847] It is yet further appreciated that a function of VGAM2420 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2420 include diagnosis, prevention and treatment of viral infection by Goatpox virus. Specific functions, and accordingly utilities, of VGAM2420 correlate with, and may be deduced from, the identity of the host target genes which VGAM2420 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[33848] Nucleotide sequences of the VGAM2420 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2420 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2420 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2420 are further described hereinbelow with reference to Table 1.

[33849] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the

complementarity of each of these host target binding sites to VGAM2420 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[33850] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2421 (VGAM2421) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[33851] VGAM2421 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2421 was detected is described hereinabove with reference to Figs. 2-8.

[33852] VGAM2421 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox virus.
VGAM2421 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[33853] VGAM2421 gene, herein designated VGAM GENE, encodes a VGAM2421 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2421 precursor RNA,

herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2421 precursor RNA is designated SEQ ID:2407, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2407 is located at position 87501 relative to the genome of Goatpox virus.

[33854] VGAM2421 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2421 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33855] An enzyme complex designated DICER COMPLEX, dices the VGAM2421 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2421 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2421 RNA is designated SEQ ID:5132, and is provided hereinbelow with reference to the sequence listing part.

[33856] VGAM2421 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2421 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2421 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33857] VGAM2421 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2421 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2421 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host

target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2421 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2421 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33858] The complementary binding of VGAM2421 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2421 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2421 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2421 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[33859] It is appreciated that VGAM2421 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2421 host target genes. The mRNA of each one of this plurality of VGAM2421 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2421 RNA, herein designated VGAM RNA, and which when bound by VGAM2421 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2421 host target proteins.

[33860] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2421 gene, herein designated VGAM GENE, on one or more VGAM2421 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33861] It is yet further appreciated that a function of VGAM2421 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2421 include diagnosis, prevention and treatment of viral infection by Goatpox virus. Specific functions, and accordingly utilities, of VGAM2421 correlate with, and may be deduced from, the identity of the host target genes which VGAM2421 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[33862] Nucleotide sequences of the VGAM2421 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2421 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2421 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2421 are further described hereinbelow with reference to Table 1.

[33863] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2421 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[33864] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2422 (VGAM2422) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[33865] VGAM2422 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2422 was detected is described hereinabove with reference to Figs. 2-8.

[33866] VGAM2422 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox virus. VGAM2422 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[33867] VGAM2422 gene, herein designated VGAM GENE, encodes a VGAM2422 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and un-

like most ordinary genes, VGAM2422 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2422 precursor RNA is designated SEQ ID:2408, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2408 is located at position 83441 relative to the genome of Goatpox virus.

[33868] VGAM2422 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2422 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33869] An enzyme complex designated DICER COMPLEX, dices the VGAM2422 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2422 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2422 RNA is designated SEQ ID:5133, and is provided hereinbelow with reference to the sequence listing part.

[33870] VGAM2422 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2422 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2422 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33871] VGAM2422 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2422 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2422 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed

sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2422 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2422 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33872] The complementary binding of VGAM2422 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2422 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2422 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2422 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target

protein is therefore outlined by a broken line.

[33873] It is appreciated that VGAM2422 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2422 host target genes. The mRNA of each one of this plurality of VGAM2422 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2422 RNA, herein designated VGAM RNA, and which when bound by VGAM2422 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2422 host target proteins.

[33874] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2422 gene, herein designated VGAM GENE, on one or more VGAM2422 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33875] It is yet further appreciated that a function of VGAM2422 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2422 include diagnosis, prevention and treatment of viral infection by Goatpox virus. Specific functions, and accordingly utilities, of VGAM2422 correlate with, and may be deduced from, the identity of the host target genes which VGAM2422 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[33876] Nucleotide sequences of the VGAM2422 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2422 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2422 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2422 are further described hereinbelow with reference to Table 1.

[33877] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2422 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[33878] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2423 (VGAM2423) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[33879] VGAM2423 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2423 was detected is described hereinabove with reference to Figs. 2-8.

[33880] VGAM2423 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox virus.
VGAM2423 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[33881] VGAM2423 gene, herein designated VGAM GENE, encodes a VGAM2423 precursor RNA, herein designated VGAM

PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2423 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2423 precursor RNA is designated SEQ ID:2409, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2409 is located at position 74429 relative to the genome of Goatpox virus.

[33882] VGAM2423 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2423 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33883] An enzyme complex designated DICER COMPLEX, dices the VGAM2423 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2423 RNA, herein designated VGAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2423 RNA is designated SEQ ID:5134, and is provided hereinbelow with reference to the sequence listing part.

[33884] VGAM2423 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2423 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2423 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33885] VGAM2423 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2423 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2423 RNA, herein designated

VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2423 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2423 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33886] The complementary binding of VGAM2423 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2423 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2423 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2423 host target protein, herein desig-

nated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[33887] It is appreciated that VGAM2423 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2423 host target genes. The mRNA of each one of this plurality of VGAM2423 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2423 RNA, herein designated VGAM RNA, and which when bound by VGAM2423 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2423 host target proteins.

[33888] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2423 gene, herein designated VGAM GENE, on one or more VGAM2423 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33889] It is yet further appreciated that a function of VGAM2423 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2423 include diagnosis, prevention and treatment of viral infection by Goatpox virus. Specific functions, and accordingly utilities, of VGAM2423 correlate with, and may be deduced from, the identity of the host target genes which VGAM2423 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[33890] Nucleotide sequences of the VGAM2423 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2423 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2423 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2423 are further described hereinbelow with reference to Table 1.

[33891] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2423 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[33892] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2424 (VGAM2424) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[33893] VGAM2424 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2424 was detected is described hereinabove with reference to Figs. 2-8.

[33894] VGAM2424 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox virus.
VGAM2424 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[33895] VGAM2424 gene, herein designated VGAM GENE, encodes

a VGAM2424 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2424 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2424 precursor RNA is designated SEQ ID:2410, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2410 is located at position 134679 relative to the genome of Goatpox virus.

[33896] VGAM2424 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2424 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33897] An enzyme complex designated DICER COMPLEX, dices the VGAM2424 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2424 RNA,

herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 66%) nucleotide sequence of VGAM2424 RNA is designated SEQ ID:5135, and is provided hereinbelow with reference to the sequence listing part.

[33898] VGAM2424 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2424 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2424 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33899] VGAM2424 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2424 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM2424 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2424 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2424 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33900] The complementary binding of VGAM2424 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2424 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2424 host target RNA, herein designated VGAM HOST TARGET

RNA, into VGAM2424 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[33901] It is appreciated that VGAM2424 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2424 host target genes. The mRNA of each one of this plurality of VGAM2424 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2424 RNA, herein designated VGAM RNA, and which when bound by VGAM2424 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2424 host target proteins.

[33902] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2424 gene, herein designated VGAM GENE, on one or more VGAM2424 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33903] It is yet further appreciated that a function of VGAM2424 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2424 include diagnosis, prevention and treatment of viral infection by Goatpox virus. Specific functions, and accordingly utilities, of VGAM2424 correlate with, and may be deduced from, the identity of the host target genes which VGAM2424 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[33904] Nucleotide sequences of the VGAM2424 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2424 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2424 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2424 are further

described hereinbelow with reference to Table 1.

[33905] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2424 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[33906] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2425 (VGAM2425) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[33907] VGAM2425 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2425 was detected is described hereinabove with reference to Figs. 2-8.

[33908] VGAM2425 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox virus.
VGAM2425 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[33909] VGAM2425 gene, herein designated VGAM GENE, encodes a VGAM2425 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2425 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2425 precursor RNA is designated SEQ ID:2411, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2411 is located at position 148298 relative to the genome of Goatpox virus.

[33910] VGAM2425 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2425 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33911] An enzyme complex designated DICER COMPLEX, dices the VGAM2425 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, into VGAM2425 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2425 RNA is designated SEQ ID:5136, and is provided hereinbelow with reference to the sequence listing part.

[33912] VGAM2425 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2425 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2425 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33913] VGAM2425 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2425 host target RNA, herein designated VGAM HOST TARGET RNA. This

complementary binding is due to the fact that the nucleotide sequence of VGAM2425 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2425 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2425 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33914] The complementary binding of VGAM2425 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2425 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2425

host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2425 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[33915] It is appreciated that VGAM2425 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2425 host target genes. The mRNA of each one of this plurality of VGAM2425 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2425 RNA, herein designated VGAM RNA, and which when bound by VGAM2425 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2425 host target proteins.

[33916] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2425 gene, herein designated VGAM GENE, on one or more VGAM2425 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33917] It is yet further appreciated that a function of VGAM2425 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2425 include diagnosis, prevention and treatment of viral infection by Goatpox virus. Specific functions, and accordingly utilities, of VGAM2425 correlate with, and may be deduced from, the identity of the host target genes which VGAM2425 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[33918] Nucleotide sequences of the VGAM2425 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2425 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2425 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM2425 are further described hereinbelow with reference to Table 1.

[33919] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2425 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[33920] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2426 (VGAM2426) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[33921] VGAM2426 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2426 was detected is described hereinabove with reference to Figs. 2-8.

[33922] VGAM2426 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox virus. VGAM2426 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the

human genome.

[33923] VGAM2426 gene, herein designated VGAM GENE, encodes a VGAM2426 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2426 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2426 precursor RNA is designated SEQ ID:2412, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2412 is located at position 51036 relative to the genome of Goatpox virus.

[33924] VGAM2426 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2426 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33925] An enzyme complex designated DICER COMPLEX, dices

the VGAM2426 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2426 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 49%) nucleotide sequence of VGAM2426 RNA is designated SEQ ID:5137, and is provided hereinbelow with reference to the sequence listing part.

[33926] VGAM2426 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2426 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2426 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33927] VGAM2426 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2426 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2426 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2426 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2426 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33928] The complementary binding of VGAM2426 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2426 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM2426 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2426 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[33929] It is appreciated that VGAM2426 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2426 host target genes. The mRNA of each one of this plurality of VGAM2426 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2426 RNA, herein designated VGAM RNA, and which when bound by VGAM2426 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2426 host target proteins.

[33930] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2426 gene, herein designated VGAM GENE, on one or more VGAM2426 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33931] It is yet further appreciated that a function of VGAM2426 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2426 include diagnosis, prevention and treatment of viral infection by Goatpox virus. Specific functions, and accordingly utilities, of VGAM2426 correlate with, and may be deduced from, the identity of the host target genes which VGAM2426 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[33932] Nucleotide sequences of the VGAM2426 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2426 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of

VGAM2426 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2426 are further described hereinbelow with reference to Table 1.

[33933] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2426 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[33934] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2427 (VGAM2427) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[33935] VGAM2427 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2427 was detected is described hereinabove with reference to Figs. 2-8.

[33936] VGAM2427 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox virus.
VGAM2427 host target gene, herein designated VGAM

HOST TARGET GENE, is a human gene contained in the human genome.

[33937] VGAM2427 gene, herein designated VGAM GENE, encodes a VGAM2427 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2427 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2427 precursor RNA is designated SEQ ID:2413, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2413 is located at position 48019 relative to the genome of Goatpox virus.

[33938] VGAM2427 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2427 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33939] An enzyme complex designated DICER COMPLEX, dices the VGAM2427 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2427 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2427 RNA is designated SEQ ID:5138, and is provided hereinbelow with reference to the sequence listing part.

[33940] VGAM2427 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2427 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2427 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33941] VGAM2427 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites

located in untranslated regions of VGAM2427 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2427 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2427 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2427 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33942] The complementary binding of VGAM2427 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2427 host target RNA, herein designated VGAM

HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2427 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2427 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[33943] It is appreciated that VGAM2427 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2427 host target genes. The mRNA of each one of this plurality of VGAM2427 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2427 RNA, herein designated VGAM RNA, and which when bound by VGAM2427 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2427 host target proteins.

[33944] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2427 gene, herein designated VGAM GENE, on one or more VGAM2427 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove

with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33945] It is yet further appreciated that a function of VGAM2427 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2427 include diagnosis, prevention and treatment of viral infection by Goatpox virus. Specific functions, and accordingly utilities, of VGAM2427 correlate with, and may be deduced from, the identity of the host target genes which VGAM2427 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[33946] Nucleotide sequences of the VGAM2427 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2427 RNA, herein designated VGAM RNA, and

a schematic representation of the secondary folding of VGAM2427 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2427 are further described hereinbelow with reference to Table 1.

[33947] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2427 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[33948] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2428 (VGAM2428) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[33949] VGAM2428 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2428 was detected is described hereinabove with reference to Figs. 2-8.

[33950] VGAM2428 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox virus.

VGAM2428 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[33951] VGAM2428 gene, herein designated VGAM GENE, encodes a VGAM2428 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2428 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2428 precursor RNA is designated SEQ ID:2414, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2414 is located at position 91853 relative to the genome of Goatpox virus.

[33952] VGAM2428 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2428 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[33953] An enzyme complex designated DICER COMPLEX, dices the VGAM2428 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2428 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 56%) nucleotide sequence of VGAM2428 RNA is designated SEQ ID:5139, and is provided hereinbelow with reference to the sequence listing part.

[33954] VGAM2428 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2428 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2428 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33955] VGAM2428 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM2428 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2428 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2428 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2428 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33956] The complementary binding of VGAM2428 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM2428 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2428 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2428 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[33957] It is appreciated that VGAM2428 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2428 host target genes. The mRNA of each one of this plurality of VGAM2428 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2428 RNA, herein designated VGAM RNA, and which when bound by VGAM2428 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2428 host target proteins.

[33958] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2428 gene, herein designated VGAM GENE, on one or more VGAM2428 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33959] It is yet further appreciated that a function of VGAM2428 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2428 include diagnosis, prevention and treatment of viral infection by Goatpox virus. Specific functions, and accordingly utilities, of VGAM2428 correlate with, and may be deduced from, the identity of the host target genes which VGAM2428 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[33960] Nucleotide sequences of the VGAM2428 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

diced VGAM2428 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2428 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2428 are further described hereinbelow with reference to Table 1.

[33961] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2428 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[33962] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2429 (VGAM2429) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[33963] VGAM2429 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2429 was detected is described hereinabove with reference to Figs. 2-8.

[33964] VGAM2429 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of Goatpox virus. VGAM2429 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[33965] VGAM2429 gene, herein designated VGAM GENE, encodes a VGAM2429 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2429 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2429 precursor RNA is designated SEQ ID:2415, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2415 is located at position 58421 relative to the genome of Goatpox virus.

[33966] VGAM2429 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2429 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33967] An enzyme complex designated DICER COMPLEX, dices the VGAM2429 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2429 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2429 RNA is designated SEQ ID:5140, and is provided hereinbelow with reference to the sequence listing part.

[33968] VGAM2429 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2429 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2429 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33969] VGAM2429 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2429 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2429 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2429 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2429 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33970] The complementary binding of VGAM2429 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM2429 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2429 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2429 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[33971] It is appreciated that VGAM2429 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2429 host target genes. The mRNA of each one of this plurality of VGAM2429 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2429 RNA, herein designated VGAM RNA, and which when bound by VGAM2429 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2429 host target proteins.

[33972] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2429 gene, herein designated VGAM GENE, on one or more VGAM2429 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33973] It is yet further appreciated that a function of VGAM2429 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2429 include diagnosis, prevention and treatment of viral infection by Goatpox virus. Specific functions, and accordingly utilities, of VGAM2429 correlate with, and may be deduced from, the identity of the host target genes which VGAM2429 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[33974] Nucleotide sequences of the VGAM2429 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the diced VGAM2429 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2429 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2429 are further described hereinbelow with reference to Table 1.

[33975] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2429 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[33976] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2430 (VGAM2430) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[33977] VGAM2430 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2430 was detected is described hereinabove with reference to Figs. 2-8.

[33978] VGAM2430 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox virus. VGAM2430 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[33979] VGAM2430 gene, herein designated VGAM GENE, encodes a VGAM2430 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2430 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2430 precursor RNA is designated SEQ ID:2416, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2416 is located at position 123911 relative to the genome of Goatpox virus.

[33980] VGAM2430 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2430 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33981] An enzyme complex designated DICER COMPLEX, dices the VGAM2430 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2430 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 58%) nucleotide sequence of VGAM2430 RNA is designated SEQ ID:5141, and is provided hereinbelow with reference to the sequence listing part.

[33982] VGAM2430 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2430 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2430 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN COD-

ING and 3UTR respectively.

[33983] VGAM2430 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2430 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2430 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2430 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2430 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33984] The complementary binding of VGAM2430 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2430 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2430 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2430 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[33985] It is appreciated that VGAM2430 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2430 host target genes. The mRNA of each one of this plurality of VGAM2430 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2430 RNA, herein designated VGAM RNA, and which when bound by VGAM2430 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2430 host target proteins.

[33986] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2430 gene, herein designated VGAM GENE, on one

or more VGAM2430 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33987] It is yet further appreciated that a function of VGAM2430 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2430 include diagnosis, prevention and treatment of viral infection by Goatpox virus. Specific functions, and accordingly utilities, of VGAM2430 correlate with, and may be deduced from, the identity of the host target genes which VGAM2430 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[33988] Nucleotide sequences of the VGAM2430 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2430 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2430 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2430 are further described hereinbelow with reference to Table 1.

[33989] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2430 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[33990] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2431 (VGAM2431) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[33991] VGAM2431 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2431 was detected is de-

scribed hereinabove with reference to Figs. 2-8.

[33992] VGAM2431 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox virus. VGAM2431 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[33993] VGAM2431 gene, herein designated VGAM GENE, encodes a VGAM2431 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2431 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2431 precursor RNA is designated SEQ ID:2417, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2417 is located at position 113097 relative to the genome of Goatpox virus.

[33994] VGAM2431 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2431 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33995] An enzyme complex designated DICER COMPLEX, dices the VGAM2431 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2431 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 82%) nucleotide sequence of VGAM2431 RNA is designated SEQ ID:5142, and is provided hereinbelow with reference to the sequence listing part.

[33996] VGAM2431 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2431 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2431 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and

a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33997] VGAM2431 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2431 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2431 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2431 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2431 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both

3UTR and 5UTR regions.

[33998] The complementary binding of VGAM2431 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2431 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2431 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2431 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[33999] It is appreciated that VGAM2431 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2431 host target genes. The mRNA of each one of this plurality of VGAM2431 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2431 RNA, herein designated VGAM RNA, and which when bound by VGAM2431 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2431 host target proteins.

[34000] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM2431 gene, herein designated VGAM GENE, on one or more VGAM2431 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34001] It is yet further appreciated that a function of VGAM2431 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2431 include diagnosis, prevention and treatment of viral infection by Goatpox virus. Specific functions, and accordingly utilities, of VGAM2431 correlate with, and may be deduced from, the identity of the host target genes which VGAM2431 binds and inhibits, and the function of these host target genes, as elaborated

hereinbelow.

[34002] Nucleotide sequences of the VGAM2431 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2431 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2431 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2431 are further described hereinbelow with reference to Table 1.

[34003] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2431 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[34004] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2432 (VGAM2432) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[34005] VGAM2432 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene.

The method by which VGAM2432 was detected is described hereinabove with reference to Figs. 2-8.

[34006] VGAM2432 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox virus. VGAM2432 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[34007] VGAM2432 gene, herein designated VGAM GENE, encodes a VGAM2432 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2432 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2432 precursor RNA is designated SEQ ID:2418, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2418 is located at position 76475 relative to the genome of Goatpox virus.

[34008] VGAM2432 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2432 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34009] An enzyme complex designated DICER COMPLEX, dices the VGAM2432 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2432 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 83%) nucleotide sequence of VGAM2432 RNA is designated SEQ ID:5143, and is provided hereinbelow with reference to the sequence listing part.

[34010] VGAM2432 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2432 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2432 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding

gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34011] VGAM2432 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2432 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2432 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2432 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2432 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be lo-

cated in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34012] The complementary binding of VGAM2432 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2432 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2432 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2432 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[34013] It is appreciated that VGAM2432 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2432 host target genes. The mRNA of each one of this plurality of VGAM2432 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2432 RNA, herein designated VGAM RNA, and which when bound by VGAM2432 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2432 host target proteins.

[34014] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM2432 gene, herein designated VGAM GENE, on one or more VGAM2432 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34015] It is yet further appreciated that a function of VGAM2432 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2432 include diagnosis, prevention and treatment of viral infection by Goatpox virus. Specific functions, and accordingly utilities, of VGAM2432 correlate with, and may be deduced from, the identity of the host target genes which VGAM2432 binds and inhibits,

and the function of these host target genes, as elaborated hereinbelow.

[34016] Nucleotide sequences of the VGAM2432 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2432 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2432 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2432 are further described hereinbelow with reference to Table 1.

[34017] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2432 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[34018] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2433 (VGAM2433) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[34019] VGAM2433 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2433 was detected is described hereinabove with reference to Figs. 2-8.

[34020] VGAM2433 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox virus. VGAM2433 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[34021] VGAM2433 gene, herein designated VGAM GENE, encodes a VGAM2433 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2433 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2433 precursor RNA is designated SEQ ID:2419, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2419 is located at position 30434 relative to the genome of Goatpox virus.

[34022] VGAM2433 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2433 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34023] An enzyme complex designated DICER COMPLEX, dices the VGAM2433 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2433 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 86%) nucleotide sequence of VGAM2433 RNA is designated SEQ ID:5144, and is provided hereinbelow with reference to the sequence listing part.

[34024] VGAM2433 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2433 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2433 host target RNA, herein designated VGAM HOST TARGET RNA, comprises

three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34025] VGAM2433 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2433 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2433 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2433 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2433 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an

example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34026] The complementary binding of VGAM2433 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2433 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2433 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2433 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[34027] It is appreciated that VGAM2433 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2433 host target genes. The mRNA of each one of this plurality of VGAM2433 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2433 RNA, herein designated VGAM RNA, and which when bound by VGAM2433 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2433 host target proteins.

[34028] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2433 gene, herein designated VGAM GENE, on one or more VGAM2433 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34029] It is yet further appreciated that a function of VGAM2433 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2433 include diagnosis, prevention and treatment of viral infection by Goatpox virus. Specific functions, and accordingly utilities, of VGAM2433 correlate with, and may be deduced from, the identity of the

host target genes which VGAM2433 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[34030] Nucleotide sequences of the VGAM2433 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2433 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2433 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2433 are further described hereinbelow with reference to Table 1.

[34031] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2433 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[34032] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2434 (VGAM2434) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[34033] VGAM2434 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2434 was detected is described hereinabove with reference to Figs. 2-8.

[34034] VGAM2434 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox virus. VGAM2434 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[34035] VGAM2434 gene, herein designated VGAM GENE, encodes a VGAM2434 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2434 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2434 precursor RNA is designated SEQ ID:2420, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2420 is located at position 130867 relative to the genome of Goatpox virus.

[34036] VGAM2434 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2434 folded precursor RNA, herein designated VGAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34037] An enzyme complex designated DICER COMPLEX, dices the VGAM2434 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2434 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2434 RNA is designated SEQ ID:5145, and is provided hereinbelow with reference to the sequence listing part.

[34038] VGAM2434 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2434 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2434 host target RNA,

herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34039] VGAM2434 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2434 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2434 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2434 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host tar-

get binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34040] The complementary binding of VGAM2434 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2434 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2434 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2434 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[34041] It is appreciated that VGAM2434 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2434 host target genes. The mRNA of each one of this plurality of VGAM2434 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2434 RNA, herein designated VGAM RNA, and which when bound by VGAM2434 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2434 host target proteins.

[34042] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2434 gene, herein designated VGAM GENE, on one or more VGAM2434 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34043] It is yet further appreciated that a function of VGAM2434 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of viral infection by Goatpox virus. Specific functions, and accordingly utilities, of VGAM2434 corre-

late with, and may be deduced from, the identity of the host target genes which VGAM2434 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[34044] Nucleotide sequences of the VGAM2434 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2434 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2434 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2434 are further described hereinbelow with reference to Table 1.

[34045] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2434 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[34046] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2435 (VGAM2435) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the

art.

[34047] VGAM2435 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2435 was detected is described hereinabove with reference to Figs. 2-8.

[34048] VGAM2435 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox virus. VGAM2435 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[34049] VGAM2435 gene, herein designated VGAM GENE, encodes a VGAM2435 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2435 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2435 precursor RNA is designated SEQ ID:2421, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2421 is located at position 35753 relative to the genome of Goatpox virus.

[34050] VGAM2435 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2435 folded

precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34051] An enzyme complex designated DICER COMPLEX, dices the VGAM2435 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2435 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 59%) nucleotide sequence of VGAM2435 RNA is designated SEQ ID:5146, and is provided hereinbelow with reference to the sequence listing part.

[34052] VGAM2435 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2435 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM2435 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34053] VGAM2435 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2435 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2435 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2435 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2435 host target RNA, herein designated VGAM HOST TARGET RNA.

It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34054] The complementary binding of VGAM2435 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2435 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2435 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2435 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[34055] It is appreciated that VGAM2435 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2435 host target genes. The mRNA of each one of this plurality of VGAM2435 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2435 RNA, herein designated VGAM RNA, and which when bound by VGAM2435 RNA, herein designated VGAM RNA, causes inhibition of translation of

respective one or more VGAM2435 host target proteins.

[34056] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2435 gene, herein designated VGAM GENE, on one or more VGAM2435 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34057] It is yet further appreciated that a function of VGAM2435 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2435 include diagnosis, prevention and treatment of viral infection by Goatpox virus. Specific

functions, and accordingly utilities, of VGAM2435 correlate with, and may be deduced from, the identity of the host target genes which VGAM2435 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[34058] Nucleotide sequences of the VGAM2435 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2435 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2435 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2435 are further described hereinbelow with reference to Table 1.

[34059] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2435 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[34060] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2436 (VGAM2436) viral gene, which modulates expression of respective host target genes thereof, the func-

tion and utility of which host target genes is known in the art.

[34061] VGAM2436 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2436 was detected is described hereinabove with reference to Figs. 2-8.

[34062] VGAM2436 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox virus. VGAM2436 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[34063] VGAM2436 gene, herein designated VGAM GENE, encodes a VGAM2436 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2436 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2436 precursor RNA is designated SEQ ID:2422, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2422 is located at position 79755 relative to the genome of Goatpox virus.

[34064] VGAM2436 precursor RNA, herein designated VGAM PRE-

CURSOR RNA, folds onto itself, forming VGAM2436 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34065] An enzyme complex designated DICER COMPLEX, dices the VGAM2436 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2436 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 66%) nucleotide sequence of VGAM2436 RNA is designated SEQ ID:5147, and is provided hereinbelow with reference to the sequence listing part.

[34066] VGAM2436 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM2436 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2436 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34067] VGAM2436 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2436 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2436 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2436 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2436 host

target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34068] The complementary binding of VGAM2436 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2436 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2436 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2436 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[34069] It is appreciated that VGAM2436 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2436 host target genes. The mRNA of each one of this plurality of VGAM2436 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2436 RNA, herein designated VGAM RNA, and which when bound by VGAM2436 RNA, herein

designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2436 host target proteins.

[34070] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2436 gene, herein designated VGAM GENE, on one or more VGAM2436 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34071] It is yet further appreciated that a function of VGAM2436 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2436 include diagnosis, prevention and

treatment of viral infection by Goatpox virus. Specific functions, and accordingly utilities, of VGAM2436 correlate with, and may be deduced from, the identity of the host target genes which VGAM2436 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[34072] Nucleotide sequences of the VGAM2436 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2436 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2436 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2436 are further described hereinbelow with reference to Table 1.

[34073] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2436 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[34074] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2437 (VGAM2437) viral gene, which modulates ex-

pression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[34075] VGAM2437 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2437 was detected is described hereinabove with reference to Figs. 2-8.

[34076] VGAM2437 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox virus. VGAM2437 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[34077] VGAM2437 gene, herein designated VGAM GENE, encodes a VGAM2437 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2437 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2437 precursor RNA is designated SEQ ID:2423, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2423 is located at position 32976 relative to the genome of Goatpox virus.

[34078] VGAM2437 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2437 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34079] An enzyme complex designated DICER COMPLEX, dices the VGAM2437 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2437 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2437 RNA is designated SEQ ID:5148, and is provided hereinbelow with reference to the sequence listing part.

[34080] VGAM2437 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2437 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2437 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34081] VGAM2437 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2437 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2437 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2437 RNA, herein designated VGAM RNA, may have a different number of host target

binding sites in untranslated regions of a VGAM2437 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34082] The complementary binding of VGAM2437 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2437 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2437 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2437 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[34083] It is appreciated that VGAM2437 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2437 host target genes. The mRNA of each one of this plurality of VGAM2437 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2437 RNA, herein designated VGAM

RNA, and which when bound by VGAM2437 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2437 host target proteins.

[34084] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2437 gene, herein designated VGAM GENE, on one or more VGAM2437 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34085] It is yet further appreciated that a function of VGAM2437 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM2437 include diagnosis, prevention and treatment of viral infection by Goatpox virus. Specific functions, and accordingly utilities, of VGAM2437 correlate with, and may be deduced from, the identity of the host target genes which VGAM2437 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[34086] Nucleotide sequences of the VGAM2437 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2437 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2437 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2437 are further described hereinbelow with reference to Table 1.

[34087] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2437 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[34088] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Mes-

senger 2438 (VGAM2438) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[34089] VGAM2438 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2438 was detected is described hereinabove with reference to Figs. 2-8.

[34090] VGAM2438 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox virus. VGAM2438 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[34091] VGAM2438 gene, herein designated VGAM GENE, encodes a VGAM2438 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2438 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2438 precursor RNA is designated SEQ ID:2424, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2424 is located at position

88305 relative to the genome of Goatpox virus.

[34092] VGAM2438 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2438 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34093] An enzyme complex designated DICER COMPLEX, dices the VGAM2438 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2438 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2438 RNA is designated SEQ ID:5149, and is provided hereinbelow with reference to the sequence listing part.

[34094] VGAM2438 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2438 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2438 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34095] VGAM2438 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2438 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2438 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2438 RNA, herein designated

VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2438 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34096] The complementary binding of VGAM2438 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2438 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2438 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2438 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[34097] It is appreciated that VGAM2438 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2438 host target genes. The mRNA of each one of this plurality of VGAM2438 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM2438 RNA, herein designated VGAM RNA, and which when bound by VGAM2438 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2438 host target proteins.

[34098] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2438 gene, herein designated VGAM GENE, on one or more VGAM2438 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34099] It is yet further appreciated that a function of VGAM2438 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2438 include diagnosis, prevention and treatment of viral infection by Goatpox virus. Specific functions, and accordingly utilities, of VGAM2438 correlate with, and may be deduced from, the identity of the host target genes which VGAM2438 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[34100] Nucleotide sequences of the VGAM2438 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2438 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2438 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2438 are further described hereinbelow with reference to Table 1.

[34101] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2438 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[34102] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present

invention, referred to here as Viral Genomic Address Messenger 2439 (VGAM2439) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[34103] VGAM2439 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2439 was detected is described hereinabove with reference to Figs. 2-8.

[34104] VGAM2439 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox virus. VGAM2439 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[34105] VGAM2439 gene, herein designated VGAM GENE, encodes a VGAM2439 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2439 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2439 precursor RNA is designated SEQ ID:2425, and is provided hereinbelow with reference to the sequence listing part. Nu-

cleotide sequence SEQ ID:2425 is located at position 129653 relative to the genome of Goatpox virus.

[34106] VGAM2439 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2439 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34107] An enzyme complex designated DICER COMPLEX, dices the VGAM2439 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2439 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2439 RNA is designated SEQ ID:5150, and is provided hereinbelow with reference to the sequence

listing part.

[34108] VGAM2439 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2439 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2439 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34109] VGAM2439 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2439 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2439 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not

meant to be limiting VGAM2439 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2439 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34110] The complementary binding of VGAM2439 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2439 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2439 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2439 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[34111] It is appreciated that VGAM2439 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2439 host target genes. The mRNA of each one of this plurality of VGAM2439 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2439 RNA, herein designated VGAM RNA, and which when bound by VGAM2439 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2439 host target proteins.

[34112] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2439 gene, herein designated VGAM GENE, on one or more VGAM2439 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34113] It is yet further appreciated that a function of VGAM2439

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2439 include diagnosis, prevention and treatment of viral infection by Goatpox virus. Specific functions, and accordingly utilities, of VGAM2439 correlate with, and may be deduced from, the identity of the host target genes which VGAM2439 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[34114] Nucleotide sequences of the VGAM2439 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2439 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2439 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2439 are further described hereinbelow with reference to Table 1.

[34115] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2439 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[34116] Fig. 1 further provides a conceptual description of another

novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2440 (VGAM2440) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[34117] VGAM2440 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2440 was detected is described hereinabove with reference to Figs. 2-8.

[34118] VGAM2440 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox virus. VGAM2440 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[34119] VGAM2440 gene, herein designated VGAM GENE, encodes a VGAM2440 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2440 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2440 precursor RNA is designated SEQ ID:2426, and is provided here-

inbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2426 is located at position 54822 relative to the genome of Goatpox virus.

[34120] VGAM2440 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2440 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34121] An enzyme complex designated DICER COMPLEX, dices the VGAM2440 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2440 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2440 RNA is designated SEQ ID:5151, and

is provided hereinbelow with reference to the sequence listing part.

[34122] VGAM2440 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2440 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2440 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34123] VGAM2440 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2440 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2440 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites

shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2440 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2440 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34124] The complementary binding of VGAM2440 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2440 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2440 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2440 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[34125] It is appreciated that VGAM2440 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2440 host target genes. The mRNA of each one of this plurality of VGAM2440 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2440 RNA, herein designated VGAM RNA, and which when bound by VGAM2440 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2440 host target proteins.

[34126] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2440 gene, herein designated VGAM GENE, on one or more VGAM2440 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34127] It is yet further appreciated that a function of VGAM2440 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2440 include diagnosis, prevention and treatment of viral infection by Goatpox virus. Specific functions, and accordingly utilities, of VGAM2440 correlate with, and may be deduced from, the identity of the host target genes which VGAM2440 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[34128] Nucleotide sequences of the VGAM2440 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2440 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2440 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2440 are further described hereinbelow with reference to Table 1.

[34129] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2440 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[34130] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2441 (VGAM2441) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[34131] VGAM2441 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2441 was detected is described hereinabove with reference to Figs. 2-8.

[34132] VGAM2441 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox virus.
VGAM2441 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[34133] VGAM2441 gene, herein designated VGAM GENE, encodes a VGAM2441 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2441 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2441 precur-

sor RNA is designated SEQ ID:2427, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2427 is located at position 482 relative to the genome of Goatpox virus.

[34134] VGAM2441 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2441 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34135] An enzyme complex designated DICER COMPLEX, dices the VGAM2441 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2441 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 58%) nucleotide se-

quence of VGAM2441 RNA is designated SEQ ID:5152, and is provided hereinbelow with reference to the sequence listing part.

[34136] VGAM2441 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2441 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2441 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34137] VGAM2441 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2441 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2441 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is ap-

preciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2441 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2441 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34138] The complementary binding of VGAM2441 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2441 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2441 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2441 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[34139] It is appreciated that VGAM2441 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2441 host target genes. The mRNA of

each one of this plurality of VGAM2441 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2441 RNA, herein designated VGAM RNA, and which when bound by VGAM2441 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2441 host target proteins.

[34140] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2441 gene, herein designated VGAM GENE, on one or more VGAM2441 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science

294,779 (2001)).

[34141] It is yet further appreciated that a function of VGAM2441 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2441 include diagnosis, prevention and treatment of viral infection by Goatpox virus. Specific functions, and accordingly utilities, of VGAM2441 correlate with, and may be deduced from, the identity of the host target genes which VGAM2441 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[34142] Nucleotide sequences of the VGAM2441 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2441 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2441 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2441 are further described hereinbelow with reference to Table 1.

[34143] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2441 RNA, herein designated VGAM RNA, are de-

scribed hereinbelow with reference to Table 2.

[34144] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2442 (VGAM2442) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[34145] VGAM2442 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2442 was detected is described hereinabove with reference to Figs. 2-8.

[34146] VGAM2442 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox virus.
VGAM2442 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[34147] VGAM2442 gene, herein designated VGAM GENE, encodes a VGAM2442 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2442 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly

similar to the nucleotide sequence of VGAM2442 precursor RNA is designated SEQ ID:2428, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2428 is located at position 110320 relative to the genome of Goatpox virus.

[34148] VGAM2442 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2442 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34149] An enzyme complex designated DICER COMPLEX, dices the VGAM2442 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2442 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2442 RNA is designated SEQ ID:5153, and is provided hereinbelow with reference to the sequence listing part.

[34150] VGAM2442 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2442 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2442 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34151] VGAM2442 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2442 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2442 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I,

BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2442 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2442 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34152] The complementary binding of VGAM2442 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2442 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2442 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2442 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[34153] It is appreciated that VGAM2442 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM2442 host target genes. The mRNA of each one of this plurality of VGAM2442 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2442 RNA, herein designated VGAM RNA, and which when bound by VGAM2442 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2442 host target proteins.

[34154] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2442 gene, herein designated VGAM GENE, on one or more VGAM2442 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34155] It is yet further appreciated that a function of VGAM2442 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2442 include diagnosis, prevention and treatment of viral infection by Goatpox virus. Specific functions, and accordingly utilities, of VGAM2442 correlate with, and may be deduced from, the identity of the host target genes which VGAM2442 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[34156] Nucleotide sequences of the VGAM2442 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2442 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2442 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2442 are further described hereinbelow with reference to Table 1.

[34157] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites

to VGAM2442 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[34158] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2443 (VGAM2443) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[34159] VGAM2443 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2443 was detected is described hereinabove with reference to Figs. 2-8.

[34160] VGAM2443 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2443 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[34161] VGAM2443 gene, herein designated VGAM GENE, encodes a VGAM2443 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2443 precursor RNA, herein designated VGAM PRECURSOR RNA, does not en-

code a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2443 precursor RNA is designated SEQ ID:2429, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2429 is located at position 167632 relative to the genome of Mouse cytomegalovirus 1.

[34162] VGAM2443 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2443 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34163] An enzyme complex designated DICER COMPLEX, dices the VGAM2443 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2443 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 70%) nucleotide sequence of VGAM2443 RNA is designated SEQ ID:5154, and is provided hereinbelow with reference to the sequence listing part.

[34164] VGAM2443 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2443 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2443 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34165] VGAM2443 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2443 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2443 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host

target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2443 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2443 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34166] The complementary binding of VGAM2443 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2443 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2443 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2443 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[34167] It is appreciated that VGAM2443 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2443 host target genes. The mRNA of each one of this plurality of VGAM2443 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2443 RNA, herein designated VGAM RNA, and which when bound by VGAM2443 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2443 host target proteins.

[34168] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2443 gene, herein designated VGAM GENE, on one or more VGAM2443 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34169] It is yet further appreciated that a function of VGAM2443 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2443 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2443 correlate with, and may be deduced from, the identity of the host target genes which VGAM2443 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[34170] Nucleotide sequences of the VGAM2443 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2443 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2443 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2443 are further described hereinbelow with reference to Table 1.

[34171] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2443 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[34172] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2444 (VGAM2444) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[34173] VGAM2444 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2444 was detected is described hereinabove with reference to Figs. 2-8.

[34174] VGAM2444 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2444 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[34175] VGAM2444 gene, herein designated VGAM GENE, encodes a VGAM2444 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and un-

like most ordinary genes, VGAM2444 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2444 precursor RNA is designated SEQ ID:2430, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2430 is located at position 180574 relative to the genome of Mouse cytomegalovirus 1.

[34176] VGAM2444 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2444 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34177] An enzyme complex designated DICER COMPLEX, dices the VGAM2444 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2444 RNA, herein designated VGAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 64%) nucleotide sequence of VGAM2444 RNA is designated SEQ ID:5155, and is provided hereinbelow with reference to the sequence listing part.

[34178] VGAM2444 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2444 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2444 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34179] VGAM2444 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2444 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2444 RNA, herein designated

VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2444 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2444 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34180] The complementary binding of VGAM2444 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2444 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2444 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2444 host target protein, herein desig-

nated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[34181] It is appreciated that VGAM2444 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2444 host target genes. The mRNA of each one of this plurality of VGAM2444 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2444 RNA, herein designated VGAM RNA, and which when bound by VGAM2444 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2444 host target proteins.

[34182] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2444 gene, herein designated VGAM GENE, on one or more VGAM2444 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34183] It is yet further appreciated that a function of VGAM2444 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2444 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2444 correlate with, and may be deduced from, the identity of the host target genes which VGAM2444 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[34184] Nucleotide sequences of the VGAM2444 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2444 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2444 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2444 are further described hereinbelow with reference to Table 1.

[34185] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2444 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[34186] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2445 (VGAM2445) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[34187] VGAM2445 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2445 was detected is described hereinabove with reference to Figs. 2-8.

[34188] VGAM2445 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2445 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[34189] VGAM2445 gene, herein designated VGAM GENE, encodes

a VGAM2445 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2445 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2445 precursor RNA is designated SEQ ID:2431, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2431 is located at position 13050 relative to the genome of Mouse cytomegalovirus 1.

[34190] VGAM2445 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2445 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34191] An enzyme complex designated DICER COMPLEX, dices the VGAM2445 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, into VGAM2445 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2445 RNA is designated SEQ ID:5156, and is provided hereinbelow with reference to the sequence listing part.

[34192] VGAM2445 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2445 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2445 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34193] VGAM2445 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2445 host target RNA, herein designated VGAM HOST TARGET RNA. This

complementary binding is due to the fact that the nucleotide sequence of VGAM2445 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2445 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2445 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34194] The complementary binding of VGAM2445 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2445 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2445

host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2445 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[34195] It is appreciated that VGAM2445 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2445 host target genes. The mRNA of each one of this plurality of VGAM2445 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2445 RNA, herein designated VGAM RNA, and which when bound by VGAM2445 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2445 host target proteins.

[34196] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2445 gene, herein designated VGAM GENE, on one or more VGAM2445 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34197] It is yet further appreciated that a function of VGAM2445 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2445 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2445 correlate with, and may be deduced from, the identity of the host target genes which VGAM2445 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[34198] Nucleotide sequences of the VGAM2445 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2445 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2445 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM2445 are further described hereinbelow with reference to Table 1.

[34199] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2445 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[34200] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2446 (VGAM2446) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[34201] VGAM2446 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2446 was detected is described hereinabove with reference to Figs. 2-8.

[34202] VGAM2446 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2446 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the

human genome.

[34203] VGAM2446 gene, herein designated VGAM GENE, encodes a VGAM2446 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2446 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2446 precursor RNA is designated SEQ ID:2432, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2432 is located at position 159425 relative to the genome of Mouse cytomegalovirus 1.

[34204] VGAM2446 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2446 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34205] An enzyme complex designated DICER COMPLEX, dices the VGAM2446 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2446 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 58%) nucleotide sequence of VGAM2446 RNA is designated SEQ ID:5157, and is provided hereinbelow with reference to the sequence listing part.

[34206] VGAM2446 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2446 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2446 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34207] VGAM2446 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites

located in untranslated regions of VGAM2446 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2446 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2446 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2446 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34208] The complementary binding of VGAM2446 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2446 host target RNA, herein designated VGAM

HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2446 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2446 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[34209] It is appreciated that VGAM2446 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2446 host target genes. The mRNA of each one of this plurality of VGAM2446 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2446 RNA, herein designated VGAM RNA, and which when bound by VGAM2446 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2446 host target proteins.

[34210] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2446 gene, herein designated VGAM GENE, on one or more VGAM2446 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove

with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34211] It is yet further appreciated that a function of VGAM2446 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2446 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2446 correlate with, and may be deduced from, the identity of the host target genes which VGAM2446 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[34212] Nucleotide sequences of the VGAM2446 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2446 RNA, herein designated VGAM RNA, and

a schematic representation of the secondary folding of VGAM2446 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2446 are further described hereinbelow with reference to Table 1.

[34213] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2446 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[34214] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2447 (VGAM2447) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[34215] VGAM2447 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2447 was detected is described hereinabove with reference to Figs. 2-8.

[34216] VGAM2447 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus

1. VGAM2447 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[34217] VGAM2447 gene, herein designated VGAM GENE, encodes a VGAM2447 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2447 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2447 precursor RNA is designated SEQ ID:2433, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2433 is located at position 2867 relative to the genome of Mouse cytomegalovirus 1.

[34218] VGAM2447 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2447 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[34219] An enzyme complex designated DICER COMPLEX, dices the VGAM2447 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2447 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 82%) nucleotide sequence of VGAM2447 RNA is designated SEQ ID:5158, and is provided hereinbelow with reference to the sequence listing part.

[34220] VGAM2447 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2447 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2447 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34221] VGAM2447 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM2447 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2447 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2447 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2447 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34222] The complementary binding of VGAM2447 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM2447 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2447 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2447 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[34223] It is appreciated that VGAM2447 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2447 host target genes. The mRNA of each one of this plurality of VGAM2447 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2447 RNA, herein designated VGAM RNA, and which when bound by VGAM2447 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2447 host target proteins.

[34224] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2447 gene, herein designated VGAM GENE, on one or more VGAM2447 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34225] It is yet further appreciated that a function of VGAM2447 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2447 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2447 correlate with, and may be deduced from, the identity of the host target genes which VGAM2447 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[34226] Nucleotide sequences of the VGAM2447 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

diced VGAM2447 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2447 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2447 are further described hereinbelow with reference to Table 1.

[34227] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2447 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[34228] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2448 (VGAM2448) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[34229] VGAM2448 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2448 was detected is described hereinabove with reference to Figs. 2-8.

[34230] VGAM2448 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of Mouse cytomegalovirus 1. VGAM2448 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[34231] VGAM2448 gene, herein designated VGAM GENE, encodes a VGAM2448 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2448 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2448 precursor RNA is designated SEQ ID:2434, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2434 is located at position 134478 relative to the genome of Mouse cytomegalovirus 1.

[34232] VGAM2448 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2448 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34233] An enzyme complex designated DICER COMPLEX, dices the VGAM2448 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2448 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2448 RNA is designated SEQ ID:5159, and is provided hereinbelow with reference to the sequence listing part.

[34234] VGAM2448 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2448 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2448 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN COD-

ING and 3UTR respectively.

[34235] VGAM2448 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2448 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2448 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2448 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2448 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34236] The complementary binding of VGAM2448 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2448 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2448 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2448 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[34237] It is appreciated that VGAM2448 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2448 host target genes. The mRNA of each one of this plurality of VGAM2448 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2448 RNA, herein designated VGAM RNA, and which when bound by VGAM2448 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2448 host target proteins.

[34238] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2448 gene, herein designated VGAM GENE, on one

or more VGAM2448 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34239] It is yet further appreciated that a function of VGAM2448 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2448 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2448 correlate with, and may be deduced from, the identity of the host target genes which VGAM2448 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[34240] Nucleotide sequences of the VGAM2448 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2448 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2448 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2448 are further described hereinbelow with reference to Table 1.

[34241] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2448 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[34242] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2449 (VGAM2449) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[34243] VGAM2449 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2449 was detected is de-

scribed hereinabove with reference to Figs. 2-8.

[34244] VGAM2449 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2449 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[34245] VGAM2449 gene, herein designated VGAM GENE, encodes a VGAM2449 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2449 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2449 precursor RNA is designated SEQ ID:2435, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2435 is located at position 53100 relative to the genome of Mouse cytomegalovirus 1.

[34246] VGAM2449 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2449 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34247] An enzyme complex designated DICER COMPLEX, dices the VGAM2449 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2449 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2449 RNA is designated SEQ ID:5160, and is provided hereinbelow with reference to the sequence listing part.

[34248] VGAM2449 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2449 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2449 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding

gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34249] VGAM2449 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2449 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2449 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2449 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2449 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be lo-

cated in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34250] The complementary binding of VGAM2449 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2449 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2449 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2449 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[34251] It is appreciated that VGAM2449 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2449 host target genes. The mRNA of each one of this plurality of VGAM2449 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2449 RNA, herein designated VGAM RNA, and which when bound by VGAM2449 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2449 host target proteins.

[34252] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM2449 gene, herein designated VGAM GENE, on one or more VGAM2449 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34253] It is yet further appreciated that a function of VGAM2449 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2449 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2449 correlate with, and may be deduced from, the identity of the host target genes which VGAM2449 binds and in-

hibits, and the function of these host target genes, as elaborated hereinbelow.

[34254] Nucleotide sequences of the VGAM2449 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2449 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2449 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2449 are further described hereinbelow with reference to Table 1.

[34255] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2449 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[34256] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2450 (VGAM2450) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[34257] VGAM2450 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2450 was detected is described hereinabove with reference to Figs. 2-8.

[34258] VGAM2450 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2450 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[34259] VGAM2450 gene, herein designated VGAM GENE, encodes a VGAM2450 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2450 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2450 precursor RNA is designated SEQ ID:2436, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2436 is located at position 39437 relative to the genome of Mouse cytomegalovirus 1.

[34260] VGAM2450 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2450 folded precursor RNA, herein designated VGAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34261] An enzyme complex designated DICER COMPLEX, dices the VGAM2450 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2450 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2450 RNA is designated SEQ ID:5161, and is provided hereinbelow with reference to the sequence listing part.

[34262] VGAM2450 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2450 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2450 host target RNA,

herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34263] VGAM2450 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2450 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2450 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2450 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2450 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host tar-

get binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34264] The complementary binding of VGAM2450 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2450 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2450 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2450 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[34265] It is appreciated that VGAM2450 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2450 host target genes. The mRNA of each one of this plurality of VGAM2450 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2450 RNA, herein designated VGAM RNA, and which when bound by VGAM2450 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2450 host target proteins.

[34266] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2450 gene, herein designated VGAM GENE, on one or more VGAM2450 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34267] It is yet further appreciated that a function of VGAM2450 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2450 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2450

correlate with, and may be deduced from, the identity of the host target genes which VGAM2450 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[34268] Nucleotide sequences of the VGAM2450 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2450 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2450 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2450 are further described hereinbelow with reference to Table 1.

[34269] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2450 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[34270] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2451 (VGAM2451) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the

art.

[34271] VGAM2451 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2451 was detected is described hereinabove with reference to Figs. 2-8.

[34272] VGAM2451 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2451 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[34273] VGAM2451 gene, herein designated VGAM GENE, encodes a VGAM2451 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2451 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2451 precursor RNA is designated SEQ ID:2437, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2437 is located at position 43825 relative to the genome of Mouse cytomegalovirus 1.

[34274] VGAM2451 precursor RNA, herein designated VGAM PRE-

CURSOR RNA, folds onto itself, forming VGAM2451 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34275] An enzyme complex designated DICER COMPLEX, dices the VGAM2451 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2451 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2451 RNA is designated SEQ ID:5162, and is provided hereinbelow with reference to the sequence listing part.

[34276] VGAM2451 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM2451 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2451 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34277] VGAM2451 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2451 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2451 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2451 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2451 host

target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34278] The complementary binding of VGAM2451 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2451 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2451 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2451 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[34279] It is appreciated that VGAM2451 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2451 host target genes. The mRNA of each one of this plurality of VGAM2451 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2451 RNA, herein designated VGAM RNA, and which when bound by VGAM2451 RNA, herein

designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2451 host target proteins.

[34280] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2451 gene, herein designated VGAM GENE, on one or more VGAM2451 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34281] It is yet further appreciated that a function of VGAM2451 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2451 include diagnosis, prevention and

treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2451 correlate with, and may be deduced from, the identity of the host target genes which VGAM2451 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[34282] Nucleotide sequences of the VGAM2451 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2451 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2451 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2451 are further described hereinbelow with reference to Table 1.

[34283] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2451 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[34284] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2452 (VGAM2452) viral gene, which modulates ex-

pression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[34285] VGAM2452 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2452 was detected is described hereinabove with reference to Figs. 2-8.

[34286] VGAM2452 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2452 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[34287] VGAM2452 gene, herein designated VGAM GENE, encodes a VGAM2452 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2452 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2452 precursor RNA is designated SEQ ID:2438, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2438 is located at position 150242 relative to the genome of Mouse cytomegalovirus

1.

[34288] VGAM2452 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2452 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34289] An enzyme complex designated DICER COMPLEX, dices the VGAM2452 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2452 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 52%) nucleotide sequence of VGAM2452 RNA is designated SEQ ID:5163, and is provided hereinbelow with reference to the sequence listing part.

[34290] VGAM2452 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2452 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2452 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34291] VGAM2452 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2452 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2452 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2452 RNA, herein designated

VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2452 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34292] The complementary binding of VGAM2452 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2452 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2452 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2452 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[34293] It is appreciated that VGAM2452 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2452 host target genes. The mRNA of each one of this plurality of VGAM2452 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM2452 RNA, herein designated VGAM RNA, and which when bound by VGAM2452 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2452 host target proteins.

[34294] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2452 gene, herein designated VGAM GENE, on one or more VGAM2452 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34295] It is yet further appreciated that a function of VGAM2452 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2452 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2452 correlate with, and may be deduced from, the identity of the host target genes which VGAM2452 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[34296] Nucleotide sequences of the VGAM2452 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2452 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2452 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2452 are further described hereinbelow with reference to Table 1.

[34297] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2452 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[34298] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present

invention, referred to here as Viral Genomic Address Messenger 2453 (VGAM2453) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[34299] VGAM2453 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2453 was detected is described hereinabove with reference to Figs. 2-8.

[34300] VGAM2453 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2453 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[34301] VGAM2453 gene, herein designated VGAM GENE, encodes a VGAM2453 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2453 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2453 precursor RNA is designated SEQ ID:2439, and is provided hereinbelow with reference to the sequence listing part. Nu-

cleotide sequence SEQ ID:2439 is located at position 45147 relative to the genome of Mouse cytomegalovirus 1.

[34302] VGAM2453 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2453 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34303] An enzyme complex designated DICER COMPLEX, dices the VGAM2453 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2453 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 50%) nucleotide sequence of VGAM2453 RNA is designated SEQ ID:5164, and

is provided hereinbelow with reference to the sequence listing part.

[34304] VGAM2453 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2453 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2453 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34305] VGAM2453 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2453 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2453 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites

shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2453 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2453 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34306] The complementary binding of VGAM2453 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2453 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2453 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2453 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[34307] It is appreciated that VGAM2453 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2453 host target genes. The mRNA of each one of this plurality of VGAM2453 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2453 RNA, herein designated VGAM RNA, and which when bound by VGAM2453 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2453 host target proteins.

[34308] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2453 gene, herein designated VGAM GENE, on one or more VGAM2453 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34309] It is yet further appreciated that a function of VGAM2453 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2453 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2453 correlate with, and may be deduced from, the identity of the host target genes which VGAM2453 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[34310] Nucleotide sequences of the VGAM2453 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2453 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2453 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2453 are further described hereinbelow with reference to Table 1.

[34311] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2453 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[34312] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2454 (VGAM2454) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[34313] VGAM2454 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2454 was detected is described hereinabove with reference to Figs. 2-8.

[34314] VGAM2454 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2454 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[34315] VGAM2454 gene, herein designated VGAM GENE, encodes a VGAM2454 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2454 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2454 precur-

sor RNA is designated SEQ ID:2440, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2440 is located at position 170592 relative to the genome of Mouse cytomegalovirus 1.

[34316] VGAM2454 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2454 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34317] An enzyme complex designated DICER COMPLEX, dices the VGAM2454 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2454 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 49%) nucleotide sequence of VGAM2454 RNA is designated SEQ ID:5165, and is provided hereinbelow with reference to the sequence listing part.

[34318] VGAM2454 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2454 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2454 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34319] VGAM2454 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2454 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2454 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I,

BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2454 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2454 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34320] The complementary binding of VGAM2454 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2454 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2454 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2454 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[34321] It is appreciated that VGAM2454 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM2454 host target genes. The mRNA of each one of this plurality of VGAM2454 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2454 RNA, herein designated VGAM RNA, and which when bound by VGAM2454 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2454 host target proteins.

[34322] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2454 gene, herein designated VGAM GENE, on one or more VGAM2454 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34323] It is yet further appreciated that a function of VGAM2454 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2454 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2454 correlate with, and may be deduced from, the identity of the host target genes which VGAM2454 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[34324] Nucleotide sequences of the VGAM2454 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2454 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2454 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2454 are further described hereinbelow with reference to Table 1.

[34325] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites

to VGAM2454 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[34326] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2455 (VGAM2455) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[34327] VGAM2455 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2455 was detected is described hereinabove with reference to Figs. 2-8.

[34328] VGAM2455 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2455 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[34329] VGAM2455 gene, herein designated VGAM GENE, encodes a VGAM2455 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2455 precursor RNA, herein designated VGAM PRECURSOR RNA, does not en-

code a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2455 precursor RNA is designated SEQ ID:2441, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2441 is located at position 3102 relative to the genome of Mouse cytomegalovirus 1.

[34330] VGAM2455 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2455 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34331] An enzyme complex designated DICER COMPLEX, dices the VGAM2455 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2455 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2455 RNA is designated SEQ ID:5166, and is provided hereinbelow with reference to the sequence listing part.

[34332] VGAM2455 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2455 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2455 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34333] VGAM2455 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2455 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2455 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3

such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2455 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2455 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34334] The complementary binding of VGAM2455 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2455 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2455 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2455 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[34335] It is appreciated that VGAM2455 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2455 host target genes. The mRNA of each one of this plurality of VGAM2455 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2455 RNA, herein designated VGAM RNA, and which when bound by VGAM2455 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2455 host target proteins.

[34336] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2455 gene, herein designated VGAM GENE, on one or more VGAM2455 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34337] It is yet further appreciated that a function of VGAM2455 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2455 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2455 correlate with, and may be deduced from, the identity of the host target genes which VGAM2455 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[34338] Nucleotide sequences of the VGAM2455 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2455 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2455 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2455 are further described hereinbelow with reference to Table 1.

[34339] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the

complementarity of each of these host target binding sites to VGAM2455 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[34340] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2456 (VGAM2456) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[34341] VGAM2456 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2456 was detected is described hereinabove with reference to Figs. 2-8.

[34342] VGAM2456 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2456 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[34343] VGAM2456 gene, herein designated VGAM GENE, encodes a VGAM2456 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2456 precursor RNA,

herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2456 precursor RNA is designated SEQ ID:2442, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2442 is located at position 166990 relative to the genome of Mouse cytomegalovirus 1.

[34344] VGAM2456 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2456 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34345] An enzyme complex designated DICER COMPLEX, dices the VGAM2456 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2456 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2456 RNA is designated SEQ ID:5167, and is provided hereinbelow with reference to the sequence listing part.

[34346] VGAM2456 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2456 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2456 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34347] VGAM2456 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2456 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2456 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed

sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2456 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2456 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34348] The complementary binding of VGAM2456 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2456 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2456 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2456 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target

protein is therefore outlined by a broken line.

[34349] It is appreciated that VGAM2456 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2456 host target genes. The mRNA of each one of this plurality of VGAM2456 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2456 RNA, herein designated VGAM RNA, and which when bound by VGAM2456 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2456 host target proteins.

[34350] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2456 gene, herein designated VGAM GENE, on one or more VGAM2456 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34351] It is yet further appreciated that a function of VGAM2456 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2456 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2456 correlate with, and may be deduced from, the identity of the host target genes which VGAM2456 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[34352] Nucleotide sequences of the VGAM2456 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2456 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2456 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2456 are further described hereinbelow with reference to Table 1.

[34353] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2456 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[34354] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2457 (VGAM2457) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[34355] VGAM2457 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2457 was detected is described hereinabove with reference to Figs. 2-8.

[34356] VGAM2457 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2457 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[34357] VGAM2457 gene, herein designated VGAM GENE, encodes a VGAM2457 precursor RNA, herein designated VGAM

PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2457 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2457 precursor RNA is designated SEQ ID:2443, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2443 is located at position 49086 relative to the genome of Mouse cytomegalovirus 1.

[34358] VGAM2457 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2457 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34359] An enzyme complex designated DICER COMPLEX, dices the VGAM2457 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2457 RNA,

herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2457 RNA is designated SEQ ID:5168, and is provided hereinbelow with reference to the sequence listing part.

[34360] VGAM2457 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2457 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2457 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34361] VGAM2457 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2457 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM2457 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2457 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2457 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34362] The complementary binding of VGAM2457 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2457 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2457 host target RNA, herein designated VGAM HOST TARGET

RNA, into VGAM2457 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[34363] It is appreciated that VGAM2457 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2457 host target genes. The mRNA of each one of this plurality of VGAM2457 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2457 RNA, herein designated VGAM RNA, and which when bound by VGAM2457 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2457 host target proteins.

[34364] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2457 gene, herein designated VGAM GENE, on one or more VGAM2457 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34365] It is yet further appreciated that a function of VGAM2457 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2457 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2457 correlate with, and may be deduced from, the identity of the host target genes which VGAM2457 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[34366] Nucleotide sequences of the VGAM2457 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2457 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2457 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2457 are further

described hereinbelow with reference to Table 1.

[34367] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2457 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[34368] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2458 (VGAM2458) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[34369] VGAM2458 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2458 was detected is described hereinabove with reference to Figs. 2-8.

[34370] VGAM2458 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2458 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[34371] VGAM2458 gene, herein designated VGAM GENE, encodes a VGAM2458 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2458 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2458 precursor RNA is designated SEQ ID:2444, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2444 is located at position 183475 relative to the genome of Mouse cytomegalovirus 1.

[34372] VGAM2458 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2458 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34373] An enzyme complex designated DICER COMPLEX, dices

the VGAM2458 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2458 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 65%) nucleotide sequence of VGAM2458 RNA is designated SEQ ID:5169, and is provided hereinbelow with reference to the sequence listing part.

[34374] VGAM2458 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2458 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2458 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34375] VGAM2458 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2458 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2458 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2458 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2458 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34376] The complementary binding of VGAM2458 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2458 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM2458 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2458 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[34377] It is appreciated that VGAM2458 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2458 host target genes. The mRNA of each one of this plurality of VGAM2458 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2458 RNA, herein designated VGAM RNA, and which when bound by VGAM2458 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2458 host target proteins.

[34378] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2458 gene, herein designated VGAM GENE, on one or more VGAM2458 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34379] It is yet further appreciated that a function of VGAM2458 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2458 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2458 correlate with, and may be deduced from, the identity of the host target genes which VGAM2458 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[34380] Nucleotide sequences of the VGAM2458 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2458 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of

VGAM2458 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2458 are further described hereinbelow with reference to Table 1.

[34381] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2458 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[34382] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2459 (VGAM2459) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[34383] VGAM2459 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2459 was detected is described hereinabove with reference to Figs. 2-8.

[34384] VGAM2459 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2459 host target gene, herein designated VGAM

HOST TARGET GENE, is a human gene contained in the human genome.

[34385] VGAM2459 gene, herein designated VGAM GENE, encodes a VGAM2459 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2459 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2459 precursor RNA is designated SEQ ID:2445, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2445 is located at position 121309 relative to the genome of Mouse cytomegalovirus 1.

[34386] VGAM2459 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2459 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[34387] An enzyme complex designated DICER COMPLEX, dices the VGAM2459 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2459 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 48%) nucleotide sequence of VGAM2459 RNA is designated SEQ ID:5170, and is provided hereinbelow with reference to the sequence listing part.

[34388] VGAM2459 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2459 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2459 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34389] VGAM2459 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM2459 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2459 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2459 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2459 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34390] The complementary binding of VGAM2459 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM2459 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2459 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2459 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[34391] It is appreciated that VGAM2459 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2459 host target genes. The mRNA of each one of this plurality of VGAM2459 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2459 RNA, herein designated VGAM RNA, and which when bound by VGAM2459 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2459 host target proteins.

[34392] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2459 gene, herein designated VGAM GENE, on one or more VGAM2459 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34393] It is yet further appreciated that a function of VGAM2459 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2459 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2459 correlate with, and may be deduced from, the identity of the host target genes which VGAM2459 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[34394] Nucleotide sequences of the VGAM2459 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

diced VGAM2459 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2459 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2459 are further described hereinbelow with reference to Table 1.

[34395] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2459 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[34396] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2460 (VGAM2460) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[34397] VGAM2460 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2460 was detected is described hereinabove with reference to Figs. 2-8.

[34398] VGAM2460 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of Mouse cytomegalovirus 1. VGAM2460 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[34399] VGAM2460 gene, herein designated VGAM GENE, encodes a VGAM2460 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2460 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2460 precursor RNA is designated SEQ ID:2446, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2446 is located at position 17895 relative to the genome of Mouse cytomegalovirus 1.

[34400] VGAM2460 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2460 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34401] An enzyme complex designated DICER COMPLEX, dices the VGAM2460 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2460 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2460 RNA is designated SEQ ID:5171, and is provided hereinbelow with reference to the sequence listing part.

[34402] VGAM2460 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2460 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2460 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN COD-

ING and 3UTR respectively.

[34403] VGAM2460 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2460 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2460 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2460 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2460 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34404] The complementary binding of VGAM2460 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2460 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2460 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2460 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[34405] It is appreciated that VGAM2460 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2460 host target genes. The mRNA of each one of this plurality of VGAM2460 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2460 RNA, herein designated VGAM RNA, and which when bound by VGAM2460 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2460 host target proteins.

[34406] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2460 gene, herein designated VGAM GENE, on one

or more VGAM2460 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34407] It is yet further appreciated that a function of VGAM2460 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2460 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2460 correlate with, and may be deduced from, the identity of the host target genes which VGAM2460 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[34408] Nucleotide sequences of the VGAM2460 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2460 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2460 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2460 are further described hereinbelow with reference to Table 1.

[34409] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2460 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[34410] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2461 (VGAM2461) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[34411] VGAM2461 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2461 was detected is de-

scribed hereinabove with reference to Figs. 2-8.

[34412] VGAM2461 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2461 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[34413] VGAM2461 gene, herein designated VGAM GENE, encodes a VGAM2461 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2461 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2461 precursor RNA is designated SEQ ID:2447, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2447 is located at position 219567 relative to the genome of Mouse cytomegalovirus 1.

[34414] VGAM2461 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2461 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34415] An enzyme complex designated DICER COMPLEX, dices the VGAM2461 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2461 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2461 RNA is designated SEQ ID:5172, and is provided hereinbelow with reference to the sequence listing part.

[34416] VGAM2461 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2461 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2461 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding

gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34417] VGAM2461 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2461 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2461 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2461 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2461 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be lo-

cated in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34418] The complementary binding of VGAM2461 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2461 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2461 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2461 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[34419] It is appreciated that VGAM2461 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2461 host target genes. The mRNA of each one of this plurality of VGAM2461 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2461 RNA, herein designated VGAM RNA, and which when bound by VGAM2461 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2461 host target proteins.

[34420] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM2461 gene, herein designated VGAM GENE, on one or more VGAM2461 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34421] It is yet further appreciated that a function of VGAM2461 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2461 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2461 correlate with, and may be deduced from, the identity of the host target genes which VGAM2461 binds and in-

hibits, and the function of these host target genes, as elaborated hereinbelow.

[34422] Nucleotide sequences of the VGAM2461 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2461 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2461 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2461 are further described hereinbelow with reference to Table 1.

[34423] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2461 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[34424] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2462 (VGAM2462) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[34425] VGAM2462 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2462 was detected is described hereinabove with reference to Figs. 2-8.

[34426] VGAM2462 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2462 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[34427] VGAM2462 gene, herein designated VGAM GENE, encodes a VGAM2462 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2462 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2462 precursor RNA is designated SEQ ID:2448, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2448 is located at position 164 relative to the genome of Mouse cytomegalovirus 1.

[34428] VGAM2462 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2462 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34429] An enzyme complex designated DICER COMPLEX, dices the VGAM2462 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2462 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 48%) nucleotide sequence of VGAM2462 RNA is designated SEQ ID:5173, and is provided hereinbelow with reference to the sequence listing part.

[34430] VGAM2462 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2462 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2462 host target RNA, herein designated VGAM HOST TARGET RNA, comprises

three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34431] VGAM2462 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2462 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2462 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2462 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2462 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an

example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34432] The complementary binding of VGAM2462 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2462 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2462 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2462 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[34433] It is appreciated that VGAM2462 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2462 host target genes. The mRNA of each one of this plurality of VGAM2462 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2462 RNA, herein designated VGAM RNA, and which when bound by VGAM2462 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2462 host target proteins.

[34434] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2462 gene, herein designated VGAM GENE, on one or more VGAM2462 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34435] It is yet further appreciated that a function of VGAM2462 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2462 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2462 correlate with, and may be deduced from, the identity of

the host target genes which VGAM2462 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[34436] Nucleotide sequences of the VGAM2462 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2462 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2462 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2462 are further described hereinbelow with reference to Table 1.

[34437] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2462 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[34438] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2463 (VGAM2463) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[34439] VGAM2463 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2463 was detected is described hereinabove with reference to Figs. 2-8.

[34440] VGAM2463 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2463 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[34441] VGAM2463 gene, herein designated VGAM GENE, encodes a VGAM2463 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2463 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2463 precursor RNA is designated SEQ ID:2449, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2449 is located at position 225478 relative to the genome of Mouse cytomegalovirus 1.

[34442] VGAM2463 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2463 folded

precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34443] An enzyme complex designated DICER COMPLEX, dices the VGAM2463 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2463 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2463 RNA is designated SEQ ID:5174, and is provided hereinbelow with reference to the sequence listing part.

[34444] VGAM2463 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2463 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM2463 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34445] VGAM2463 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2463 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2463 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2463 host target RNA, herein designated VGAM HOST TARGET RNA.

It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34446] The complementary binding of VGAM2463 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2463 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2463 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2463 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[34447] It is appreciated that VGAM2463 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2463 host target genes. The mRNA of each one of this plurality of VGAM2463 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2463 RNA, herein designated VGAM RNA, and which when bound by VGAM2463 RNA, herein designated VGAM RNA, causes inhibition of translation of

respective one or more VGAM2463 host target proteins.

[34448] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2463 gene, herein designated VGAM GENE, on one or more VGAM2463 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34449] It is yet further appreciated that a function of VGAM2463 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1.

Specific functions, and accordingly utilities, of VGAM2463 correlate with, and may be deduced from, the identity of the host target genes which VGAM2463 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[34450] Nucleotide sequences of the VGAM2463 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2463 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2463 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2463 are further described hereinbelow with reference to Table 1.

[34451] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2463 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[34452] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2464 (VGAM2464) viral gene, which modulates expression of respective host target genes thereof, the func-

tion and utility of which host target genes is known in the art.

[34453] VGAM2464 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2464 was detected is described hereinabove with reference to Figs. 2-8.

[34454] VGAM2464 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2464 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[34455] VGAM2464 gene, herein designated VGAM GENE, encodes a VGAM2464 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2464 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2464 precursor RNA is designated SEQ ID:2450, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2450 is located at position 225307 relative to the genome of Mouse cytomegalovirus 1.

[34456] VGAM2464 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2464 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34457] An enzyme complex designated DICER COMPLEX, dices the VGAM2464 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2464 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2464 RNA is designated SEQ ID:5175, and is provided hereinbelow with reference to the sequence listing part.

[34458] VGAM2464 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2464 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2464 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34459] VGAM2464 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2464 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2464 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2464 RNA, herein designated VGAM RNA, may have a different number of host target

binding sites in untranslated regions of a VGAM2464 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34460] The complementary binding of VGAM2464 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2464 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2464 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2464 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[34461] It is appreciated that VGAM2464 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2464 host target genes. The mRNA of each one of this plurality of VGAM2464 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2464 RNA, herein designated VGAM

RNA, and which when bound by VGAM2464 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2464 host target proteins.

[34462] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2464 gene, herein designated VGAM GENE, on one or more VGAM2464 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34463] It is yet further appreciated that a function of VGAM2464 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM2464 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2464 correlate with, and may be deduced from, the identity of the host target genes which VGAM2464 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[34464] Nucleotide sequences of the VGAM2464 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2464 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2464 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2464 are further described hereinbelow with reference to Table 1.

[34465] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2464 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[34466] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Mes-

senger 2465 (VGAM2465) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[34467] VGAM2465 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2465 was detected is described hereinabove with reference to Figs. 2-8.

[34468] VGAM2465 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2465 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[34469] VGAM2465 gene, herein designated VGAM GENE, encodes a VGAM2465 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2465 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2465 precursor RNA is designated SEQ ID:2451, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2451 is located at position

161125 relative to the genome of Mouse cytomegalovirus 1.

[34470] VGAM2465 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2465 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34471] An enzyme complex designated DICER COMPLEX, dices the VGAM2465 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2465 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2465 RNA is designated SEQ ID:5176, and is provided hereinbelow with reference to the sequence

listing part.

[34472] VGAM2465 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2465 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2465 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34473] VGAM2465 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2465 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2465 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not

meant to be limiting VGAM2465 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2465 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34474] The complementary binding of VGAM2465 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2465 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2465 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2465 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[34475] It is appreciated that VGAM2465 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2465 host target genes. The mRNA of each one of this plurality of VGAM2465 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2465 RNA, herein designated VGAM RNA, and which when bound by VGAM2465 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2465 host target proteins.

[34476] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2465 gene, herein designated VGAM GENE, on one or more VGAM2465 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34477] It is yet further appreciated that a function of VGAM2465

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2465 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2465 correlate with, and may be deduced from, the identity of the host target genes which VGAM2465 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[34478] Nucleotide sequences of the VGAM2465 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2465 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2465 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2465 are further described hereinbelow with reference to Table 1.

[34479] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2465 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[34480] Fig. 1 further provides a conceptual description of another

novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2466 (VGAM2466) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[34481] VGAM2466 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2466 was detected is described hereinabove with reference to Figs. 2-8.

[34482] VGAM2466 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2466 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[34483] VGAM2466 gene, herein designated VGAM GENE, encodes a VGAM2466 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2466 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2466 precursor RNA is designated SEQ ID:2452, and is provided here-

inbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2452 is located at position 94468 relative to the genome of Mouse cytomegalovirus 1.

[34484] VGAM2466 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2466 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34485] An enzyme complex designated DICER COMPLEX, dices the VGAM2466 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2466 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 52%) nucleotide se-

quence of VGAM2466 RNA is designated SEQ ID:5177, and is provided hereinbelow with reference to the sequence listing part.

[34486] VGAM2466 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2466 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2466 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34487] VGAM2466 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2466 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2466 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is ap-

preciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2466 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2466 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34488] The complementary binding of VGAM2466 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2466 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2466 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2466 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[34489] It is appreciated that VGAM2466 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2466 host target genes. The mRNA of

each one of this plurality of VGAM2466 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2466 RNA, herein designated VGAM RNA, and which when bound by VGAM2466 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2466 host target proteins.

[34490] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2466 gene, herein designated VGAM GENE, on one or more VGAM2466 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science

294,779 (2001)).

[34491] It is yet further appreciated that a function of VGAM2466 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2466 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2466 correlate with, and may be deduced from, the identity of the host target genes which VGAM2466 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[34492] Nucleotide sequences of the VGAM2466 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2466 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2466 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2466 are further described hereinbelow with reference to Table 1.

[34493] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2466 RNA, herein designated VGAM RNA, are de-

scribed hereinbelow with reference to Table 2.

[34494] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2467 (VGAM2467) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[34495] VGAM2467 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2467 was detected is described hereinabove with reference to Figs. 2-8.

[34496] VGAM2467 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2467 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[34497] VGAM2467 gene, herein designated VGAM GENE, encodes a VGAM2467 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2467 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly

similar to the nucleotide sequence of VGAM2467 precursor RNA is designated SEQ ID:2453, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2453 is located at position 175100 relative to the genome of Mouse cytomegalovirus 1.

[34498] VGAM2467 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2467 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34499] An enzyme complex designated DICER COMPLEX, dices the VGAM2467 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2467 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2467 RNA is designated SEQ ID:5178, and is provided hereinbelow with reference to the sequence listing part.

[34500] VGAM2467 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2467 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2467 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34501] VGAM2467 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2467 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2467 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3

such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2467 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2467 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34502] The complementary binding of VGAM2467 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2467 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2467 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2467 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[34503] It is appreciated that VGAM2467 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2467 host target genes. The mRNA of each one of this plurality of VGAM2467 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2467 RNA, herein designated VGAM RNA, and which when bound by VGAM2467 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2467 host target proteins.

[34504] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2467 gene, herein designated VGAM GENE, on one or more VGAM2467 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34505] It is yet further appreciated that a function of VGAM2467 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2467 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2467 correlate with, and may be deduced from, the identity of the host target genes which VGAM2467 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[34506] Nucleotide sequences of the VGAM2467 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2467 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2467 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2467 are further described hereinbelow with reference to Table 1.

[34507] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the

complementarity of each of these host target binding sites to VGAM2467 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[34508] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2468 (VGAM2468) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[34509] VGAM2468 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2468 was detected is described hereinabove with reference to Figs. 2-8.

[34510] VGAM2468 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2468 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[34511] VGAM2468 gene, herein designated VGAM GENE, encodes a VGAM2468 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2468 precursor RNA,

herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2468 precursor RNA is designated SEQ ID:2454, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2454 is located at position 64210 relative to the genome of Mouse cytomegalovirus 1.

[34512] VGAM2468 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2468 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34513] An enzyme complex designated DICER COMPLEX, dices the VGAM2468 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2468 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2468 RNA is designated SEQ ID:5179, and is provided hereinbelow with reference to the sequence listing part.

[34514] VGAM2468 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2468 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2468 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34515] VGAM2468 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2468 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2468 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed

sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2468 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2468 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34516] The complementary binding of VGAM2468 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2468 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2468 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2468 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target

protein is therefore outlined by a broken line.

[34517] It is appreciated that VGAM2468 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2468 host target genes. The mRNA of each one of this plurality of VGAM2468 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2468 RNA, herein designated VGAM RNA, and which when bound by VGAM2468 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2468 host target proteins.

[34518] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2468 gene, herein designated VGAM GENE, on one or more VGAM2468 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34519] It is yet further appreciated that a function of VGAM2468 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2468 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2468 correlate with, and may be deduced from, the identity of the host target genes which VGAM2468 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[34520] Nucleotide sequences of the VGAM2468 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2468 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2468 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2468 are further described hereinbelow with reference to Table 1.

[34521] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2468 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[34522] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2469 (VGAM2469) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[34523] VGAM2469 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2469 was detected is described hereinabove with reference to Figs. 2-8.

[34524] VGAM2469 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2469 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[34525] VGAM2469 gene, herein designated VGAM GENE, encodes a VGAM2469 precursor RNA, herein designated VGAM

PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2469 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2469 precursor RNA is designated SEQ ID:2455, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2455 is located at position 226054 relative to the genome of Mouse cytomegalovirus 1.

[34526] VGAM2469 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2469 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34527] An enzyme complex designated DICER COMPLEX, dices the VGAM2469 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2469 RNA,

herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2469 RNA is designated SEQ ID:5180, and is provided hereinbelow with reference to the sequence listing part.

[34528] VGAM2469 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2469 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2469 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34529] VGAM2469 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2469 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM2469 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2469 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2469 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34530] The complementary binding of VGAM2469 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2469 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2469 host target RNA, herein designated VGAM HOST TARGET

RNA, into VGAM2469 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[34531] It is appreciated that VGAM2469 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2469 host target genes. The mRNA of each one of this plurality of VGAM2469 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2469 RNA, herein designated VGAM RNA, and which when bound by VGAM2469 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2469 host target proteins.

[34532] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2469 gene, herein designated VGAM GENE, on one or more VGAM2469 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34533] It is yet further appreciated that a function of VGAM2469 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2469 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2469 correlate with, and may be deduced from, the identity of the host target genes which VGAM2469 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[34534] Nucleotide sequences of the VGAM2469 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2469 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2469 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2469 are further

described hereinbelow with reference to Table 1.

[34535] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2469 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[34536] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2470 (VGAM2470) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[34537] VGAM2470 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2470 was detected is described hereinabove with reference to Figs. 2-8.

[34538] VGAM2470 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2470 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[34539] VGAM2470 gene, herein designated VGAM GENE, encodes a VGAM2470 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2470 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2470 precursor RNA is designated SEQ ID:2456, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2456 is located at position 195573 relative to the genome of Mouse cytomegalovirus 1.

[34540] VGAM2470 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2470 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34541] An enzyme complex designated DICER COMPLEX, dices

the VGAM2470 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2470 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2470 RNA is designated SEQ ID:5181, and is provided hereinbelow with reference to the sequence listing part.

[34542] VGAM2470 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2470 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2470 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34543] VGAM2470 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2470 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2470 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2470 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2470 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34544] The complementary binding of VGAM2470 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2470 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM2470 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2470 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[34545] It is appreciated that VGAM2470 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2470 host target genes. The mRNA of each one of this plurality of VGAM2470 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2470 RNA, herein designated VGAM RNA, and which when bound by VGAM2470 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2470 host target proteins.

[34546] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2470 gene, herein designated VGAM GENE, on one or more VGAM2470 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34547] It is yet further appreciated that a function of VGAM2470 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2470 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2470 correlate with, and may be deduced from, the identity of the host target genes which VGAM2470 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[34548] Nucleotide sequences of the VGAM2470 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2470 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of

VGAM2470 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2470 are further described hereinbelow with reference to Table 1.

[34549] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2470 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[34550] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2471 (VGAM2471) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[34551] VGAM2471 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2471 was detected is described hereinabove with reference to Figs. 2-8.

[34552] VGAM2471 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2471 host target gene, herein designated VGAM

HOST TARGET GENE, is a human gene contained in the human genome.

[34553] VGAM2471 gene, herein designated VGAM GENE, encodes a VGAM2471 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2471 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2471 precursor RNA is designated SEQ ID:2457, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2457 is located at position 2006 relative to the genome of Mouse cytomegalovirus 1.

[34554] VGAM2471 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2471 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34555] An enzyme complex designated DICER COMPLEX, dices the VGAM2471 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2471 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2471 RNA is designated SEQ ID:5182, and is provided hereinbelow with reference to the sequence listing part.

[34556] VGAM2471 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2471 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2471 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34557] VGAM2471 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites

located in untranslated regions of VGAM2471 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2471 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2471 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2471 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34558] The complementary binding of VGAM2471 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2471 host target RNA, herein designated VGAM

HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2471 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2471 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[34559] It is appreciated that VGAM2471 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2471 host target genes. The mRNA of each one of this plurality of VGAM2471 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2471 RNA, herein designated VGAM RNA, and which when bound by VGAM2471 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2471 host target proteins.

[34560] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2471 gene, herein designated VGAM GENE, on one or more VGAM2471 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove

with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34561] It is yet further appreciated that a function of VGAM2471 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2471 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2471 correlate with, and may be deduced from, the identity of the host target genes which VGAM2471 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[34562] Nucleotide sequences of the VGAM2471 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2471 RNA, herein designated VGAM RNA, and

a schematic representation of the secondary folding of VGAM2471 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2471 are further described hereinbelow with reference to Table 1.

[34563] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2471 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[34564] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2472 (VGAM2472) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[34565] VGAM2472 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2472 was detected is described hereinabove with reference to Figs. 2-8.

[34566] VGAM2472 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus

1. VGAM2472 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[34567] VGAM2472 gene, herein designated VGAM GENE, encodes a VGAM2472 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2472 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2472 precursor RNA is designated SEQ ID:2458, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2458 is located at position 116628 relative to the genome of Mouse cytomegalovirus 1.

[34568] VGAM2472 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2472 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34569] An enzyme complex designated DICER COMPLEX, dices the VGAM2472 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2472 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2472 RNA is designated SEQ ID:5183, and is provided hereinbelow with reference to the sequence listing part.

[34570] VGAM2472 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2472 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2472 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34571] VGAM2472 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2472 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2472 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2472 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2472 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34572] The complementary binding of VGAM2472 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM2472 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2472 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2472 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[34573] It is appreciated that VGAM2472 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2472 host target genes. The mRNA of each one of this plurality of VGAM2472 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2472 RNA, herein designated VGAM RNA, and which when bound by VGAM2472 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2472 host target proteins.

[34574] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2472 gene, herein designated VGAM GENE, on one or more VGAM2472 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34575] It is yet further appreciated that a function of VGAM2472 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2472 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2472 correlate with, and may be deduced from, the identity of the host target genes which VGAM2472 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[34576] Nucleotide sequences of the VGAM2472 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the diced VGAM2472 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2472 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2472 are further described hereinbelow with reference to Table 1.

[34577] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2472 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[34578] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2473 (VGAM2473) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[34579] VGAM2473 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2473 was detected is described hereinabove with reference to Figs. 2-8.

[34580] VGAM2473 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2473 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[34581] VGAM2473 gene, herein designated VGAM GENE, encodes a VGAM2473 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2473 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2473 precursor RNA is designated SEQ ID:2459, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2459 is located at position 101492 relative to the genome of Mouse cytomegalovirus 1.

[34582] VGAM2473 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2473 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34583] An enzyme complex designated DICER COMPLEX, dices the VGAM2473 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2473 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2473 RNA is designated SEQ ID:5184, and is provided hereinbelow with reference to the sequence listing part.

[34584] VGAM2473 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2473 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2473 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and

a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34585] VGAM2473 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2473 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2473 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2473 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2473 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both

3UTR and 5UTR regions.

[34586] The complementary binding of VGAM2473 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2473 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2473 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2473 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[34587] It is appreciated that VGAM2473 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2473 host target genes. The mRNA of each one of this plurality of VGAM2473 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2473 RNA, herein designated VGAM RNA, and which when bound by VGAM2473 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2473 host target proteins.

[34588] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM2473 gene, herein designated VGAM GENE, on one or more VGAM2473 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34589] It is yet further appreciated that a function of VGAM2473 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2473 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2473 correlate with, and may be deduced from, the identity of the host target genes which VGAM2473 binds and inhibits, and the function of these host target genes, as

elaborated hereinbelow.

[34590] Nucleotide sequences of the VGAM2473 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2473 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2473 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2473 are further described hereinbelow with reference to Table 1.

[34591] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2473 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[34592] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2474 (VGAM2474) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[34593] VGAM2474 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene.

The method by which VGAM2474 was detected is described hereinabove with reference to Figs. 2-8.

[34594] VGAM2474 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2474 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[34595] VGAM2474 gene, herein designated VGAM GENE, encodes a VGAM2474 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2474 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2474 precursor RNA is designated SEQ ID:2460, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2460 is located at position 82294 relative to the genome of Mouse cytomegalovirus 1.

[34596] VGAM2474 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2474 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34597] An enzyme complex designated DICER COMPLEX, dices the VGAM2474 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2474 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2474 RNA is designated SEQ ID:5185, and is provided hereinbelow with reference to the sequence listing part.

[34598] VGAM2474 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2474 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2474 host target RNA, herein designated VGAM HOST TARGET RNA, comprises

three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34599] VGAM2474 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2474 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2474 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2474 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2474 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an

example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34600] The complementary binding of VGAM2474 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2474 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2474 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2474 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[34601] It is appreciated that VGAM2474 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2474 host target genes. The mRNA of each one of this plurality of VGAM2474 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2474 RNA, herein designated VGAM RNA, and which when bound by VGAM2474 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2474 host target proteins.

[34602] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2474 gene, herein designated VGAM GENE, on one or more VGAM2474 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34603] It is yet further appreciated that a function of VGAM2474 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2474 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2474 correlate with, and may be deduced from, the identity of

the host target genes which VGAM2474 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[34604] Nucleotide sequences of the VGAM2474 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2474 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2474 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2474 are further described hereinbelow with reference to Table 1.

[34605] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2474 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[34606] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2475 (VGAM2475) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[34607] VGAM2475 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2475 was detected is described hereinabove with reference to Figs. 2-8.

[34608] VGAM2475 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2475 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[34609] VGAM2475 gene, herein designated VGAM GENE, encodes a VGAM2475 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2475 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2475 precursor RNA is designated SEQ ID:2461, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2461 is located at position 190173 relative to the genome of Mouse cytomegalovirus 1.

[34610] VGAM2475 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2475 folded

precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34611] An enzyme complex designated DICER COMPLEX, dices the VGAM2475 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2475 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2475 RNA is designated SEQ ID:5186, and is provided hereinbelow with reference to the sequence listing part.

[34612] VGAM2475 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2475 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM2475 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34613] VGAM2475 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2475 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2475 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2475 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2475 host target RNA, herein designated VGAM HOST TARGET RNA.

It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34614] The complementary binding of VGAM2475 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2475 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2475 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2475 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[34615] It is appreciated that VGAM2475 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2475 host target genes. The mRNA of each one of this plurality of VGAM2475 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2475 RNA, herein designated VGAM RNA, and which when bound by VGAM2475 RNA, herein designated VGAM RNA, causes inhibition of translation of

respective one or more VGAM2475 host target proteins.

[34616] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2475 gene, herein designated VGAM GENE, on one or more VGAM2475 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34617] It is yet further appreciated that a function of VGAM2475 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2475 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1.

Specific functions, and accordingly utilities, of VGAM2475 correlate with, and may be deduced from, the identity of the host target genes which VGAM2475 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[34618] Nucleotide sequences of the VGAM2475 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2475 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2475 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2475 are further described hereinbelow with reference to Table 1.

[34619] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2475 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[34620] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2476 (VGAM2476) viral gene, which modulates expression of respective host target genes thereof, the func-

tion and utility of which host target genes is known in the art.

[34621] VGAM2476 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2476 was detected is described hereinabove with reference to Figs. 2-8.

[34622] VGAM2476 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2476 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[34623] VGAM2476 gene, herein designated VGAM GENE, encodes a VGAM2476 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2476 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2476 precursor RNA is designated SEQ ID:2462, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2462 is located at position 136488 relative to the genome of Mouse cytomegalovirus 1.

[34624] VGAM2476 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2476 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34625] An enzyme complex designated DICER COMPLEX, dices the VGAM2476 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2476 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2476 RNA is designated SEQ ID:5187, and is provided hereinbelow with reference to the sequence listing part.

[34626] VGAM2476 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2476 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2476 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34627] VGAM2476 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2476 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2476 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2476 RNA, herein designated VGAM RNA, may have a different number of host target

binding sites in untranslated regions of a VGAM2476 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34628] The complementary binding of VGAM2476 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2476 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2476 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2476 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[34629] It is appreciated that VGAM2476 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2476 host target genes. The mRNA of each one of this plurality of VGAM2476 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2476 RNA, herein designated VGAM

RNA, and which when bound by VGAM2476 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2476 host target proteins.

[34630] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2476 gene, herein designated VGAM GENE, on one or more VGAM2476 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34631] It is yet further appreciated that a function of VGAM2476 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM2476 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2476 correlate with, and may be deduced from, the identity of the host target genes which VGAM2476 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[34632] Nucleotide sequences of the VGAM2476 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2476 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2476 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2476 are further described hereinbelow with reference to Table 1.

[34633] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2476 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[34634] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Mes-

senger 2477 (VGAM2477) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[34635] VGAM2477 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2477 was detected is described hereinabove with reference to Figs. 2-8.

[34636] VGAM2477 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2477 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[34637] VGAM2477 gene, herein designated VGAM GENE, encodes a VGAM2477 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2477 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2477 precursor RNA is designated SEQ ID:2463, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2463 is located at position

205607 relative to the genome of Mouse cytomegalovirus 1.

[34638] VGAM2477 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2477 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34639] An enzyme complex designated DICER COMPLEX, dices the VGAM2477 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2477 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2477 RNA is designated SEQ ID:5188, and is provided hereinbelow with reference to the sequence

listing part.

[34640] VGAM2477 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2477 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2477 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34641] VGAM2477 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2477 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2477 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not

meant to be limiting VGAM2477 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2477 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34642] The complementary binding of VGAM2477 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2477 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2477 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2477 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[34643] It is appreciated that VGAM2477 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2477 host target genes. The mRNA of each one of this plurality of VGAM2477 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2477 RNA, herein designated VGAM RNA, and which when bound by VGAM2477 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2477 host target proteins.

[34644] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2477 gene, herein designated VGAM GENE, on one or more VGAM2477 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34645] It is yet further appreciated that a function of VGAM2477

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2477 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2477 correlate with, and may be deduced from, the identity of the host target genes which VGAM2477 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[34646] Nucleotide sequences of the VGAM2477 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2477 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2477 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2477 are further described hereinbelow with reference to Table 1.

[34647] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2477 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[34648] Fig. 1 further provides a conceptual description of another

novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2478 (VGAM2478) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[34649] VGAM2478 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2478 was detected is described hereinabove with reference to Figs. 2-8.

[34650] VGAM2478 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2478 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[34651] VGAM2478 gene, herein designated VGAM GENE, encodes a VGAM2478 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2478 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2478 precursor RNA is designated SEQ ID:2464, and is provided here-

inbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2464 is located at position 55947 relative to the genome of Mouse cytomegalovirus 1.

[34652] VGAM2478 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2478 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34653] An enzyme complex designated DICER COMPLEX, dices the VGAM2478 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2478 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide se-

quence of VGAM2478 RNA is designated SEQ ID:5189, and is provided hereinbelow with reference to the sequence listing part.

[34654] VGAM2478 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2478 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2478 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34655] VGAM2478 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2478 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2478 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is ap-

preciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2478 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2478 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34656] The complementary binding of VGAM2478 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2478 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2478 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2478 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[34657] It is appreciated that VGAM2478 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2478 host target genes. The mRNA of

each one of this plurality of VGAM2478 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2478 RNA, herein designated VGAM RNA, and which when bound by VGAM2478 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2478 host target proteins.

[34658] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2478 gene, herein designated VGAM GENE, on one or more VGAM2478 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science

294,779 (2001)).

[34659] It is yet further appreciated that a function of VGAM2478 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2478 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2478 correlate with, and may be deduced from, the identity of the host target genes which VGAM2478 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[34660] Nucleotide sequences of the VGAM2478 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2478 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2478 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2478 are further described hereinbelow with reference to Table 1.

[34661] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2478 RNA, herein designated VGAM RNA, are de-

scribed hereinbelow with reference to Table 2.

[34662] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2479 (VGAM2479) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[34663] VGAM2479 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2479 was detected is described hereinabove with reference to Figs. 2-8.

[34664] VGAM2479 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2479 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[34665] VGAM2479 gene, herein designated VGAM GENE, encodes a VGAM2479 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2479 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2479 precursor RNA is designated SEQ ID:2465, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2465 is located at position 167759 relative to the genome of Mouse cytomegalovirus 1.

[34666] VGAM2479 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2479 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34667] An enzyme complex designated DICER COMPLEX, dices

the VGAM2479 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2479 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2479 RNA is designated SEQ ID:5190, and is provided hereinbelow with reference to the sequence listing part.

[34668] VGAM2479 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2479 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2479 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34669] VGAM2479 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2479 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2479 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2479 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2479 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34670] The complementary binding of VGAM2479 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2479 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM2479 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2479 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[34671] It is appreciated that VGAM2479 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2479 host target genes. The mRNA of each one of this plurality of VGAM2479 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2479 RNA, herein designated VGAM RNA, and which when bound by VGAM2479 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2479 host target proteins.

[34672] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2479 gene, herein designated VGAM GENE, on one or more VGAM2479 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34673] It is yet further appreciated that a function of VGAM2479 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2479 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2479 correlate with, and may be deduced from, the identity of the host target genes which VGAM2479 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[34674] Nucleotide sequences of the VGAM2479 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2479 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of

VGAM2479 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2479 are further described hereinbelow with reference to Table 1.

[34675] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2479 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[34676] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2480 (VGAM2480) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[34677] VGAM2480 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2480 was detected is described hereinabove with reference to Figs. 2-8.

[34678] VGAM2480 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2480 host target gene, herein designated VGAM

HOST TARGET GENE, is a human gene contained in the human genome.

[34679] VGAM2480 gene, herein designated VGAM GENE, encodes a VGAM2480 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2480 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2480 precursor RNA is designated SEQ ID:2466, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2466 is located at position 131305 relative to the genome of Mouse cytomegalovirus 1.

[34680] VGAM2480 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2480 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[34681] An enzyme complex designated DICER COMPLEX, dices the VGAM2480 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2480 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2480 RNA is designated SEQ ID:5191, and is provided hereinbelow with reference to the sequence listing part.

[34682] VGAM2480 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2480 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2480 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34683] VGAM2480 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM2480 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2480 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2480 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2480 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34684] The complementary binding of VGAM2480 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM2480 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2480 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2480 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[34685] It is appreciated that VGAM2480 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2480 host target genes. The mRNA of each one of this plurality of VGAM2480 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2480 RNA, herein designated VGAM RNA, and which when bound by VGAM2480 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2480 host target proteins.

[34686] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2480 gene, herein designated VGAM GENE, on one or more VGAM2480 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34687] It is yet further appreciated that a function of VGAM2480 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2480 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2480 correlate with, and may be deduced from, the identity of the host target genes which VGAM2480 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[34688] Nucleotide sequences of the VGAM2480 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

diced VGAM2480 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2480 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2480 are further described hereinbelow with reference to Table 1.

[34689] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2480 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[34690] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2481 (VGAM2481) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[34691] VGAM2481 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2481 was detected is described hereinabove with reference to Figs. 2-8.

[34692] VGAM2481 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of Mouse cytomegalovirus 1. VGAM2481 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[34693] VGAM2481 gene, herein designated VGAM GENE, encodes a VGAM2481 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2481 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2481 precursor RNA is designated SEQ ID:2467, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2467 is located at position 96988 relative to the genome of Mouse cytomegalovirus 1.

[34694] VGAM2481 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2481 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34695] An enzyme complex designated DICER COMPLEX, dices the VGAM2481 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2481 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 68%) nucleotide sequence of VGAM2481 RNA is designated SEQ ID:5192, and is provided hereinbelow with reference to the sequence listing part.

[34696] VGAM2481 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2481 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2481 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN COD-

ING and 3UTR respectively.

[34697] VGAM2481 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2481 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2481 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2481 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2481 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34698] The complementary binding of VGAM2481 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2481 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2481 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2481 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[34699] It is appreciated that VGAM2481 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2481 host target genes. The mRNA of each one of this plurality of VGAM2481 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2481 RNA, herein designated VGAM RNA, and which when bound by VGAM2481 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2481 host target proteins.

[34700] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2481 gene, herein designated VGAM GENE, on one

or more VGAM2481 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34701] It is yet further appreciated that a function of VGAM2481 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2481 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2481 correlate with, and may be deduced from, the identity of the host target genes which VGAM2481 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[34702] Nucleotide sequences of the VGAM2481 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2481 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2481 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2481 are further described hereinbelow with reference to Table 1.

[34703] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2481 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[34704] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2482 (VGAM2482) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[34705] VGAM2482 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2482 was detected is de-

scribed hereinabove with reference to Figs. 2-8.

[34706] VGAM2482 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2482 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[34707] VGAM2482 gene, herein designated VGAM GENE, encodes a VGAM2482 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2482 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2482 precursor RNA is designated SEQ ID:2468, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2468 is located at position 182861 relative to the genome of Mouse cytomegalovirus 1.

[34708] VGAM2482 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2482 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34709] An enzyme complex designated DICER COMPLEX, dices the VGAM2482 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2482 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2482 RNA is designated SEQ ID:5193, and is provided hereinbelow with reference to the sequence listing part.

[34710] VGAM2482 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2482 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2482 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding

gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34711] VGAM2482 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2482 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2482 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2482 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2482 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be lo-

cated in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34712] The complementary binding of VGAM2482 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2482 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2482 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2482 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[34713] It is appreciated that VGAM2482 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2482 host target genes. The mRNA of each one of this plurality of VGAM2482 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2482 RNA, herein designated VGAM RNA, and which when bound by VGAM2482 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2482 host target proteins.

[34714] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM2482 gene, herein designated VGAM GENE, on one or more VGAM2482 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34715] It is yet further appreciated that a function of VGAM2482 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2482 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2482 correlate with, and may be deduced from, the identity of the host target genes which VGAM2482 binds and in-

hibits, and the function of these host target genes, as elaborated hereinbelow.

[34716] Nucleotide sequences of the VGAM2482 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2482 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2482 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2482 are further described hereinbelow with reference to Table 1.

[34717] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2482 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[34718] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2483 (VGAM2483) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[34719] VGAM2483 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2483 was detected is described hereinabove with reference to Figs. 2-8.

[34720] VGAM2483 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2483 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[34721] VGAM2483 gene, herein designated VGAM GENE, encodes a VGAM2483 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2483 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2483 precursor RNA is designated SEQ ID:2469, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2469 is located at position 166603 relative to the genome of Mouse cytomegalovirus 1.

[34722] VGAM2483 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2483 folded precursor RNA, herein designated VGAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34723] An enzyme complex designated DICER COMPLEX, dices the VGAM2483 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2483 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 52%) nucleotide sequence of VGAM2483 RNA is designated SEQ ID:5194, and is provided hereinbelow with reference to the sequence listing part.

[34724] VGAM2483 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2483 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2483 host target RNA,

herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34725] VGAM2483 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2483 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2483 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2483 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2483 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host tar-

get binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34726] The complementary binding of VGAM2483 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2483 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2483 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2483 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[34727] It is appreciated that VGAM2483 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2483 host target genes. The mRNA of each one of this plurality of VGAM2483 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2483 RNA, herein designated VGAM RNA, and which when bound by VGAM2483 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2483 host target proteins.

[34728] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2483 gene, herein designated VGAM GENE, on one or more VGAM2483 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34729] It is yet further appreciated that a function of VGAM2483 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2483 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2483

correlate with, and may be deduced from, the identity of the host target genes which VGAM2483 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[34730] Nucleotide sequences of the VGAM2483 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2483 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2483 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2483 are further described hereinbelow with reference to Table 1.

[34731] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2483 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[34732] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2484 (VGAM2484) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the

art.

[34733] VGAM2484 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2484 was detected is described hereinabove with reference to Figs. 2-8.

[34734] VGAM2484 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2484 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[34735] VGAM2484 gene, herein designated VGAM GENE, encodes a VGAM2484 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2484 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2484 precursor RNA is designated SEQ ID:2470, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2470 is located at position 183727 relative to the genome of Mouse cytomegalovirus 1.

[34736] VGAM2484 precursor RNA, herein designated VGAM PRE-

CURSOR RNA, folds onto itself, forming VGAM2484 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34737] An enzyme complex designated DICER COMPLEX, dices the VGAM2484 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2484 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide sequence of VGAM2484 RNA is designated SEQ ID:5195, and is provided hereinbelow with reference to the sequence listing part.

[34738] VGAM2484 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM2484 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2484 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34739] VGAM2484 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2484 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2484 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2484 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2484 host

target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34740] The complementary binding of VGAM2484 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2484 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2484 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2484 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[34741] It is appreciated that VGAM2484 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2484 host target genes. The mRNA of each one of this plurality of VGAM2484 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2484 RNA, herein designated VGAM RNA, and which when bound by VGAM2484 RNA, herein

designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2484 host target proteins.

[34742] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2484 gene, herein designated VGAM GENE, on one or more VGAM2484 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34743] It is yet further appreciated that a function of VGAM2484 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2484 include diagnosis, prevention and

treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2484 correlate with, and may be deduced from, the identity of the host target genes which VGAM2484 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[34744] Nucleotide sequences of the VGAM2484 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2484 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2484 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2484 are further described hereinbelow with reference to Table 1.

[34745] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2484 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[34746] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2485 (VGAM2485) viral gene, which modulates ex-

pression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[34747] VGAM2485 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2485 was detected is described hereinabove with reference to Figs. 2-8.

[34748] VGAM2485 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2485 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[34749] VGAM2485 gene, herein designated VGAM GENE, encodes a VGAM2485 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2485 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2485 precursor RNA is designated SEQ ID:2471, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2471 is located at position 214191 relative to the genome of Mouse cytomegalovirus

1.

[34750] VGAM2485 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2485 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34751] An enzyme complex designated DICER COMPLEX, dices the VGAM2485 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2485 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 49%) nucleotide sequence of VGAM2485 RNA is designated SEQ ID:5196, and is provided hereinbelow with reference to the sequence listing part.

[34752] VGAM2485 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2485 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2485 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34753] VGAM2485 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2485 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2485 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2485 RNA, herein designated

VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2485 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34754] The complementary binding of VGAM2485 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2485 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2485 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2485 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[34755] It is appreciated that VGAM2485 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2485 host target genes. The mRNA of each one of this plurality of VGAM2485 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM2485 RNA, herein designated VGAM RNA, and which when bound by VGAM2485 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2485 host target proteins.

[34756] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2485 gene, herein designated VGAM GENE, on one or more VGAM2485 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34757] It is yet further appreciated that a function of VGAM2485 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2485 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2485 correlate with, and may be deduced from, the identity of the host target genes which VGAM2485 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[34758] Nucleotide sequences of the VGAM2485 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2485 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2485 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2485 are further described hereinbelow with reference to Table 1.

[34759] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2485 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[34760] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present

invention, referred to here as Viral Genomic Address Messenger 2486 (VGAM2486) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[34761] VGAM2486 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2486 was detected is described hereinabove with reference to Figs. 2-8.

[34762] VGAM2486 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2486 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[34763] VGAM2486 gene, herein designated VGAM GENE, encodes a VGAM2486 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2486 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2486 precursor RNA is designated SEQ ID:2472, and is provided hereinbelow with reference to the sequence listing part. Nu-

cleotide sequence SEQ ID:2472 is located at position 54581 relative to the genome of Mouse cytomegalovirus 1.

[34764] VGAM2486 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2486 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34765] An enzyme complex designated DICER COMPLEX, dices the VGAM2486 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2486 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2486 RNA is designated SEQ ID:5197, and

is provided hereinbelow with reference to the sequence listing part.

[34766] VGAM2486 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2486 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2486 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34767] VGAM2486 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2486 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2486 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites

shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2486 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2486 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34768] The complementary binding of VGAM2486 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2486 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2486 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2486 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[34769] It is appreciated that VGAM2486 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2486 host target genes. The mRNA of each one of this plurality of VGAM2486 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2486 RNA, herein designated VGAM RNA, and which when bound by VGAM2486 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2486 host target proteins.

[34770] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2486 gene, herein designated VGAM GENE, on one or more VGAM2486 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34771] It is yet further appreciated that a function of VGAM2486 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2486 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2486 correlate with, and may be deduced from, the identity of the host target genes which VGAM2486 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[34772] Nucleotide sequences of the VGAM2486 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2486 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2486 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2486 are further described hereinbelow with reference to Table 1.

[34773] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2486 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[34774] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2487 (VGAM2487) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[34775] VGAM2487 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2487 was detected is described hereinabove with reference to Figs. 2-8.

[34776] VGAM2487 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2487 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[34777] VGAM2487 gene, herein designated VGAM GENE, encodes a VGAM2487 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2487 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2487 precur-

sor RNA is designated SEQ ID:2473, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2473 is located at position 105519 relative to the genome of Mouse cytomegalovirus 1.

[34778] VGAM2487 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2487 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34779] An enzyme complex designated DICER COMPLEX, dices the VGAM2487 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2487 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2487 RNA is designated SEQ ID:5198, and is provided hereinbelow with reference to the sequence listing part.

[34780] VGAM2487 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2487 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2487 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34781] VGAM2487 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2487 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2487 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I,

BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2487 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2487 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34782] The complementary binding of VGAM2487 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2487 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2487 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2487 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[34783] It is appreciated that VGAM2487 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM2487 host target genes. The mRNA of each one of this plurality of VGAM2487 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2487 RNA, herein designated VGAM RNA, and which when bound by VGAM2487 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2487 host target proteins.

[34784] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2487 gene, herein designated VGAM GENE, on one or more VGAM2487 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34785] It is yet further appreciated that a function of VGAM2487 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2487 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2487 correlate with, and may be deduced from, the identity of the host target genes which VGAM2487 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[34786] Nucleotide sequences of the VGAM2487 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2487 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2487 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2487 are further described hereinbelow with reference to Table 1.

[34787] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites

to VGAM2487 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[34788] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2488 (VGAM2488) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[34789] VGAM2488 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2488 was detected is described hereinabove with reference to Figs. 2-8.

[34790] VGAM2488 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2488 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[34791] VGAM2488 gene, herein designated VGAM GENE, encodes a VGAM2488 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2488 precursor RNA, herein designated VGAM PRECURSOR RNA, does not en-

code a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2488 precursor RNA is designated SEQ ID:2474, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2474 is located at position 77638 relative to the genome of Mouse cytomegalovirus 1.

[34792] VGAM2488 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2488 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34793] An enzyme complex designated DICER COMPLEX, dices the VGAM2488 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2488 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2488 RNA is designated SEQ ID:5199, and is provided hereinbelow with reference to the sequence listing part.

[34794] VGAM2488 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2488 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2488 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34795] VGAM2488 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2488 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2488 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host

target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2488 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2488 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34796] The complementary binding of VGAM2488 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2488 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2488 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2488 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[34797] It is appreciated that VGAM2488 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2488 host target genes. The mRNA of each one of this plurality of VGAM2488 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2488 RNA, herein designated VGAM RNA, and which when bound by VGAM2488 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2488 host target proteins.

[34798] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2488 gene, herein designated VGAM GENE, on one or more VGAM2488 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34799] It is yet further appreciated that a function of VGAM2488 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2488 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2488 correlate with, and may be deduced from, the identity of the host target genes which VGAM2488 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[34800] Nucleotide sequences of the VGAM2488 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2488 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2488 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2488 are further described hereinbelow with reference to Table 1.

[34801] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2488 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[34802] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2489 (VGAM2489) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[34803] VGAM2489 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2489 was detected is described hereinabove with reference to Figs. 2-8.

[34804] VGAM2489 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2489 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[34805] VGAM2489 gene, herein designated VGAM GENE, encodes a VGAM2489 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and un-

like most ordinary genes, VGAM2489 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2489 precursor RNA is designated SEQ ID:2475, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2475 is located at position 131589 relative to the genome of Mouse cytomegalovirus 1.

[34806] VGAM2489 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2489 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34807] An enzyme complex designated DICER COMPLEX, dices the VGAM2489 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2489 RNA, herein designated VGAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of VGAM2489 RNA is designated SEQ ID:5200, and is provided hereinbelow with reference to the sequence listing part.

[34808] VGAM2489 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2489 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2489 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34809] VGAM2489 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2489 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2489 RNA, herein designated

VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2489 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2489 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34810] The complementary binding of VGAM2489 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2489 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2489 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2489 host target protein, herein desig-

nated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[34811] It is appreciated that VGAM2489 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2489 host target genes. The mRNA of each one of this plurality of VGAM2489 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2489 RNA, herein designated VGAM RNA, and which when bound by VGAM2489 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2489 host target proteins.

[34812] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2489 gene, herein designated VGAM GENE, on one or more VGAM2489 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34813] It is yet further appreciated that a function of VGAM2489 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2489 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2489 correlate with, and may be deduced from, the identity of the host target genes which VGAM2489 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[34814] Nucleotide sequences of the VGAM2489 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2489 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2489 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2489 are further described hereinbelow with reference to Table 1.

[34815] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2489 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[34816] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2490 (VGAM2490) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[34817] VGAM2490 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2490 was detected is described hereinabove with reference to Figs. 2-8.

[34818] VGAM2490 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2490 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[34819] VGAM2490 gene, herein designated VGAM GENE, encodes

a VGAM2490 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2490 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2490 precursor RNA is designated SEQ ID:2476, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2476 is located at position 47693 relative to the genome of Mouse cytomegalovirus 1.

[34820] VGAM2490 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2490 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34821] An enzyme complex designated DICER COMPLEX, dices the VGAM2490 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, into VGAM2490 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2490 RNA is designated SEQ ID:5201, and is provided hereinbelow with reference to the sequence listing part.

[34822] VGAM2490 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2490 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2490 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34823] VGAM2490 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2490 host target RNA, herein designated VGAM HOST TARGET RNA. This

complementary binding is due to the fact that the nucleotide sequence of VGAM2490 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2490 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2490 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34824] The complementary binding of VGAM2490 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2490 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2490

host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2490 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[34825] It is appreciated that VGAM2490 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2490 host target genes. The mRNA of each one of this plurality of VGAM2490 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2490 RNA, herein designated VGAM RNA, and which when bound by VGAM2490 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2490 host target proteins.

[34826] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2490 gene, herein designated VGAM GENE, on one or more VGAM2490 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34827] It is yet further appreciated that a function of VGAM2490 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2490 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2490 correlate with, and may be deduced from, the identity of the host target genes which VGAM2490 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[34828] Nucleotide sequences of the VGAM2490 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2490 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2490 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM2490 are further described hereinbelow with reference to Table 1.

[34829] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2490 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[34830] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2491 (VGAM2491) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[34831] VGAM2491 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2491 was detected is described hereinabove with reference to Figs. 2-8.

[34832] VGAM2491 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2491 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the

human genome.

[34833] VGAM2491 gene, herein designated VGAM GENE, encodes a VGAM2491 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2491 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2491 precursor RNA is designated SEQ ID:2477, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2477 is located at position 198448 relative to the genome of Mouse cytomegalovirus 1.

[34834] VGAM2491 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2491 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34835] An enzyme complex designated DICER COMPLEX, dices the VGAM2491 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2491 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2491 RNA is designated SEQ ID:5202, and is provided hereinbelow with reference to the sequence listing part.

[34836] VGAM2491 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2491 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2491 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34837] VGAM2491 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites

located in untranslated regions of VGAM2491 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2491 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2491 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2491 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34838] The complementary binding of VGAM2491 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2491 host target RNA, herein designated VGAM

HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2491 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2491 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[34839] It is appreciated that VGAM2491 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2491 host target genes. The mRNA of each one of this plurality of VGAM2491 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2491 RNA, herein designated VGAM RNA, and which when bound by VGAM2491 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2491 host target proteins.

[34840] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2491 gene, herein designated VGAM GENE, on one or more VGAM2491 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove

with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34841] It is yet further appreciated that a function of VGAM2491 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2491 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2491 correlate with, and may be deduced from, the identity of the host target genes which VGAM2491 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[34842] Nucleotide sequences of the VGAM2491 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2491 RNA, herein designated VGAM RNA, and

a schematic representation of the secondary folding of VGAM2491 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2491 are further described hereinbelow with reference to Table 1.

[34843] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2491 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[34844] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2492 (VGAM2492) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[34845] VGAM2492 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2492 was detected is described hereinabove with reference to Figs. 2-8.

[34846] VGAM2492 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus

1. VGAM2492 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[34847] VGAM2492 gene, herein designated VGAM GENE, encodes a VGAM2492 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2492 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2492 precursor RNA is designated SEQ ID:2478, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2478 is located at position 124024 relative to the genome of Mouse cytomegalovirus 1.

[34848] VGAM2492 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2492 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34849] An enzyme complex designated DICER COMPLEX, dices the VGAM2492 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2492 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 56%) nucleotide sequence of VGAM2492 RNA is designated SEQ ID:5203, and is provided hereinbelow with reference to the sequence listing part.

[34850] VGAM2492 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2492 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2492 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34851] VGAM2492 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2492 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2492 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2492 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2492 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34852] The complementary binding of VGAM2492 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM2492 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2492 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2492 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[34853] It is appreciated that VGAM2492 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2492 host target genes. The mRNA of each one of this plurality of VGAM2492 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2492 RNA, herein designated VGAM RNA, and which when bound by VGAM2492 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2492 host target proteins.

[34854] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2492 gene, herein designated VGAM GENE, on one or more VGAM2492 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34855] It is yet further appreciated that a function of VGAM2492 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2492 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2492 correlate with, and may be deduced from, the identity of the host target genes which VGAM2492 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[34856] Nucleotide sequences of the VGAM2492 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the diced VGAM2492 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2492 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2492 are further described hereinbelow with reference to Table 1.

[34857] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2492 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[34858] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2493 (VGAM2493) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[34859] VGAM2493 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2493 was detected is described hereinabove with reference to Figs. 2-8.

[34860] VGAM2493 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2493 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[34861] VGAM2493 gene, herein designated VGAM GENE, encodes a VGAM2493 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2493 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2493 precursor RNA is designated SEQ ID:2479, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2479 is located at position 160440 relative to the genome of Mouse cytomegalovirus 1.

[34862] VGAM2493 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2493 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34863] An enzyme complex designated DICER COMPLEX, dices the VGAM2493 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2493 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2493 RNA is designated SEQ ID:5204, and is provided hereinbelow with reference to the sequence listing part.

[34864] VGAM2493 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2493 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2493 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and

a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34865] VGAM2493 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2493 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2493 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2493 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2493 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both

3UTR and 5UTR regions.

[34866] The complementary binding of VGAM2493 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2493 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2493 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2493 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[34867] It is appreciated that VGAM2493 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2493 host target genes. The mRNA of each one of this plurality of VGAM2493 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2493 RNA, herein designated VGAM RNA, and which when bound by VGAM2493 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2493 host target proteins.

[34868] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM2493 gene, herein designated VGAM GENE, on one or more VGAM2493 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34869] It is yet further appreciated that a function of VGAM2493 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2493 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2493 correlate with, and may be deduced from, the identity of the host target genes which VGAM2493 binds and inhibits, and the function of these host target genes, as

elaborated hereinbelow.

[34870] Nucleotide sequences of the VGAM2493 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2493 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2493 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2493 are further described hereinbelow with reference to Table 1.

[34871] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2493 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[34872] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2494 (VGAM2494) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[34873] VGAM2494 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene.

The method by which VGAM2494 was detected is described hereinabove with reference to Figs. 2-8.

[34874] VGAM2494 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2494 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[34875] VGAM2494 gene, herein designated VGAM GENE, encodes a VGAM2494 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2494 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2494 precursor RNA is designated SEQ ID:2480, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2480 is located at position 208377 relative to the genome of Mouse cytomegalovirus 1.

[34876] VGAM2494 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2494 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34877] An enzyme complex designated DICER COMPLEX, dices the VGAM2494 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2494 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of VGAM2494 RNA is designated SEQ ID:5205, and is provided hereinbelow with reference to the sequence listing part.

[34878] VGAM2494 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2494 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2494 host target RNA, herein designated VGAM HOST TARGET RNA, comprises

three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34879] VGAM2494 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2494 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2494 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2494 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2494 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an

example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34880] The complementary binding of VGAM2494 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2494 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2494 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2494 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[34881] It is appreciated that VGAM2494 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2494 host target genes. The mRNA of each one of this plurality of VGAM2494 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2494 RNA, herein designated VGAM RNA, and which when bound by VGAM2494 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2494 host target proteins.

[34882] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2494 gene, herein designated VGAM GENE, on one or more VGAM2494 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34883] It is yet further appreciated that a function of VGAM2494 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2494 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2494 correlate with, and may be deduced from, the identity of

the host target genes which VGAM2494 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[34884] Nucleotide sequences of the VGAM2494 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2494 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2494 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2494 are further described hereinbelow with reference to Table 1.

[34885] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2494 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[34886] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2495 (VGAM2495) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[34887] VGAM2495 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2495 was detected is described hereinabove with reference to Figs. 2-8.

[34888] VGAM2495 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2495 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[34889] VGAM2495 gene, herein designated VGAM GENE, encodes a VGAM2495 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2495 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2495 precursor RNA is designated SEQ ID:2481, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2481 is located at position 106389 relative to the genome of Mouse cytomegalovirus 1.

[34890] VGAM2495 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2495 folded

precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34891] An enzyme complex designated DICER COMPLEX, dices the VGAM2495 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2495 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2495 RNA is designated SEQ ID:5206, and is provided hereinbelow with reference to the sequence listing part.

[34892] VGAM2495 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2495 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM2495 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34893] VGAM2495 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2495 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2495 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2495 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2495 host target RNA, herein designated VGAM HOST TARGET RNA.

It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34894] The complementary binding of VGAM2495 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2495 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2495 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2495 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[34895] It is appreciated that VGAM2495 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2495 host target genes. The mRNA of each one of this plurality of VGAM2495 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2495 RNA, herein designated VGAM RNA, and which when bound by VGAM2495 RNA, herein designated VGAM RNA, causes inhibition of translation of

respective one or more VGAM2495 host target proteins.

[34896] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2495 gene, herein designated VGAM GENE, on one or more VGAM2495 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34897] It is yet further appreciated that a function of VGAM2495 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2495 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1.

Specific functions, and accordingly utilities, of VGAM2495 correlate with, and may be deduced from, the identity of the host target genes which VGAM2495 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[34898] Nucleotide sequences of the VGAM2495 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2495 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2495 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2495 are further described hereinbelow with reference to Table 1.

[34899] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2495 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[34900] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2496 (VGAM2496) viral gene, which modulates expression of respective host target genes thereof, the func-

tion and utility of which host target genes is known in the art.

[34901] VGAM2496 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2496 was detected is described hereinabove with reference to Figs. 2-8.

[34902] VGAM2496 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2496 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[34903] VGAM2496 gene, herein designated VGAM GENE, encodes a VGAM2496 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2496 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2496 precursor RNA is designated SEQ ID:2482, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2482 is located at position 186483 relative to the genome of Mouse cytomegalovirus 1.

[34904] VGAM2496 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2496 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34905] An enzyme complex designated DICER COMPLEX, dices the VGAM2496 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2496 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2496 RNA is designated SEQ ID:5207, and is provided hereinbelow with reference to the sequence listing part.

[34906] VGAM2496 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2496 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2496 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34907] VGAM2496 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2496 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2496 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2496 RNA, herein designated VGAM RNA, may have a different number of host target

binding sites in untranslated regions of a VGAM2496 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34908] The complementary binding of VGAM2496 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2496 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2496 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2496 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[34909] It is appreciated that VGAM2496 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2496 host target genes. The mRNA of each one of this plurality of VGAM2496 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2496 RNA, herein designated VGAM

RNA, and which when bound by VGAM2496 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2496 host target proteins.

[34910] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2496 gene, herein designated VGAM GENE, on one or more VGAM2496 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34911] It is yet further appreciated that a function of VGAM2496 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM2496 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2496 correlate with, and may be deduced from, the identity of the host target genes which VGAM2496 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[34912] Nucleotide sequences of the VGAM2496 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2496 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2496 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2496 are further described hereinbelow with reference to Table 1.

[34913] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2496 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[34914] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Mes-

senger 2497 (VGAM2497) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[34915] VGAM2497 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2497 was detected is described hereinabove with reference to Figs. 2-8.

[34916] VGAM2497 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2497 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[34917] VGAM2497 gene, herein designated VGAM GENE, encodes a VGAM2497 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2497 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2497 precursor RNA is designated SEQ ID:2483, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2483 is located at position

212016 relative to the genome of Mouse cytomegalovirus 1.

[34918] VGAM2497 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2497 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34919] An enzyme complex designated DICER COMPLEX, dices the VGAM2497 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2497 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2497 RNA is designated SEQ ID:5208, and is provided hereinbelow with reference to the sequence

listing part.

[34920] VGAM2497 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2497 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2497 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34921] VGAM2497 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2497 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2497 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not

meant to be limiting VGAM2497 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2497 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34922] The complementary binding of VGAM2497 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2497 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2497 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2497 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[34923] It is appreciated that VGAM2497 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2497 host target genes. The mRNA of each one of this plurality of VGAM2497 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2497 RNA, herein designated VGAM RNA, and which when bound by VGAM2497 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2497 host target proteins.

[34924] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2497 gene, herein designated VGAM GENE, on one or more VGAM2497 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34925] It is yet further appreciated that a function of VGAM2497

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2497 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2497 correlate with, and may be deduced from, the identity of the host target genes which VGAM2497 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[34926] Nucleotide sequences of the VGAM2497 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2497 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2497 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2497 are further described hereinbelow with reference to Table 1.

[34927] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2497 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[34928] Fig. 1 further provides a conceptual description of another

novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2498 (VGAM2498) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[34929] VGAM2498 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2498 was detected is described hereinabove with reference to Figs. 2-8.

[34930] VGAM2498 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2498 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[34931] VGAM2498 gene, herein designated VGAM GENE, encodes a VGAM2498 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2498 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2498 precursor RNA is designated SEQ ID:2484, and is provided here-

inbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2484 is located at position 211848 relative to the genome of Mouse cytomegalovirus 1.

[34932] VGAM2498 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2498 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34933] An enzyme complex designated DICER COMPLEX, dices the VGAM2498 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2498 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 61%) nucleotide se-

quence of VGAM2498 RNA is designated SEQ ID:5209, and is provided hereinbelow with reference to the sequence listing part.

[34934] VGAM2498 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2498 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2498 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34935] VGAM2498 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2498 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2498 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is ap-

preciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2498 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2498 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34936] The complementary binding of VGAM2498 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2498 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2498 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2498 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[34937] It is appreciated that VGAM2498 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2498 host target genes. The mRNA of

each one of this plurality of VGAM2498 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2498 RNA, herein designated VGAM RNA, and which when bound by VGAM2498 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2498 host target proteins.

[34938] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2498 gene, herein designated VGAM GENE, on one or more VGAM2498 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science

294,779 (2001)).

[34939] It is yet further appreciated that a function of VGAM2498 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2498 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2498 correlate with, and may be deduced from, the identity of the host target genes which VGAM2498 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[34940] Nucleotide sequences of the VGAM2498 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2498 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2498 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2498 are further described hereinbelow with reference to Table 1.

[34941] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2498 RNA, herein designated VGAM RNA, are de-

scribed hereinbelow with reference to Table 2.

[34942] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2499 (VGAM2499) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[34943] VGAM2499 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2499 was detected is described hereinabove with reference to Figs. 2-8.

[34944] VGAM2499 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2499 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[34945] VGAM2499 gene, herein designated VGAM GENE, encodes a VGAM2499 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2499 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly

similar to the nucleotide sequence of VGAM2499 precursor RNA is designated SEQ ID:2485, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2485 is located at position 88282 relative to the genome of Mouse cytomegalovirus 1.

[34946] VGAM2499 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2499 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34947] An enzyme complex designated DICER COMPLEX, dices the VGAM2499 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2499 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2499 RNA is designated SEQ ID:5210, and is provided hereinbelow with reference to the sequence listing part.

[34948] VGAM2499 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2499 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2499 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34949] VGAM2499 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2499 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2499 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3

such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2499 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2499 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34950] The complementary binding of VGAM2499 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2499 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2499 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2499 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[34951] It is appreciated that VGAM2499 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2499 host target genes. The mRNA of each one of this plurality of VGAM2499 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2499 RNA, herein designated VGAM RNA, and which when bound by VGAM2499 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2499 host target proteins.

[34952] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2499 gene, herein designated VGAM GENE, on one or more VGAM2499 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34953] It is yet further appreciated that a function of VGAM2499 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2499 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2499 correlate with, and may be deduced from, the identity of the host target genes which VGAM2499 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[34954] Nucleotide sequences of the VGAM2499 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2499 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2499 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2499 are further described hereinbelow with reference to Table 1.

[34955] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the

complementarity of each of these host target binding sites to VGAM2499 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[34956] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2500 (VGAM2500) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[34957] VGAM2500 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2500 was detected is described hereinabove with reference to Figs. 2-8.

[34958] VGAM2500 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2500 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[34959] VGAM2500 gene, herein designated VGAM GENE, encodes a VGAM2500 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2500 precursor RNA,

herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2500 precursor RNA is designated SEQ ID:2486, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2486 is located at position 173739 relative to the genome of Mouse cytomegalovirus 1.

[34960] VGAM2500 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2500 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34961] An enzyme complex designated DICER COMPLEX, dices the VGAM2500 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2500 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 81%) nucleotide sequence of VGAM2500 RNA is designated SEQ ID:5211, and is provided hereinbelow with reference to the sequence listing part.

[34962] VGAM2500 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2500 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2500 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34963] VGAM2500 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2500 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2500 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed

sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2500 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2500 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34964] The complementary binding of VGAM2500 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2500 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2500 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2500 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target

protein is therefore outlined by a broken line.

[34965] It is appreciated that VGAM2500 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2500 host target genes. The mRNA of each one of this plurality of VGAM2500 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2500 RNA, herein designated VGAM RNA, and which when bound by VGAM2500 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2500 host target proteins.

[34966] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2500 gene, herein designated VGAM GENE, on one or more VGAM2500 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34967] It is yet further appreciated that a function of VGAM2500 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2500 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2500 correlate with, and may be deduced from, the identity of the host target genes which VGAM2500 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[34968] Nucleotide sequences of the VGAM2500 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2500 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2500 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2500 are further described hereinbelow with reference to Table 1.

[34969] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2500 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[34970] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2501 (VGAM2501) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[34971] VGAM2501 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2501 was detected is described hereinabove with reference to Figs. 2-8.

[34972] VGAM2501 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2501 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[34973] VGAM2501 gene, herein designated VGAM GENE, encodes a VGAM2501 precursor RNA, herein designated VGAM

PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2501 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2501 precursor RNA is designated SEQ ID:2487, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2487 is located at position 72060 relative to the genome of Mouse cytomegalovirus 1.

[34974] VGAM2501 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2501 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34975] An enzyme complex designated DICER COMPLEX, dices the VGAM2501 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2501 RNA,

herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 47%) nucleotide sequence of VGAM2501 RNA is designated SEQ ID:5212, and is provided hereinbelow with reference to the sequence listing part.

[34976] VGAM2501 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2501 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2501 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34977] VGAM2501 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2501 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM2501 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2501 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2501 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34978] The complementary binding of VGAM2501 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2501 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2501 host target RNA, herein designated VGAM HOST TARGET

RNA, into VGAM2501 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[34979] It is appreciated that VGAM2501 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2501 host target genes. The mRNA of each one of this plurality of VGAM2501 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2501 RNA, herein designated VGAM RNA, and which when bound by VGAM2501 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2501 host target proteins.

[34980] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2501 gene, herein designated VGAM GENE, on one or more VGAM2501 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34981] It is yet further appreciated that a function of VGAM2501 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2501 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2501 correlate with, and may be deduced from, the identity of the host target genes which VGAM2501 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[34982] Nucleotide sequences of the VGAM2501 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2501 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2501 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2501 are further

described hereinbelow with reference to Table 1.

[34983] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2501 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[34984] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2502 (VGAM2502) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[34985] VGAM2502 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2502 was detected is described hereinabove with reference to Figs. 2-8.

[34986] VGAM2502 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2502 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[34987] VGAM2502 gene, herein designated VGAM GENE, encodes a VGAM2502 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2502 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2502 precursor RNA is designated SEQ ID:2488, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2488 is located at position 192021 relative to the genome of Mouse cytomegalovirus 1.

[34988] VGAM2502 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2502 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34989] An enzyme complex designated DICER COMPLEX, dices

the VGAM2502 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2502 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2502 RNA is designated SEQ ID:5213, and is provided hereinbelow with reference to the sequence listing part.

[34990] VGAM2502 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2502 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2502 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34991] VGAM2502 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2502 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2502 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2502 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2502 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34992] The complementary binding of VGAM2502 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2502 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM2502 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2502 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[34993] It is appreciated that VGAM2502 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2502 host target genes. The mRNA of each one of this plurality of VGAM2502 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2502 RNA, herein designated VGAM RNA, and which when bound by VGAM2502 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2502 host target proteins.

[34994] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2502 gene, herein designated VGAM GENE, on one or more VGAM2502 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34995] It is yet further appreciated that a function of VGAM2502 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2502 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2502 correlate with, and may be deduced from, the identity of the host target genes which VGAM2502 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[34996] Nucleotide sequences of the VGAM2502 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2502 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of

VGAM2502 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2502 are further described hereinbelow with reference to Table 1.

[34997] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2502 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[34998] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2503 (VGAM2503) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[34999] VGAM2503 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2503 was detected is described hereinabove with reference to Figs. 2-8.

[35000] VGAM2503 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2503 host target gene, herein designated VGAM

HOST TARGET GENE, is a human gene contained in the human genome.

[35001] VGAM2503 gene, herein designated VGAM GENE, encodes a VGAM2503 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2503 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2503 precursor RNA is designated SEQ ID:2489, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2489 is located at position 125983 relative to the genome of Mouse cytomegalovirus 1.

[35002] VGAM2503 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2503 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[35003] An enzyme complex designated DICER COMPLEX, dices the VGAM2503 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2503 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 81%) nucleotide sequence of VGAM2503 RNA is designated SEQ ID:5214, and is provided hereinbelow with reference to the sequence listing part.

[35004] VGAM2503 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2503 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2503 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35005] VGAM2503 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM2503 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2503 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2503 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2503 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35006] The complementary binding of VGAM2503 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM2503 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2503 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2503 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[35007] It is appreciated that VGAM2503 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2503 host target genes. The mRNA of each one of this plurality of VGAM2503 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2503 RNA, herein designated VGAM RNA, and which when bound by VGAM2503 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2503 host target proteins.

[35008] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2503 gene, herein designated VGAM GENE, on one or more VGAM2503 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35009] It is yet further appreciated that a function of VGAM2503 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2503 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2503 correlate with, and may be deduced from, the identity of the host target genes which VGAM2503 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[35010] Nucleotide sequences of the VGAM2503 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

diced VGAM2503 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2503 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2503 are further described hereinbelow with reference to Table 1.

[35011] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2503 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[35012] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2504 (VGAM2504) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[35013] VGAM2504 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2504 was detected is described hereinabove with reference to Figs. 2-8.

[35014] VGAM2504 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of Mouse cytomegalovirus 1. VGAM2504 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[35015] VGAM2504 gene, herein designated VGAM GENE, encodes a VGAM2504 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2504 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2504 precursor RNA is designated SEQ ID:2490, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2490 is located at position 179418 relative to the genome of Mouse cytomegalovirus 1.

[35016] VGAM2504 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2504 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35017] An enzyme complex designated DICER COMPLEX, dices the VGAM2504 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2504 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of VGAM2504 RNA is designated SEQ ID:5215, and is provided hereinbelow with reference to the sequence listing part.

[35018] VGAM2504 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2504 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2504 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN COD-

ING and 3UTR respectively.

[35019] VGAM2504 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2504 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2504 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2504 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2504 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35020] The complementary binding of VGAM2504 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2504 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2504 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2504 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[35021] It is appreciated that VGAM2504 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2504 host target genes. The mRNA of each one of this plurality of VGAM2504 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2504 RNA, herein designated VGAM RNA, and which when bound by VGAM2504 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2504 host target proteins.

[35022] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2504 gene, herein designated VGAM GENE, on one

or more VGAM2504 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35023] It is yet further appreciated that a function of VGAM2504 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2504 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2504 correlate with, and may be deduced from, the identity of the host target genes which VGAM2504 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[35024] Nucleotide sequences of the VGAM2504 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2504 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2504 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2504 are further described hereinbelow with reference to Table 1.

[35025] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2504 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[35026] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2505 (VGAM2505) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[35027] VGAM2505 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2505 was detected is de-

scribed hereinabove with reference to Figs. 2-8.

[35028] VGAM2505 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2505 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[35029] VGAM2505 gene, herein designated VGAM GENE, encodes a VGAM2505 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2505 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2505 precursor RNA is designated SEQ ID:2491, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2491 is located at position 75695 relative to the genome of Mouse cytomegalovirus 1.

[35030] VGAM2505 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2505 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35031] An enzyme complex designated DICER COMPLEX, dices the VGAM2505 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2505 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2505 RNA is designated SEQ ID:5216, and is provided hereinbelow with reference to the sequence listing part.

[35032] VGAM2505 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2505 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2505 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding

gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35033] VGAM2505 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2505 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2505 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2505 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be lo-

cated in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35034] The complementary binding of VGAM2505 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2505 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2505 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2505 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[35035] It is appreciated that VGAM2505 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2505 host target genes. The mRNA of each one of this plurality of VGAM2505 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2505 RNA, herein designated VGAM RNA, and which when bound by VGAM2505 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2505 host target proteins.

[35036] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM2505 gene, herein designated VGAM GENE, on one or more VGAM2505 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35037] It is yet further appreciated that a function of VGAM2505 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2505 correlate with, and may be deduced from, the identity of the host target genes which VGAM2505 binds and in-

hibits, and the function of these host target genes, as elaborated hereinbelow.

[35038] Nucleotide sequences of the VGAM2505 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2505 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2505 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2505 are further described hereinbelow with reference to Table 1.

[35039] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2505 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[35040] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2506 (VGAM2506) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[35041] VGAM2506 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2506 was detected is described hereinabove with reference to Figs. 2-8.

[35042] VGAM2506 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2506 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[35043] VGAM2506 gene, herein designated VGAM GENE, encodes a VGAM2506 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2506 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2506 precursor RNA is designated SEQ ID:2492, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2492 is located at position 165224 relative to the genome of Mouse cytomegalovirus 1.

[35044] VGAM2506 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2506 folded precursor RNA, herein designated VGAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35045] An enzyme complex designated DICER COMPLEX, dices the VGAM2506 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2506 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 59%) nucleotide sequence of VGAM2506 RNA is designated SEQ ID:5217, and is provided hereinbelow with reference to the sequence listing part.

[35046] VGAM2506 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2506 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2506 host target RNA,

herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35047] VGAM2506 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2506 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2506 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2506 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2506 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host tar-

get binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35048] The complementary binding of VGAM2506 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2506 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2506 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2506 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[35049] It is appreciated that VGAM2506 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2506 host target genes. The mRNA of each one of this plurality of VGAM2506 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2506 RNA, herein designated VGAM RNA, and which when bound by VGAM2506 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2506 host target proteins.

[35050] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2506 gene, herein designated VGAM GENE, on one or more VGAM2506 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35051] It is yet further appreciated that a function of VGAM2506 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2506 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2506

correlate with, and may be deduced from, the identity of the host target genes which VGAM2506 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[35052] Nucleotide sequences of the VGAM2506 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2506 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2506 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2506 are further described hereinbelow with reference to Table 1.

[35053] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2506 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[35054] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2507 (VGAM2507) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the

art.

[35055] VGAM2507 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2507 was detected is described hereinabove with reference to Figs. 2-8.

[35056] VGAM2507 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2507 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[35057] VGAM2507 gene, herein designated VGAM GENE, encodes a VGAM2507 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2507 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2507 precursor RNA is designated SEQ ID:2493, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2493 is located at position 38544 relative to the genome of Mouse cytomegalovirus 1.

[35058] VGAM2507 precursor RNA, herein designated VGAM PRE-

CURSOR RNA, folds onto itself, forming VGAM2507 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35059] An enzyme complex designated DICER COMPLEX, dices the VGAM2507 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2507 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2507 RNA is designated SEQ ID:5218, and is provided hereinbelow with reference to the sequence listing part.

[35060] VGAM2507 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM2507 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2507 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35061] VGAM2507 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2507 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2507 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2507 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2507 host

target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35062] The complementary binding of VGAM2507 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2507 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2507 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2507 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[35063] It is appreciated that VGAM2507 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2507 host target genes. The mRNA of each one of this plurality of VGAM2507 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2507 RNA, herein designated VGAM RNA, and which when bound by VGAM2507 RNA, herein

designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2507 host target proteins.

[35064] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2507 gene, herein designated VGAM GENE, on one or more VGAM2507 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35065] It is yet further appreciated that a function of VGAM2507 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2507 include diagnosis, prevention and

treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2507 correlate with, and may be deduced from, the identity of the host target genes which VGAM2507 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[35066] Nucleotide sequences of the VGAM2507 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2507 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2507 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2507 are further described hereinbelow with reference to Table 1.

[35067] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2507 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[35068] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2508 (VGAM2508) viral gene, which modulates ex-

pression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[35069] VGAM2508 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2508 was detected is described hereinabove with reference to Figs. 2-8.

[35070] VGAM2508 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2508 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[35071] VGAM2508 gene, herein designated VGAM GENE, encodes a VGAM2508 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2508 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2508 precursor RNA is designated SEQ ID:2494, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2494 is located at position 168766 relative to the genome of Mouse cytomegalovirus

1.

[35072] VGAM2508 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2508 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35073] An enzyme complex designated DICER COMPLEX, dices the VGAM2508 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2508 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2508 RNA is designated SEQ ID:5219, and is provided hereinbelow with reference to the sequence listing part.

[35074] VGAM2508 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2508 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2508 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35075] VGAM2508 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2508 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2508 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2508 RNA, herein designated

VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2508 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35076] The complementary binding of VGAM2508 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2508 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2508 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2508 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[35077] It is appreciated that VGAM2508 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2508 host target genes. The mRNA of each one of this plurality of VGAM2508 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM2508 RNA, herein designated VGAM RNA, and which when bound by VGAM2508 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2508 host target proteins.

[35078] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2508 gene, herein designated VGAM GENE, on one or more VGAM2508 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35079] It is yet further appreciated that a function of VGAM2508 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2508 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2508 correlate with, and may be deduced from, the identity of the host target genes which VGAM2508 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[35080] Nucleotide sequences of the VGAM2508 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2508 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2508 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2508 are further described hereinbelow with reference to Table 1.

[35081] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2508 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[35082] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present

invention, referred to here as Viral Genomic Address Messenger 2509 (VGAM2509) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[35083] VGAM2509 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2509 was detected is described hereinabove with reference to Figs. 2-8.

[35084] VGAM2509 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2509 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[35085] VGAM2509 gene, herein designated VGAM GENE, encodes a VGAM2509 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2509 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2509 precursor RNA is designated SEQ ID:2495, and is provided hereinbelow with reference to the sequence listing part. Nu-

cleotide sequence SEQ ID:2495 is located at position 220001 relative to the genome of Mouse cytomegalovirus 1.

[35086] VGAM2509 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2509 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35087] An enzyme complex designated DICER COMPLEX, dices the VGAM2509 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2509 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2509 RNA is designated SEQ ID:5220, and

is provided hereinbelow with reference to the sequence listing part.

[35088] VGAM2509 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2509 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2509 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35089] VGAM2509 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2509 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2509 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites

shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2509 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2509 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35090] The complementary binding of VGAM2509 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2509 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2509 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2509 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[35091] It is appreciated that VGAM2509 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2509 host target genes. The mRNA of each one of this plurality of VGAM2509 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2509 RNA, herein designated VGAM RNA, and which when bound by VGAM2509 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2509 host target proteins.

[35092] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2509 gene, herein designated VGAM GENE, on one or more VGAM2509 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35093] It is yet further appreciated that a function of VGAM2509 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2509 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2509 correlate with, and may be deduced from, the identity of the host target genes which VGAM2509 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[35094] Nucleotide sequences of the VGAM2509 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2509 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2509 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2509 are further described hereinbelow with reference to Table 1.

[35095] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2509 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[35096] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2510 (VGAM2510) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[35097] VGAM2510 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2510 was detected is described hereinabove with reference to Figs. 2-8.

[35098] VGAM2510 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2510 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[35099] VGAM2510 gene, herein designated VGAM GENE, encodes a VGAM2510 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2510 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2510 precur-

sor RNA is designated SEQ ID:2496, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2496 is located at position 226893 relative to the genome of Mouse cytomegalovirus 1.

[35100] VGAM2510 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2510 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35101] An enzyme complex designated DICER COMPLEX, dices the VGAM2510 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2510 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2510 RNA is designated SEQ ID:5221, and is provided hereinbelow with reference to the sequence listing part.

[35102] VGAM2510 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2510 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2510 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35103] VGAM2510 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2510 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2510 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I,

BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2510 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2510 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35104] The complementary binding of VGAM2510 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2510 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2510 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2510 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[35105] It is appreciated that VGAM2510 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM2510 host target genes. The mRNA of each one of this plurality of VGAM2510 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2510 RNA, herein designated VGAM RNA, and which when bound by VGAM2510 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2510 host target proteins.

[35106] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2510 gene, herein designated VGAM GENE, on one or more VGAM2510 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35107] It is yet further appreciated that a function of VGAM2510 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2510 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2510 correlate with, and may be deduced from, the identity of the host target genes which VGAM2510 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[35108] Nucleotide sequences of the VGAM2510 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2510 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2510 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2510 are further described hereinbelow with reference to Table 1.

[35109] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites

to VGAM2510 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[35110] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2511 (VGAM2511) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[35111] VGAM2511 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2511 was detected is described hereinabove with reference to Figs. 2-8.

[35112] VGAM2511 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2511 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[35113] VGAM2511 gene, herein designated VGAM GENE, encodes a VGAM2511 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2511 precursor RNA, herein designated VGAM PRECURSOR RNA, does not en-

code a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2511 precursor RNA is designated SEQ ID:2497, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2497 is located at position 36653 relative to the genome of Mouse cytomegalovirus 1.

[35114] VGAM2511 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2511 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35115] An enzyme complex designated DICER COMPLEX, dices the VGAM2511 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2511 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2511 RNA is designated SEQ ID:5222, and is provided hereinbelow with reference to the sequence listing part.

[35116] VGAM2511 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2511 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2511 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35117] VGAM2511 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2511 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2511 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host

target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2511 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2511 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35118] The complementary binding of VGAM2511 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2511 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2511 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2511 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[35119] It is appreciated that VGAM2511 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2511 host target genes. The mRNA of each one of this plurality of VGAM2511 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2511 RNA, herein designated VGAM RNA, and which when bound by VGAM2511 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2511 host target proteins.

[35120] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2511 gene, herein designated VGAM GENE, on one or more VGAM2511 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35121] It is yet further appreciated that a function of VGAM2511 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2511 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2511 correlate with, and may be deduced from, the identity of the host target genes which VGAM2511 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[35122] Nucleotide sequences of the VGAM2511 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2511 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2511 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2511 are further described hereinbelow with reference to Table 1.

[35123] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2511 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[35124] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2512 (VGAM2512) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[35125] VGAM2512 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2512 was detected is described hereinabove with reference to Figs. 2-8.

[35126] VGAM2512 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2512 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[35127] VGAM2512 gene, herein designated VGAM GENE, encodes a VGAM2512 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and un-

like most ordinary genes, VGAM2512 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2512 precursor RNA is designated SEQ ID:2498, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2498 is located at position 84643 relative to the genome of Mouse cytomegalovirus 1.

[35128] VGAM2512 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2512 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35129] An enzyme complex designated DICER COMPLEX, dices the VGAM2512 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2512 RNA, herein designated VGAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2512 RNA is designated SEQ ID:5223, and is provided hereinbelow with reference to the sequence listing part.

[35130] VGAM2512 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2512 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2512 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35131] VGAM2512 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2512 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2512 RNA, herein designated

VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2512 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2512 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35132] The complementary binding of VGAM2512 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2512 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2512 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2512 host target protein, herein desig-

nated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[35133] It is appreciated that VGAM2512 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2512 host target genes. The mRNA of each one of this plurality of VGAM2512 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2512 RNA, herein designated VGAM RNA, and which when bound by VGAM2512 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2512 host target proteins.

[35134] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2512 gene, herein designated VGAM GENE, on one or more VGAM2512 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35135] It is yet further appreciated that a function of VGAM2512 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2512 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2512 correlate with, and may be deduced from, the identity of the host target genes which VGAM2512 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[35136] Nucleotide sequences of the VGAM2512 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2512 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2512 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2512 are further described hereinbelow with reference to Table 1.

[35137] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2512 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[35138] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2513 (VGAM2513) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[35139] VGAM2513 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2513 was detected is described hereinabove with reference to Figs. 2-8.

[35140] VGAM2513 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2513 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[35141] VGAM2513 gene, herein designated VGAM GENE, encodes

a VGAM2513 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2513 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2513 precursor RNA is designated SEQ ID:2499, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2499 is located at position 157900 relative to the genome of Mouse cytomegalovirus 1.

[35142] VGAM2513 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2513 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35143] An enzyme complex designated DICER COMPLEX, dices the VGAM2513 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, into VGAM2513 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2513 RNA is designated SEQ ID:5224, and is provided hereinbelow with reference to the sequence listing part.

[35144] VGAM2513 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2513 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2513 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35145] VGAM2513 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2513 host target RNA, herein designated VGAM HOST TARGET RNA. This

complementary binding is due to the fact that the nucleotide sequence of VGAM2513 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2513 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2513 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35146] The complementary binding of VGAM2513 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2513 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2513

host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2513 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[35147] It is appreciated that VGAM2513 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2513 host target genes. The mRNA of each one of this plurality of VGAM2513 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2513 RNA, herein designated VGAM RNA, and which when bound by VGAM2513 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2513 host target proteins.

[35148] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2513 gene, herein designated VGAM GENE, on one or more VGAM2513 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35149] It is yet further appreciated that a function of VGAM2513 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2513 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2513 correlate with, and may be deduced from, the identity of the host target genes which VGAM2513 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[35150] Nucleotide sequences of the VGAM2513 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2513 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2513 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM2513 are further described hereinbelow with reference to Table 1.

[35151] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2513 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[35152] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2514 (VGAM2514) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[35153] VGAM2514 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2514 was detected is described hereinabove with reference to Figs. 2-8.

[35154] VGAM2514 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2514 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the

human genome.

[35155] VGAM2514 gene, herein designated VGAM GENE, encodes a VGAM2514 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2514 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2514 precursor RNA is designated SEQ ID:2500, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2500 is located at position 127106 relative to the genome of Mouse cytomegalovirus 1.

[35156] VGAM2514 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2514 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35157] An enzyme complex designated DICER COMPLEX, dices the VGAM2514 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2514 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2514 RNA is designated SEQ ID:5225, and is provided hereinbelow with reference to the sequence listing part.

[35158] VGAM2514 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2514 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2514 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35159] VGAM2514 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites

located in untranslated regions of VGAM2514 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2514 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2514 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2514 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35160] The complementary binding of VGAM2514 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2514 host target RNA, herein designated VGAM

HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2514 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2514 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[35161] It is appreciated that VGAM2514 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2514 host target genes. The mRNA of each one of this plurality of VGAM2514 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2514 RNA, herein designated VGAM RNA, and which when bound by VGAM2514 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2514 host target proteins.

[35162] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2514 gene, herein designated VGAM GENE, on one or more VGAM2514 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove

with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35163] It is yet further appreciated that a function of VGAM2514 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2514 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2514 correlate with, and may be deduced from, the identity of the host target genes which VGAM2514 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[35164] Nucleotide sequences of the VGAM2514 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2514 RNA, herein designated VGAM RNA, and

a schematic representation of the secondary folding of VGAM2514 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2514 are further described hereinbelow with reference to Table 1.

[35165] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2514 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[35166] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2515 (VGAM2515) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[35167] VGAM2515 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2515 was detected is described hereinabove with reference to Figs. 2-8.

[35168] VGAM2515 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus

1. VGAM2515 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[35169] VGAM2515 gene, herein designated VGAM GENE, encodes a VGAM2515 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2515 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2515 precursor RNA is designated SEQ ID:2501, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2501 is located at position 35144 relative to the genome of Mouse cytomegalovirus 1.

[35170] VGAM2515 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2515 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35171] An enzyme complex designated DICER COMPLEX, dices the VGAM2515 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2515 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2515 RNA is designated SEQ ID:5226, and is provided hereinbelow with reference to the sequence listing part.

[35172] VGAM2515 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2515 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2515 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35173] VGAM2515 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2515 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2515 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2515 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2515 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35174] The complementary binding of VGAM2515 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM2515 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2515 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2515 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[35175] It is appreciated that VGAM2515 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2515 host target genes. The mRNA of each one of this plurality of VGAM2515 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2515 RNA, herein designated VGAM RNA, and which when bound by VGAM2515 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2515 host target proteins.

[35176] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2515 gene, herein designated VGAM GENE, on one or more VGAM2515 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35177] It is yet further appreciated that a function of VGAM2515 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2515 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2515 correlate with, and may be deduced from, the identity of the host target genes which VGAM2515 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[35178] Nucleotide sequences of the VGAM2515 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the diced VGAM2515 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2515 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2515 are further described hereinbelow with reference to Table 1.

[35179] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2515 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[35180] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2516 (VGAM2516) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[35181] VGAM2516 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2516 was detected is described hereinabove with reference to Figs. 2-8.

[35182] VGAM2516 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2516 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[35183] VGAM2516 gene, herein designated VGAM GENE, encodes a VGAM2516 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2516 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2516 precursor RNA is designated SEQ ID:2502, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2502 is located at position 84255 relative to the genome of Mouse cytomegalovirus 1.

[35184] VGAM2516 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2516 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35185] An enzyme complex designated DICER COMPLEX, dices the VGAM2516 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2516 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2516 RNA is designated SEQ ID:5227, and is provided hereinbelow with reference to the sequence listing part.

[35186] VGAM2516 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2516 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2516 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and

a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35187] VGAM2516 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2516 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2516 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2516 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2516 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both

3UTR and 5UTR regions.

[35188] The complementary binding of VGAM2516 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2516 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2516 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2516 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[35189] It is appreciated that VGAM2516 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2516 host target genes. The mRNA of each one of this plurality of VGAM2516 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2516 RNA, herein designated VGAM RNA, and which when bound by VGAM2516 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2516 host target proteins.

[35190] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM2516 gene, herein designated VGAM GENE, on one or more VGAM2516 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35191] It is yet further appreciated that a function of VGAM2516 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2516 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2516 correlate with, and may be deduced from, the identity of the host target genes which VGAM2516 binds and inhibits, and the function of these host target genes, as

elaborated hereinbelow.

[35192] Nucleotide sequences of the VGAM2516 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2516 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2516 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2516 are further described hereinbelow with reference to Table 1.

[35193] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2516 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[35194] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2517 (VGAM2517) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[35195] VGAM2517 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene.

The method by which VGAM2517 was detected is described hereinabove with reference to Figs. 2-8.

[35196] VGAM2517 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2517 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[35197] VGAM2517 gene, herein designated VGAM GENE, encodes a VGAM2517 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2517 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2517 precursor RNA is designated SEQ ID:2503, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2503 is located at position 158132 relative to the genome of Mouse cytomegalovirus 1.

[35198] VGAM2517 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2517 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35199] An enzyme complex designated DICER COMPLEX, dices the VGAM2517 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2517 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 61%) nucleotide sequence of VGAM2517 RNA is designated SEQ ID:5228, and is provided hereinbelow with reference to the sequence listing part.

[35200] VGAM2517 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2517 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2517 host target RNA, herein designated VGAM HOST TARGET RNA, comprises

three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35201] VGAM2517 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2517 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2517 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2517 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2517 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an

example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35202] The complementary binding of VGAM2517 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2517 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2517 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2517 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[35203] It is appreciated that VGAM2517 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2517 host target genes. The mRNA of each one of this plurality of VGAM2517 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2517 RNA, herein designated VGAM RNA, and which when bound by VGAM2517 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2517 host target proteins.

[35204] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2517 gene, herein designated VGAM GENE, on one or more VGAM2517 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35205] It is yet further appreciated that a function of VGAM2517 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2517 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2517 correlate with, and may be deduced from, the identity of

the host target genes which VGAM2517 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[35206] Nucleotide sequences of the VGAM2517 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2517 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2517 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2517 are further described hereinbelow with reference to Table 1.

[35207] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2517 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[35208] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2518 (VGAM2518) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[35209] VGAM2518 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2518 was detected is described hereinabove with reference to Figs. 2-8.

[35210] VGAM2518 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2518 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[35211] VGAM2518 gene, herein designated VGAM GENE, encodes a VGAM2518 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2518 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2518 precursor RNA is designated SEQ ID:2504, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2504 is located at position 3872 relative to the genome of Mouse cytomegalovirus 1.

[35212] VGAM2518 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2518 folded precursor RNA, herein designated VGAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35213] An enzyme complex designated DICER COMPLEX, dices the VGAM2518 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2518 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2518 RNA is designated SEQ ID:5229, and is provided hereinbelow with reference to the sequence listing part.

[35214] VGAM2518 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2518 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2518 host target RNA,

herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35215] VGAM2518 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2518 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2518 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2518 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2518 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host tar-

get binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35216] The complementary binding of VGAM2518 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2518 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2518 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2518 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[35217] It is appreciated that VGAM2518 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2518 host target genes. The mRNA of each one of this plurality of VGAM2518 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2518 RNA, herein designated VGAM RNA, and which when bound by VGAM2518 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2518 host target proteins.

[35218] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2518 gene, herein designated VGAM GENE, on one or more VGAM2518 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35219] It is yet further appreciated that a function of VGAM2518 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2518 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2518

correlate with, and may be deduced from, the identity of the host target genes which VGAM2518 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[35220] Nucleotide sequences of the VGAM2518 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2518 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2518 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2518 are further described hereinbelow with reference to Table 1.

[35221] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2518 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[35222] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2519 (VGAM2519) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the

art.

[35223] VGAM2519 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2519 was detected is described hereinabove with reference to Figs. 2-8.

[35224] VGAM2519 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2519 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[35225] VGAM2519 gene, herein designated VGAM GENE, encodes a VGAM2519 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2519 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2519 precursor RNA is designated SEQ ID:2505, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2505 is located at position 59910 relative to the genome of Mouse cytomegalovirus 1.

[35226] VGAM2519 precursor RNA, herein designated VGAM PRE-

CURSOR RNA, folds onto itself, forming VGAM2519 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35227] An enzyme complex designated DICER COMPLEX, dices the VGAM2519 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2519 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 75%) nucleotide sequence of VGAM2519 RNA is designated SEQ ID:5230, and is provided hereinbelow with reference to the sequence listing part.

[35228] VGAM2519 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM2519 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2519 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35229] VGAM2519 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2519 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2519 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2519 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2519 host

target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35230] The complementary binding of VGAM2519 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2519 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2519 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2519 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[35231] It is appreciated that VGAM2519 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2519 host target genes. The mRNA of each one of this plurality of VGAM2519 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2519 RNA, herein designated VGAM RNA, and which when bound by VGAM2519 RNA, herein

designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2519 host target proteins.

[35232] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2519 gene, herein designated VGAM GENE, on one or more VGAM2519 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35233] It is yet further appreciated that a function of VGAM2519 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2519 include diagnosis, prevention and

treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2519 correlate with, and may be deduced from, the identity of the host target genes which VGAM2519 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[35234] Nucleotide sequences of the VGAM2519 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2519 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2519 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2519 are further described hereinbelow with reference to Table 1.

[35235] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2519 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[35236] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2520 (VGAM2520) viral gene, which modulates ex-

pression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[35237] VGAM2520 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2520 was detected is described hereinabove with reference to Figs. 2-8.

[35238] VGAM2520 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2520 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[35239] VGAM2520 gene, herein designated VGAM GENE, encodes a VGAM2520 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2520 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2520 precursor RNA is designated SEQ ID:2506, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2506 is located at position 173931 relative to the genome of Mouse cytomegalovirus

1.

[35240] VGAM2520 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2520 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35241] An enzyme complex designated DICER COMPLEX, dices the VGAM2520 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2520 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2520 RNA is designated SEQ ID:5231, and is provided hereinbelow with reference to the sequence listing part.

[35242] VGAM2520 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2520 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2520 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35243] VGAM2520 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2520 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2520 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2520 RNA, herein designated

VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2520 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35244] The complementary binding of VGAM2520 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2520 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2520 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2520 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[35245] It is appreciated that VGAM2520 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2520 host target genes. The mRNA of each one of this plurality of VGAM2520 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM2520 RNA, herein designated VGAM RNA, and which when bound by VGAM2520 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2520 host target proteins.

[35246] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2520 gene, herein designated VGAM GENE, on one or more VGAM2520 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35247] It is yet further appreciated that a function of VGAM2520 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2520 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2520 correlate with, and may be deduced from, the identity of the host target genes which VGAM2520 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[35248] Nucleotide sequences of the VGAM2520 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2520 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2520 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2520 are further described hereinbelow with reference to Table 1.

[35249] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2520 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[35250] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present

invention, referred to here as Viral Genomic Address Messenger 2521 (VGAM2521) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[35251] VGAM2521 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2521 was detected is described hereinabove with reference to Figs. 2-8.

[35252] VGAM2521 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2521 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[35253] VGAM2521 gene, herein designated VGAM GENE, encodes a VGAM2521 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2521 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2521 precursor RNA is designated SEQ ID:2507, and is provided hereinbelow with reference to the sequence listing part. Nu-

cleotide sequence SEQ ID:2507 is located at position 9443 relative to the genome of Mouse cytomegalovirus 1.

[35254] VGAM2521 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2521 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35255] An enzyme complex designated DICER COMPLEX, dices the VGAM2521 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2521 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2521 RNA is designated SEQ ID:5232, and is provided hereinbelow with reference to the sequence

listing part.

[35256] VGAM2521 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2521 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2521 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35257] VGAM2521 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2521 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2521 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not

meant to be limiting VGAM2521 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2521 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35258] The complementary binding of VGAM2521 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2521 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2521 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2521 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[35259] It is appreciated that VGAM2521 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2521 host target genes. The mRNA of each one of this plurality of VGAM2521 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2521 RNA, herein designated VGAM RNA, and which when bound by VGAM2521 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2521 host target proteins.

[35260] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2521 gene, herein designated VGAM GENE, on one or more VGAM2521 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35261] It is yet further appreciated that a function of VGAM2521

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2521 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2521 correlate with, and may be deduced from, the identity of the host target genes which VGAM2521 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[35262] Nucleotide sequences of the VGAM2521 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2521 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2521 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2521 are further described hereinbelow with reference to Table 1.

[35263] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2521 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[35264] Fig. 1 further provides a conceptual description of another

novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2522 (VGAM2522) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[35265] VGAM2522 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2522 was detected is described hereinabove with reference to Figs. 2-8.

[35266] VGAM2522 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2522 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[35267] VGAM2522 gene, herein designated VGAM GENE, encodes a VGAM2522 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2522 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2522 precursor RNA is designated SEQ ID:2508, and is provided here-

inbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2508 is located at position 116189 relative to the genome of Mouse cytomegalovirus 1.

[35268] VGAM2522 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2522 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35269] An enzyme complex designated DICER COMPLEX, dices the VGAM2522 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2522 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide se-

quence of VGAM2522 RNA is designated SEQ ID:5233, and is provided hereinbelow with reference to the sequence listing part.

[35270] VGAM2522 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2522 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2522 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35271] VGAM2522 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2522 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2522 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is ap-

preciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2522 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2522 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35272] The complementary binding of VGAM2522 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2522 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2522 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2522 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[35273] It is appreciated that VGAM2522 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2522 host target genes. The mRNA of

each one of this plurality of VGAM2522 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2522 RNA, herein designated VGAM RNA, and which when bound by VGAM2522 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2522 host target proteins.

[35274] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2522 gene, herein designated VGAM GENE, on one or more VGAM2522 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science

294,779 (2001)).

[35275] It is yet further appreciated that a function of VGAM2522 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2522 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2522 correlate with, and may be deduced from, the identity of the host target genes which VGAM2522 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[35276] Nucleotide sequences of the VGAM2522 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2522 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2522 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2522 are further described hereinbelow with reference to Table 1.

[35277] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2522 RNA, herein designated VGAM RNA, are de-

scribed hereinbelow with reference to Table 2.

[35278] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2523 (VGAM2523) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[35279] VGAM2523 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2523 was detected is described hereinabove with reference to Figs. 2-8.

[35280] VGAM2523 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2523 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[35281] VGAM2523 gene, herein designated VGAM GENE, encodes a VGAM2523 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2523 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly

similar to the nucleotide sequence of VGAM2523 precursor RNA is designated SEQ ID:2509, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2509 is located at position 122311 relative to the genome of Mouse cytomegalovirus 1.

[35282] VGAM2523 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2523 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35283] An enzyme complex designated DICER COMPLEX, dices the VGAM2523 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2523 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 70%) nucleotide sequence of VGAM2523 RNA is designated SEQ ID:5234, and is provided hereinbelow with reference to the sequence listing part.

[35284] VGAM2523 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2523 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2523 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35285] VGAM2523 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2523 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2523 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3

such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2523 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2523 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35286] The complementary binding of VGAM2523 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2523 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2523 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2523 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[35287] It is appreciated that VGAM2523 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2523 host target genes. The mRNA of each one of this plurality of VGAM2523 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2523 RNA, herein designated VGAM RNA, and which when bound by VGAM2523 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2523 host target proteins.

[35288] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2523 gene, herein designated VGAM GENE, on one or more VGAM2523 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35289] It is yet further appreciated that a function of VGAM2523 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2523 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2523 correlate with, and may be deduced from, the identity of the host target genes which VGAM2523 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[35290] Nucleotide sequences of the VGAM2523 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2523 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2523 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2523 are further described hereinbelow with reference to Table 1.

[35291] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the

complementarity of each of these host target binding sites to VGAM2523 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[35292] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2524 (VGAM2524) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[35293] VGAM2524 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2524 was detected is described hereinabove with reference to Figs. 2-8.

[35294] VGAM2524 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2524 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[35295] VGAM2524 gene, herein designated VGAM GENE, encodes a VGAM2524 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2524 precursor RNA,

herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2524 precursor RNA is designated SEQ ID:2510, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2510 is located at position 180093 relative to the genome of Mouse cytomegalovirus 1.

[35296] VGAM2524 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2524 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35297] An enzyme complex designated DICER COMPLEX, dices the VGAM2524 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2524 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2524 RNA is designated SEQ ID:5235, and is provided hereinbelow with reference to the sequence listing part.

[35298] VGAM2524 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2524 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2524 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35299] VGAM2524 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2524 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2524 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed

sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2524 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2524 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35300] The complementary binding of VGAM2524 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2524 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2524 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2524 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target

protein is therefore outlined by a broken line.

[35301] It is appreciated that VGAM2524 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2524 host target genes. The mRNA of each one of this plurality of VGAM2524 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2524 RNA, herein designated VGAM RNA, and which when bound by VGAM2524 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2524 host target proteins.

[35302] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2524 gene, herein designated VGAM GENE, on one or more VGAM2524 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35303] It is yet further appreciated that a function of VGAM2524 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2524 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2524 correlate with, and may be deduced from, the identity of the host target genes which VGAM2524 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[35304] Nucleotide sequences of the VGAM2524 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2524 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2524 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2524 are further described hereinbelow with reference to Table 1.

[35305] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2524 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[35306] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2525 (VGAM2525) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[35307] VGAM2525 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2525 was detected is described hereinabove with reference to Figs. 2-8.

[35308] VGAM2525 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2525 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[35309] VGAM2525 gene, herein designated VGAM GENE, encodes a VGAM2525 precursor RNA, herein designated VGAM

PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2525 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2525 precursor RNA is designated SEQ ID:2511, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2511 is located at position 213327 relative to the genome of Mouse cytomegalovirus 1.

[35310] VGAM2525 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2525 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35311] An enzyme complex designated DICER COMPLEX, dices the VGAM2525 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2525 RNA,

herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2525 RNA is designated SEQ ID:5236, and is provided hereinbelow with reference to the sequence listing part.

[35312] VGAM2525 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2525 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2525 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35313] VGAM2525 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2525 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM2525 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2525 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2525 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35314] The complementary binding of VGAM2525 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2525 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2525 host target RNA, herein designated VGAM HOST TARGET

RNA, into VGAM2525 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[35315] It is appreciated that VGAM2525 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2525 host target genes. The mRNA of each one of this plurality of VGAM2525 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2525 RNA, herein designated VGAM RNA, and which when bound by VGAM2525 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2525 host target proteins.

[35316] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2525 gene, herein designated VGAM GENE, on one or more VGAM2525 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35317] It is yet further appreciated that a function of VGAM2525 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2525 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2525 correlate with, and may be deduced from, the identity of the host target genes which VGAM2525 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[35318] Nucleotide sequences of the VGAM2525 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2525 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2525 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2525 are further

described hereinbelow with reference to Table 1.

[35319] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2525 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[35320] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2526 (VGAM2526) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[35321] VGAM2526 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2526 was detected is described hereinabove with reference to Figs. 2-8.

[35322] VGAM2526 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2526 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[35323] VGAM2526 gene, herein designated VGAM GENE, encodes a VGAM2526 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2526 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2526 precursor RNA is designated SEQ ID:2512, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2512 is located at position 85449 relative to the genome of Mouse cytomegalovirus 1.

[35324] VGAM2526 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2526 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35325] An enzyme complex designated DICER COMPLEX, dices

the VGAM2526 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2526 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2526 RNA is designated SEQ ID:5237, and is provided hereinbelow with reference to the sequence listing part.

[35326] VGAM2526 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2526 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2526 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35327] VGAM2526 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2526 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2526 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2526 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2526 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35328] The complementary binding of VGAM2526 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2526 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM2526 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2526 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[35329] It is appreciated that VGAM2526 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2526 host target genes. The mRNA of each one of this plurality of VGAM2526 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2526 RNA, herein designated VGAM RNA, and which when bound by VGAM2526 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2526 host target proteins.

[35330] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2526 gene, herein designated VGAM GENE, on one or more VGAM2526 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35331] It is yet further appreciated that a function of VGAM2526 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2526 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2526 correlate with, and may be deduced from, the identity of the host target genes which VGAM2526 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[35332] Nucleotide sequences of the VGAM2526 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2526 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of

VGAM2526 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2526 are further described hereinbelow with reference to Table 1.

[35333] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2526 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[35334] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2527 (VGAM2527) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[35335] VGAM2527 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2527 was detected is described hereinabove with reference to Figs. 2-8.

[35336] VGAM2527 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse cytomegalovirus 1. VGAM2527 host target gene, herein designated VGAM

HOST TARGET GENE, is a human gene contained in the human genome.

[35337] VGAM2527 gene, herein designated VGAM GENE, encodes a VGAM2527 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2527 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2527 precursor RNA is designated SEQ ID:2513, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2513 is located at position 157147 relative to the genome of Mouse cytomegalovirus 1.

[35338] VGAM2527 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2527 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[35339] An enzyme complex designated DICER COMPLEX, dices the VGAM2527 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2527 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2527 RNA is designated SEQ ID:5238, and is provided hereinbelow with reference to the sequence listing part.

[35340] VGAM2527 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2527 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2527 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35341] VGAM2527 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM2527 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2527 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2527 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2527 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35342] The complementary binding of VGAM2527 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM2527 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2527 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2527 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[35343] It is appreciated that VGAM2527 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2527 host target genes. The mRNA of each one of this plurality of VGAM2527 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2527 RNA, herein designated VGAM RNA, and which when bound by VGAM2527 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2527 host target proteins.

[35344] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2527 gene, herein designated VGAM GENE, on one or more VGAM2527 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35345] It is yet further appreciated that a function of VGAM2527 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2527 include diagnosis, prevention and treatment of viral infection by Mouse cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2527 correlate with, and may be deduced from, the identity of the host target genes which VGAM2527 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[35346] Nucleotide sequences of the VGAM2527 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

diced VGAM2527 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2527 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2527 are further described hereinbelow with reference to Table 1.

[35347] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2527 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[35348] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2528 (VGAM2528) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[35349] VGAM2528 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2528 was detected is described hereinabove with reference to Figs. 2-8.

[35350] VGAM2528 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of Cowpox virus. VGAM2528 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[35351] VGAM2528 gene, herein designated VGAM GENE, encodes a VGAM2528 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2528 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2528 precursor RNA is designated SEQ ID:2514, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2514 is located at position 17101 relative to the genome of Cowpox virus.

[35352] VGAM2528 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2528 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35353] An enzyme complex designated DICER COMPLEX, dices the VGAM2528 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2528 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of VGAM2528 RNA is designated SEQ ID:5239, and is provided hereinbelow with reference to the sequence listing part.

[35354] VGAM2528 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2528 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2528 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35355] VGAM2528 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2528 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2528 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2528 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2528 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35356] The complementary binding of VGAM2528 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM2528 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2528 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2528 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[35357] It is appreciated that VGAM2528 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2528 host target genes. The mRNA of each one of this plurality of VGAM2528 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2528 RNA, herein designated VGAM RNA, and which when bound by VGAM2528 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2528 host target proteins.

[35358] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2528 gene, herein designated VGAM GENE, on one or more VGAM2528 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35359] It is yet further appreciated that a function of VGAM2528 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2528 include diagnosis, prevention and treatment of viral infection by Cowpox virus. Specific functions, and accordingly utilities, of VGAM2528 correlate with, and may be deduced from, the identity of the host target genes which VGAM2528 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[35360] Nucleotide sequences of the VGAM2528 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the diced VGAM2528 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2528 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2528 are further described hereinbelow with reference to Table 1.

[35361] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2528 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[35362] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2529 (VGAM2529) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[35363] VGAM2529 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2529 was detected is described hereinabove with reference to Figs. 2-8.

[35364] VGAM2529 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Pepper ringspot virus. VGAM2529 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[35365] VGAM2529 gene, herein designated VGAM GENE, encodes a VGAM2529 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2529 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2529 precursor RNA is designated SEQ ID:2515, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2515 is located at position 4230 relative to the genome of Pepper ringspot virus.

[35366] VGAM2529 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2529 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35367] An enzyme complex designated DICER COMPLEX, dices the VGAM2529 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2529 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 53%) nucleotide sequence of VGAM2529 RNA is designated SEQ ID:5240, and is provided hereinbelow with reference to the sequence listing part.

[35368] VGAM2529 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2529 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2529 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN COD-

ING and 3UTR respectively.

[35369] VGAM2529 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2529 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2529 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2529 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2529 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35370] The complementary binding of VGAM2529 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2529 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2529 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2529 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[35371] It is appreciated that VGAM2529 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2529 host target genes. The mRNA of each one of this plurality of VGAM2529 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2529 RNA, herein designated VGAM RNA, and which when bound by VGAM2529 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2529 host target proteins.

[35372] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2529 gene, herein designated VGAM GENE, on one

or more VGAM2529 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35373] It is yet further appreciated that a function of VGAM2529 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2529 include diagnosis, prevention and treatment of viral infection by Pepper ringspot virus. Specific functions, and accordingly utilities, of VGAM2529 correlate with, and may be deduced from, the identity of the host target genes which VGAM2529 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[35374] Nucleotide sequences of the VGAM2529 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2529 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2529 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2529 are further described hereinbelow with reference to Table 1.

[35375] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2529 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[35376] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2530 (VGAM2530) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[35377] VGAM2530 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2530 was detected is de-

scribed hereinabove with reference to Figs. 2-8.

[35378] VGAM2530 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Pepper ringspot virus. VGAM2530 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[35379] VGAM2530 gene, herein designated VGAM GENE, encodes a VGAM2530 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2530 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2530 precursor RNA is designated SEQ ID:2516, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2516 is located at position 1886 relative to the genome of Pepper ringspot virus.

[35380] VGAM2530 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2530 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35381] An enzyme complex designated DICER COMPLEX, dices the VGAM2530 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2530 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide sequence of VGAM2530 RNA is designated SEQ ID:5241, and is provided hereinbelow with reference to the sequence listing part.

[35382] VGAM2530 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2530 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2530 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and

a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35383] VGAM2530 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2530 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2530 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2530 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2530 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both

3UTR and 5UTR regions.

[35384] The complementary binding of VGAM2530 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2530 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2530 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2530 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[35385] It is appreciated that VGAM2530 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2530 host target genes. The mRNA of each one of this plurality of VGAM2530 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2530 RNA, herein designated VGAM RNA, and which when bound by VGAM2530 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2530 host target proteins.

[35386] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM2530 gene, herein designated VGAM GENE, on one or more VGAM2530 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35387] It is yet further appreciated that a function of VGAM2530 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2530 include diagnosis, prevention and treatment of viral infection by Pepper ringspot virus. Specific functions, and accordingly utilities, of VGAM2530 correlate with, and may be deduced from, the identity of the host target genes which VGAM2530 binds and inhibits, and the function of these host target genes, as

elaborated hereinbelow.

[35388] Nucleotide sequences of the VGAM2530 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2530 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2530 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2530 are further described hereinbelow with reference to Table 1.

[35389] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2530 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[35390] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2531 (VGAM2531) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[35391] VGAM2531 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene.

The method by which VGAM2531 was detected is described hereinabove with reference to Figs. 2-8.

[35392] VGAM2531 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Pepper ringspot virus. VGAM2531 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[35393] VGAM2531 gene, herein designated VGAM GENE, encodes a VGAM2531 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2531 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2531 precursor RNA is designated SEQ ID:2517, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2517 is located at position 2562 relative to the genome of Pepper ringspot virus.

[35394] VGAM2531 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2531 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35395] An enzyme complex designated DICER COMPLEX, dices the VGAM2531 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2531 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 57%) nucleotide sequence of VGAM2531 RNA is designated SEQ ID:5242, and is provided hereinbelow with reference to the sequence listing part.

[35396] VGAM2531 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2531 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2531 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding

gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35397] VGAM2531 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2531 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2531 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2531 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2531 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be lo-

cated in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35398] The complementary binding of VGAM2531 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2531 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2531 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2531 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[35399] It is appreciated that VGAM2531 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2531 host target genes. The mRNA of each one of this plurality of VGAM2531 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2531 RNA, herein designated VGAM RNA, and which when bound by VGAM2531 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2531 host target proteins.

[35400] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM2531 gene, herein designated VGAM GENE, on one or more VGAM2531 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35401] It is yet further appreciated that a function of VGAM2531 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2531 include diagnosis, prevention and treatment of viral infection by Pepper ringspot virus. Specific functions, and accordingly utilities, of VGAM2531 correlate with, and may be deduced from, the identity of the host target genes which VGAM2531 binds and in-

hibits, and the function of these host target genes, as elaborated hereinbelow.

[35402] Nucleotide sequences of the VGAM2531 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2531 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2531 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2531 are further described hereinbelow with reference to Table 1.

[35403] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2531 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[35404] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2532 (VGAM2532) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[35405] VGAM2532 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2532 was detected is described hereinabove with reference to Figs. 2-8.

[35406] VGAM2532 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rio Bravo virus. VGAM2532 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[35407] VGAM2532 gene, herein designated VGAM GENE, encodes a VGAM2532 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2532 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2532 precursor RNA is designated SEQ ID:2518, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2518 is located at position 643 relative to the genome of Rio Bravo virus.

[35408] VGAM2532 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2532 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35409] An enzyme complex designated DICER COMPLEX, dices the VGAM2532 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2532 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2532 RNA is designated SEQ ID:5243, and is provided hereinbelow with reference to the sequence listing part.

[35410] VGAM2532 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2532 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2532 host target RNA, herein designated VGAM HOST TARGET RNA, comprises

three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35411] VGAM2532 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2532 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2532 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2532 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2532 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an

example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35412] The complementary binding of VGAM2532 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2532 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2532 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2532 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[35413] It is appreciated that VGAM2532 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2532 host target genes. The mRNA of each one of this plurality of VGAM2532 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2532 RNA, herein designated VGAM RNA, and which when bound by VGAM2532 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2532 host target proteins.

[35414] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2532 gene, herein designated VGAM GENE, on one or more VGAM2532 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35415] It is yet further appreciated that a function of VGAM2532 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2532 include diagnosis, prevention and treatment of viral infection by Rio Bravo virus. Specific functions, and accordingly utilities, of VGAM2532 correlate with, and may be deduced from, the identity of the

host target genes which VGAM2532 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[35416] Nucleotide sequences of the VGAM2532 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2532 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2532 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2532 are further described hereinbelow with reference to Table 1.

[35417] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2532 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[35418] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2533 (VGAM2533) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[35419] VGAM2533 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2533 was detected is described hereinabove with reference to Figs. 2-8.

[35420] VGAM2533 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rio Bravo virus. VGAM2533 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[35421] VGAM2533 gene, herein designated VGAM GENE, encodes a VGAM2533 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2533 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2533 precursor RNA is designated SEQ ID:2519, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2519 is located at position 3063 relative to the genome of Rio Bravo virus.

[35422] VGAM2533 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2533 folded precursor RNA, herein designated VGAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35423] An enzyme complex designated DICER COMPLEX, dices the VGAM2533 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2533 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2533 RNA is designated SEQ ID:5244, and is provided hereinbelow with reference to the sequence listing part.

[35424] VGAM2533 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2533 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2533 host target RNA,

herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35425] VGAM2533 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2533 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2533 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2533 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2533 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host tar-

get binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35426] The complementary binding of VGAM2533 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2533 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2533 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2533 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[35427] It is appreciated that VGAM2533 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2533 host target genes. The mRNA of each one of this plurality of VGAM2533 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2533 RNA, herein designated VGAM RNA, and which when bound by VGAM2533 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2533 host target proteins.

[35428] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2533 gene, herein designated VGAM GENE, on one or more VGAM2533 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35429] It is yet further appreciated that a function of VGAM2533 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2533 include diagnosis, prevention and treatment of viral infection by Rio Bravo virus. Specific functions, and accordingly utilities, of VGAM2533 corre-

late with, and may be deduced from, the identity of the host target genes which VGAM2533 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[35430] Nucleotide sequences of the VGAM2533 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2533 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2533 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2533 are further described hereinbelow with reference to Table 1.

[35431] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2533 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[35432] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2534 (VGAM2534) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the

art.

[35433] VGAM2534 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2534 was detected is described hereinabove with reference to Figs. 2-8.

[35434] VGAM2534 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rio Bravo virus. VGAM2534 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[35435] VGAM2534 gene, herein designated VGAM GENE, encodes a VGAM2534 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2534 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2534 precursor RNA is designated SEQ ID:2520, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2520 is located at position 7314 relative to the genome of Rio Bravo virus.

[35436] VGAM2534 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2534 folded

precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35437] An enzyme complex designated DICER COMPLEX, dices the VGAM2534 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2534 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 90%) nucleotide sequence of VGAM2534 RNA is designated SEQ ID:5245, and is provided hereinbelow with reference to the sequence listing part.

[35438] VGAM2534 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2534 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM2534 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35439] VGAM2534 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2534 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2534 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2534 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2534 host target RNA, herein designated VGAM HOST TARGET RNA.

It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35440] The complementary binding of VGAM2534 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2534 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2534 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2534 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[35441] It is appreciated that VGAM2534 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2534 host target genes. The mRNA of each one of this plurality of VGAM2534 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2534 RNA, herein designated VGAM RNA, and which when bound by VGAM2534 RNA, herein designated VGAM RNA, causes inhibition of translation of

respective one or more VGAM2534 host target proteins.

[35442] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2534 gene, herein designated VGAM GENE, on one or more VGAM2534 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35443] It is yet further appreciated that a function of VGAM2534 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2534 include diagnosis, prevention and treatment of viral infection by Rio Bravo virus. Specific

functions, and accordingly utilities, of VGAM2534 correlate with, and may be deduced from, the identity of the host target genes which VGAM2534 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[35444] Nucleotide sequences of the VGAM2534 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2534 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2534 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2534 are further described hereinbelow with reference to Table 1.

[35445] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2534 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[35446] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2535 (VGAM2535) viral gene, which modulates expression of respective host target genes thereof, the func-

tion and utility of which host target genes is known in the art.

[35447] VGAM2535 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2535 was detected is described hereinabove with reference to Figs. 2-8.

[35448] VGAM2535 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rio Bravo virus. VGAM2535 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[35449] VGAM2535 gene, herein designated VGAM GENE, encodes a VGAM2535 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2535 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2535 precursor RNA is designated SEQ ID:2521, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2521 is located at position 5612 relative to the genome of Rio Bravo virus.

[35450] VGAM2535 precursor RNA, herein designated VGAM PRE-

CURSOR RNA, folds onto itself, forming VGAM2535 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35451] An enzyme complex designated DICER COMPLEX, dices the VGAM2535 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2535 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2535 RNA is designated SEQ ID:5246, and is provided hereinbelow with reference to the sequence listing part.

[35452] VGAM2535 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM2535 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2535 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35453] VGAM2535 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2535 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2535 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2535 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2535 host

target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35454] The complementary binding of VGAM2535 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2535 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2535 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2535 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[35455] It is appreciated that VGAM2535 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2535 host target genes. The mRNA of each one of this plurality of VGAM2535 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2535 RNA, herein designated VGAM RNA, and which when bound by VGAM2535 RNA, herein

designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2535 host target proteins.

[35456] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2535 gene, herein designated VGAM GENE, on one or more VGAM2535 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35457] It is yet further appreciated that a function of VGAM2535 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2535 include diagnosis, prevention and

treatment of viral infection by Rio Bravo virus. Specific functions, and accordingly utilities, of VGAM2535 correlate with, and may be deduced from, the identity of the host target genes which VGAM2535 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[35458] Nucleotide sequences of the VGAM2535 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2535 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2535 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2535 are further described hereinbelow with reference to Table 1.

[35459] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2535 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[35460] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2536 (VGAM2536) viral gene, which modulates ex-

pression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[35461] VGAM2536 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2536 was detected is described hereinabove with reference to Figs. 2-8.

[35462] VGAM2536 gene, herein designated VGAM GENE, is a viral gene contained in the genome of pestivirus Reindeer-1. VGAM2536 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[35463] VGAM2536 gene, herein designated VGAM GENE, encodes a VGAM2536 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2536 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2536 precursor RNA is designated SEQ ID:2522, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2522 is located at position 4448 relative to the genome of pestivirus Reindeer-1.

[35464] VGAM2536 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2536 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35465] An enzyme complex designated DICER COMPLEX, dices the VGAM2536 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2536 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2536 RNA is designated SEQ ID:5247, and is provided hereinbelow with reference to the sequence listing part.

[35466] VGAM2536 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2536 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2536 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35467] VGAM2536 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2536 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2536 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2536 RNA, herein designated VGAM RNA, may have a different number of host target

binding sites in untranslated regions of a VGAM2536 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35468] The complementary binding of VGAM2536 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2536 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2536 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2536 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[35469] It is appreciated that VGAM2536 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2536 host target genes. The mRNA of each one of this plurality of VGAM2536 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2536 RNA, herein designated VGAM

RNA, and which when bound by VGAM2536 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2536 host target proteins.

[35470] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2536 gene, herein designated VGAM GENE, on one or more VGAM2536 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35471] It is yet further appreciated that a function of VGAM2536 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM2536 include diagnosis, prevention and treatment of viral infection by pestivirus Reindeer-1. Specific functions, and accordingly utilities, of VGAM2536 correlate with, and may be deduced from, the identity of the host target genes which VGAM2536 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[35472] Nucleotide sequences of the VGAM2536 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2536 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2536 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2536 are further described hereinbelow with reference to Table 1.

[35473] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2536 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[35474] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Mes-

senger 2537 (VGAM2537) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[35475] VGAM2537 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2537 was detected is described hereinabove with reference to Figs. 2-8.

[35476] VGAM2537 gene, herein designated VGAM GENE, is a viral gene contained in the genome of pestivirus Reindeer-1. VGAM2537 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[35477] VGAM2537 gene, herein designated VGAM GENE, encodes a VGAM2537 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2537 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2537 precursor RNA is designated SEQ ID:2523, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2523 is located at position 4253

relative to the genome of pestivirus Reindeer-1.

[35478] VGAM2537 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2537 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35479] An enzyme complex designated DICER COMPLEX, dices the VGAM2537 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2537 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2537 RNA is designated SEQ ID:5248, and is provided hereinbelow with reference to the sequence listing part.

[35480] VGAM2537 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2537 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2537 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35481] VGAM2537 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2537 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2537 RNA, herein designated

VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2537 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35482] The complementary binding of VGAM2537 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2537 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2537 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2537 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[35483] It is appreciated that VGAM2537 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2537 host target genes. The mRNA of each one of this plurality of VGAM2537 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM2537 RNA, herein designated VGAM RNA, and which when bound by VGAM2537 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2537 host target proteins.

[35484] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2537 gene, herein designated VGAM GENE, on one or more VGAM2537 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35485] It is yet further appreciated that a function of VGAM2537 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of viral infection by pestivirus Reindeer-1. Specific functions, and accordingly utilities, of VGAM2537 correlate with, and may be deduced from, the identity of the host target genes which VGAM2537 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[35486] Nucleotide sequences of the VGAM2537 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2537 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2537 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2537 are further described hereinbelow with reference to Table 1.

[35487] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2537 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[35488] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present

invention, referred to here as Viral Genomic Address Messenger 2538 (VGAM2538) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[35489] VGAM2538 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2538 was detected is described hereinabove with reference to Figs. 2-8.

[35490] VGAM2538 gene, herein designated VGAM GENE, is a viral gene contained in the genome of pestivirus Reindeer-1. VGAM2538 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[35491] VGAM2538 gene, herein designated VGAM GENE, encodes a VGAM2538 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2538 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2538 precursor RNA is designated SEQ ID:2524, and is provided hereinbelow with reference to the sequence listing part. Nu-

cleotide sequence SEQ ID:2524 is located at position 2796 relative to the genome of pestivirus Reindeer-1.

[35492] VGAM2538 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2538 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35493] An enzyme complex designated DICER COMPLEX, dices the VGAM2538 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2538 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 81%) nucleotide sequence of VGAM2538 RNA is designated SEQ ID:5249, and is provided hereinbelow with reference to the sequence

listing part.

[35494] VGAM2538 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2538 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2538 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35495] VGAM2538 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2538 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2538 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not

meant to be limiting VGAM2538 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2538 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35496] The complementary binding of VGAM2538 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2538 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2538 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2538 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[35497] It is appreciated that VGAM2538 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2538 host target genes. The mRNA of each one of this plurality of VGAM2538 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2538 RNA, herein designated VGAM RNA, and which when bound by VGAM2538 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2538 host target proteins.

[35498] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2538 gene, herein designated VGAM GENE, on one or more VGAM2538 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35499] It is yet further appreciated that a function of VGAM2538

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2538 include diagnosis, prevention and treatment of viral infection by pestivirus Reindeer-1. Specific functions, and accordingly utilities, of VGAM2538 correlate with, and may be deduced from, the identity of the host target genes which VGAM2538 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[35500] Nucleotide sequences of the VGAM2538 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2538 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2538 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2538 are further described hereinbelow with reference to Table 1.

[35501] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2538 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[35502] Fig. 1 further provides a conceptual description of another

novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2539 (VGAM2539) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[35503] VGAM2539 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2539 was detected is described hereinabove with reference to Figs. 2-8.

[35504] VGAM2539 gene, herein designated VGAM GENE, is a viral gene contained in the genome of pestivirus Giraffe-1. VGAM2539 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[35505] VGAM2539 gene, herein designated VGAM GENE, encodes a VGAM2539 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2539 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2539 precursor RNA is designated SEQ ID:2525, and is provided here-

inbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2525 is located at position 1159 relative to the genome of pestivirus Giraffe-1.

[35506] VGAM2539 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2539 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35507] An enzyme complex designated DICER COMPLEX, dices the VGAM2539 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2539 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2539 RNA is designated SEQ ID:5250, and

is provided hereinbelow with reference to the sequence listing part.

[35508] VGAM2539 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2539 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2539 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35509] VGAM2539 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2539 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2539 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites

shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2539 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2539 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35510] The complementary binding of VGAM2539 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2539 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2539 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2539 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[35511] It is appreciated that VGAM2539 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2539 host target genes. The mRNA of each one of this plurality of VGAM2539 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2539 RNA, herein designated VGAM RNA, and which when bound by VGAM2539 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2539 host target proteins.

[35512] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2539 gene, herein designated VGAM GENE, on one or more VGAM2539 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35513] It is yet further appreciated that a function of VGAM2539 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2539 include diagnosis, prevention and treatment of viral infection by pestivirus Giraffe-1. Specific functions, and accordingly utilities, of VGAM2539 correlate with, and may be deduced from, the identity of the host target genes which VGAM2539 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[35514] Nucleotide sequences of the VGAM2539 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2539 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2539 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2539 are further described hereinbelow with reference to Table 1.

[35515] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2539 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[35516] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2540 (VGAM2540) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[35517] VGAM2540 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2540 was detected is described hereinabove with reference to Figs. 2-8.

[35518] VGAM2540 gene, herein designated VGAM GENE, is a viral gene contained in the genome of pestivirus Giraffe-1. VGAM2540 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[35519] VGAM2540 gene, herein designated VGAM GENE, encodes a VGAM2540 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2540 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2540 precur-

sor RNA is designated SEQ ID:2526, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2526 is located at position 4480 relative to the genome of pestivirus Giraffe-1.

[35520] VGAM2540 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2540 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35521] An enzyme complex designated DICER COMPLEX, dices the VGAM2540 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2540 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide se-

quence of VGAM2540 RNA is designated SEQ ID:5251, and is provided hereinbelow with reference to the sequence listing part.

[35522] VGAM2540 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2540 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2540 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35523] VGAM2540 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2540 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2540 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is ap-

preciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2540 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2540 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35524] The complementary binding of VGAM2540 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2540 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2540 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2540 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[35525] It is appreciated that VGAM2540 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2540 host target genes. The mRNA of

each one of this plurality of VGAM2540 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2540 RNA, herein designated VGAM RNA, and which when bound by VGAM2540 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2540 host target proteins.

[35526] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2540 gene, herein designated VGAM GENE, on one or more VGAM2540 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science

294,779 (2001)).

[35527] It is yet further appreciated that a function of VGAM2540 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2540 include diagnosis, prevention and treatment of viral infection by pestivirus Giraffe-1. Specific functions, and accordingly utilities, of VGAM2540 correlate with, and may be deduced from, the identity of the host target genes which VGAM2540 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[35528] Nucleotide sequences of the VGAM2540 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2540 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2540 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2540 are further described hereinbelow with reference to Table 1.

[35529] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2540 RNA, herein designated VGAM RNA, are de-

scribed hereinbelow with reference to Table 2.

[35530] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2541 (VGAM2541) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[35531] VGAM2541 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2541 was detected is described hereinabove with reference to Figs. 2-8.

[35532] VGAM2541 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Langat virus. VGAM2541 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[35533] VGAM2541 gene, herein designated VGAM GENE, encodes a VGAM2541 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2541 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2541 precur-

sor RNA is designated SEQ ID:2527, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2527 is located at position 1698 relative to the genome of Langat virus.

[35534] VGAM2541 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2541 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35535] An enzyme complex designated DICER COMPLEX, dices the VGAM2541 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2541 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide se-

quence of VGAM2541 RNA is designated SEQ ID:5252, and is provided hereinbelow with reference to the sequence listing part.

[35536] VGAM2541 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2541 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2541 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35537] VGAM2541 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2541 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2541 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is ap-

preciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2541 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2541 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35538] The complementary binding of VGAM2541 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2541 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2541 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2541 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[35539] It is appreciated that VGAM2541 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2541 host target genes. The mRNA of

each one of this plurality of VGAM2541 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2541 RNA, herein designated VGAM RNA, and which when bound by VGAM2541 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2541 host target proteins.

[35540] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2541 gene, herein designated VGAM GENE, on one or more VGAM2541 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science

294,779 (2001)).

[35541] It is yet further appreciated that a function of VGAM2541 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2541 include diagnosis, prevention and treatment of viral infection by Langat virus. Specific functions, and accordingly utilities, of VGAM2541 correlate with, and may be deduced from, the identity of the host target genes which VGAM2541 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[35542] Nucleotide sequences of the VGAM2541 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2541 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2541 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2541 are further described hereinbelow with reference to Table 1.

[35543] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2541 RNA, herein designated VGAM RNA, are de-

scribed hereinbelow with reference to Table 2.

[35544] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2542 (VGAM2542) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[35545] VGAM2542 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2542 was detected is described hereinabove with reference to Figs. 2-8.

[35546] VGAM2542 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Langat virus. VGAM2542 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[35547] VGAM2542 gene, herein designated VGAM GENE, encodes a VGAM2542 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2542 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2542 precur-

sor RNA is designated SEQ ID:2528, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2528 is located at position 9086 relative to the genome of Langat virus.

[35548] VGAM2542 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2542 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35549] An enzyme complex designated DICER COMPLEX, dices the VGAM2542 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2542 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide se-

quence of VGAM2542 RNA is designated SEQ ID:5253, and is provided hereinbelow with reference to the sequence listing part.

[35550] VGAM2542 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2542 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2542 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35551] VGAM2542 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2542 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2542 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is ap-

preciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2542 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2542 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35552] The complementary binding of VGAM2542 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2542 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2542 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2542 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[35553] It is appreciated that VGAM2542 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2542 host target genes. The mRNA of

each one of this plurality of VGAM2542 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2542 RNA, herein designated VGAM RNA, and which when bound by VGAM2542 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2542 host target proteins.

[35554] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2542 gene, herein designated VGAM GENE, on one or more VGAM2542 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science

294,779 (2001)).

[35555] It is yet further appreciated that a function of VGAM2542 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2542 include diagnosis, prevention and treatment of viral infection by Langat virus. Specific functions, and accordingly utilities, of VGAM2542 correlate with, and may be deduced from, the identity of the host target genes which VGAM2542 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[35556] Nucleotide sequences of the VGAM2542 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2542 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2542 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2542 are further described hereinbelow with reference to Table 1.

[35557] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2542 RNA, herein designated VGAM RNA, are de-

scribed hereinbelow with reference to Table 2.

[35558] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2543 (VGAM2543) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[35559] VGAM2543 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2543 was detected is described hereinabove with reference to Figs. 2-8.

[35560] VGAM2543 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Langat virus. VGAM2543 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[35561] VGAM2543 gene, herein designated VGAM GENE, encodes a VGAM2543 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2543 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2543 precur-

sor RNA is designated SEQ ID:2529, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2529 is located at position 976 relative to the genome of Langat virus.

[35562] VGAM2543 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2543 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35563] An enzyme complex designated DICER COMPLEX, dices the VGAM2543 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2543 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide se-

quence of VGAM2543 RNA is designated SEQ ID:5254, and is provided hereinbelow with reference to the sequence listing part.

[35564] VGAM2543 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2543 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2543 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35565] VGAM2543 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2543 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2543 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is ap-

preciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2543 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2543 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35566] The complementary binding of VGAM2543 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2543 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2543 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2543 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[35567] It is appreciated that VGAM2543 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2543 host target genes. The mRNA of

each one of this plurality of VGAM2543 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2543 RNA, herein designated VGAM RNA, and which when bound by VGAM2543 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2543 host target proteins.

[35568] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2543 gene, herein designated VGAM GENE, on one or more VGAM2543 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science

294,779 (2001)).

[35569] It is yet further appreciated that a function of VGAM2543 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2543 include diagnosis, prevention and treatment of viral infection by Langat virus. Specific functions, and accordingly utilities, of VGAM2543 correlate with, and may be deduced from, the identity of the host target genes which VGAM2543 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[35570] Nucleotide sequences of the VGAM2543 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2543 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2543 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2543 are further described hereinbelow with reference to Table 1.

[35571] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2543 RNA, herein designated VGAM RNA, are de-

scribed hereinbelow with reference to Table 2.

[35572] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2544 (VGAM2544) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[35573] VGAM2544 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2544 was detected is described hereinabove with reference to Figs. 2-8.

[35574] VGAM2544 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Langat virus. VGAM2544 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[35575] VGAM2544 gene, herein designated VGAM GENE, encodes a VGAM2544 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2544 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2544 precur-

sor RNA is designated SEQ ID:2530, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2530 is located at position 9387 relative to the genome of Langat virus.

[35576] VGAM2544 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2544 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35577] An enzyme complex designated DICER COMPLEX, dices the VGAM2544 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2544 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide se-

quence of VGAM2544 RNA is designated SEQ ID:5255, and is provided hereinbelow with reference to the sequence listing part.

[35578] VGAM2544 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2544 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2544 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35579] VGAM2544 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2544 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2544 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is ap-

preciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2544 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2544 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35580] The complementary binding of VGAM2544 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2544 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2544 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2544 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[35581] It is appreciated that VGAM2544 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2544 host target genes. The mRNA of

each one of this plurality of VGAM2544 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2544 RNA, herein designated VGAM RNA, and which when bound by VGAM2544 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2544 host target proteins.

[35582] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2544 gene, herein designated VGAM GENE, on one or more VGAM2544 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science

294,779 (2001)).

[35583] It is yet further appreciated that a function of VGAM2544 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2544 include diagnosis, prevention and treatment of viral infection by Langat virus. Specific functions, and accordingly utilities, of VGAM2544 correlate with, and may be deduced from, the identity of the host target genes which VGAM2544 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[35584] Nucleotide sequences of the VGAM2544 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2544 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2544 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2544 are further described hereinbelow with reference to Table 1.

[35585] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2544 RNA, herein designated VGAM RNA, are de-

scribed hereinbelow with reference to Table 2.

[35586] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2545 (VGAM2545) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[35587] VGAM2545 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2545 was detected is described hereinabove with reference to Figs. 2-8.

[35588] VGAM2545 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Langat virus. VGAM2545 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[35589] VGAM2545 gene, herein designated VGAM GENE, encodes a VGAM2545 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2545 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2545 precur-

sor RNA is designated SEQ ID:2531, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2531 is located at position 3636 relative to the genome of Langat virus.

[35590] VGAM2545 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2545 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35591] An enzyme complex designated DICER COMPLEX, dices the VGAM2545 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2545 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide se-

quence of VGAM2545 RNA is designated SEQ ID:5256, and is provided hereinbelow with reference to the sequence listing part.

[35592] VGAM2545 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2545 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2545 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35593] VGAM2545 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2545 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2545 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is ap-

preciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2545 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2545 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35594] The complementary binding of VGAM2545 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2545 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2545 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2545 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[35595] It is appreciated that VGAM2545 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2545 host target genes. The mRNA of

each one of this plurality of VGAM2545 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2545 RNA, herein designated VGAM RNA, and which when bound by VGAM2545 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2545 host target proteins.

[35596] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2545 gene, herein designated VGAM GENE, on one or more VGAM2545 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science

294,779 (2001)).

[35597] It is yet further appreciated that a function of VGAM2545 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2545 include diagnosis, prevention and treatment of viral infection by Langat virus. Specific functions, and accordingly utilities, of VGAM2545 correlate with, and may be deduced from, the identity of the host target genes which VGAM2545 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[35598] Nucleotide sequences of the VGAM2545 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2545 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2545 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2545 are further described hereinbelow with reference to Table 1.

[35599] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2545 RNA, herein designated VGAM RNA, are de-

scribed hereinbelow with reference to Table 2.

[35600] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2546 (VGAM2546) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[35601] VGAM2546 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2546 was detected is described hereinabove with reference to Figs. 2-8.

[35602] VGAM2546 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Langat virus. VGAM2546 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[35603] VGAM2546 gene, herein designated VGAM GENE, encodes a VGAM2546 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2546 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2546 precur-

sor RNA is designated SEQ ID:2532, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2532 is located at position 3420 relative to the genome of Langat virus.

[35604] VGAM2546 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2546 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35605] An enzyme complex designated DICER COMPLEX, dices the VGAM2546 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2546 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 47%) nucleotide se-

quence of VGAM2546 RNA is designated SEQ ID:5257, and is provided hereinbelow with reference to the sequence listing part.

[35606] VGAM2546 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2546 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2546 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35607] VGAM2546 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2546 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2546 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is ap-

preciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2546 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2546 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35608] The complementary binding of VGAM2546 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2546 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2546 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2546 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[35609] It is appreciated that VGAM2546 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2546 host target genes. The mRNA of

each one of this plurality of VGAM2546 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2546 RNA, herein designated VGAM RNA, and which when bound by VGAM2546 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2546 host target proteins.

[35610] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2546 gene, herein designated VGAM GENE, on one or more VGAM2546 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science

294,779 (2001)).

[35611] It is yet further appreciated that a function of VGAM2546 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2546 include diagnosis, prevention and treatment of viral infection by Langat virus. Specific functions, and accordingly utilities, of VGAM2546 correlate with, and may be deduced from, the identity of the host target genes which VGAM2546 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[35612] Nucleotide sequences of the VGAM2546 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2546 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2546 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2546 are further described hereinbelow with reference to Table 1.

[35613] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2546 RNA, herein designated VGAM RNA, are de-

scribed hereinbelow with reference to Table 2.

[35614] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2547 (VGAM2547) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[35615] VGAM2547 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2547 was detected is described hereinabove with reference to Figs. 2-8.

[35616] VGAM2547 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Langat virus. VGAM2547 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[35617] VGAM2547 gene, herein designated VGAM GENE, encodes a VGAM2547 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2547 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2547 precur-

sor RNA is designated SEQ ID:2533, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2533 is located at position 6689 relative to the genome of Langat virus.

[35618] VGAM2547 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2547 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35619] An enzyme complex designated DICER COMPLEX, dices the VGAM2547 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2547 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide se-

quence of VGAM2547 RNA is designated SEQ ID:5258, and is provided hereinbelow with reference to the sequence listing part.

[35620] VGAM2547 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2547 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2547 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35621] VGAM2547 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2547 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2547 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is ap-

preciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2547 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2547 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35622] The complementary binding of VGAM2547 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2547 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2547 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2547 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[35623] It is appreciated that VGAM2547 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2547 host target genes. The mRNA of

each one of this plurality of VGAM2547 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2547 RNA, herein designated VGAM RNA, and which when bound by VGAM2547 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2547 host target proteins.

[35624] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2547 gene, herein designated VGAM GENE, on one or more VGAM2547 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science

294,779 (2001)).

[35625] It is yet further appreciated that a function of VGAM2547 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2547 include diagnosis, prevention and treatment of viral infection by Langat virus. Specific functions, and accordingly utilities, of VGAM2547 correlate with, and may be deduced from, the identity of the host target genes which VGAM2547 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[35626] Nucleotide sequences of the VGAM2547 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2547 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2547 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2547 are further described hereinbelow with reference to Table 1.

[35627] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2547 RNA, herein designated VGAM RNA, are de-

scribed hereinbelow with reference to Table 2.

[35628] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2548 (VGAM2548) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[35629] VGAM2548 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2548 was detected is described hereinabove with reference to Figs. 2-8.

[35630] VGAM2548 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Saccharomyces cerevisiae virus L-A. VGAM2548 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[35631] VGAM2548 gene, herein designated VGAM GENE, encodes a VGAM2548 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2548 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly

similar to the nucleotide sequence of VGAM2548 precursor RNA is designated SEQ ID:2534, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2534 is located at position 4007 relative to the genome of Saccharomyces cerevisiae virus L-A.

[35632] VGAM2548 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2548 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35633] An enzyme complex designated DICER COMPLEX, dices the VGAM2548 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2548 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2548 RNA is designated SEQ ID:5259, and is provided hereinbelow with reference to the sequence listing part.

[35634] VGAM2548 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2548 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2548 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35635] VGAM2548 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2548 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2548 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3

such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2548 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2548 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35636] The complementary binding of VGAM2548 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2548 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2548 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2548 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[35637] It is appreciated that VGAM2548 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2548 host target genes. The mRNA of each one of this plurality of VGAM2548 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2548 RNA, herein designated VGAM RNA, and which when bound by VGAM2548 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2548 host target proteins.

[35638] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2548 gene, herein designated VGAM GENE, on one or more VGAM2548 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35639] It is yet further appreciated that a function of VGAM2548 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2548 include diagnosis, prevention and treatment of viral infection by Saccharomyces cerevisiae virus L-A. Specific functions, and accordingly utilities, of VGAM2548 correlate with, and may be deduced from, the identity of the host target genes which VGAM2548 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[35640] Nucleotide sequences of the VGAM2548 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2548 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2548 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2548 are further described hereinbelow with reference to Table 1.

[35641] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the

complementarity of each of these host target binding sites to VGAM2548 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[35642] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2549 (VGAM2549) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[35643] VGAM2549 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2549 was detected is described hereinabove with reference to Figs. 2-8.

[35644] VGAM2549 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Saccharomyces cerevisiae virus L-A. VGAM2549 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[35645] VGAM2549 gene, herein designated VGAM GENE, encodes a VGAM2549 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2549 precursor RNA,

herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2549 precursor RNA is designated SEQ ID:2535, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2535 is located at position 2612 relative to the genome of Saccharomyces cerevisiae virus L-A.

[35646] VGAM2549 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2549 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35647] An enzyme complex designated DICER COMPLEX, dices the VGAM2549 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2549 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2549 RNA is designated SEQ ID:5260, and is provided hereinbelow with reference to the sequence listing part.

[35648] VGAM2549 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2549 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2549 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35649] VGAM2549 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2549 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2549 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed

sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2549 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2549 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35650] The complementary binding of VGAM2549 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2549 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2549 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2549 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target

protein is therefore outlined by a broken line.

[35651] It is appreciated that VGAM2549 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2549 host target genes. The mRNA of each one of this plurality of VGAM2549 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2549 RNA, herein designated VGAM RNA, and which when bound by VGAM2549 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2549 host target proteins.

[35652] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2549 gene, herein designated VGAM GENE, on one or more VGAM2549 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35653] It is yet further appreciated that a function of VGAM2549 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2549 include diagnosis, prevention and treatment of viral infection by Saccharomyces cerevisiae virus L-A. Specific functions, and accordingly utilities, of VGAM2549 correlate with, and may be deduced from, the identity of the host target genes which VGAM2549 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[35654] Nucleotide sequences of the VGAM2549 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2549 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2549 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2549 are further described hereinbelow with reference to Table 1.

[35655] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2549 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[35656] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2550 (VGAM2550) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[35657] VGAM2550 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2550 was detected is described hereinabove with reference to Figs. 2-8.

[35658] VGAM2550 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Saccharomyces cerevisiae virus L-A. VGAM2550 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[35659] VGAM2550 gene, herein designated VGAM GENE, encodes a VGAM2550 precursor RNA, herein designated VGAM

PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2550 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2550 precursor RNA is designated SEQ ID:2536, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2536 is located at position 4405 relative to the genome of Saccharomyces cerevisiae virus L-A.

[35660] VGAM2550 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2550 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35661] An enzyme complex designated DICER COMPLEX, dices the VGAM2550 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2550 RNA,

herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2550 RNA is designated SEQ ID:5261, and is provided hereinbelow with reference to the sequence listing part.

[35662] VGAM2550 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2550 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2550 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35663] VGAM2550 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2550 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM2550 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2550 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2550 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35664] The complementary binding of VGAM2550 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2550 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2550 host target RNA, herein designated VGAM HOST TARGET

RNA, into VGAM2550 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[35665] It is appreciated that VGAM2550 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2550 host target genes. The mRNA of each one of this plurality of VGAM2550 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2550 RNA, herein designated VGAM RNA, and which when bound by VGAM2550 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2550 host target proteins.

[35666] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2550 gene, herein designated VGAM GENE, on one or more VGAM2550 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35667] It is yet further appreciated that a function of VGAM2550 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2550 include diagnosis, prevention and treatment of viral infection by Saccharomyces cerevisiae virus L-A. Specific functions, and accordingly utilities, of VGAM2550 correlate with, and may be deduced from, the identity of the host target genes which VGAM2550 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[35668] Nucleotide sequences of the VGAM2550 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2550 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2550 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2550 are further

described hereinbelow with reference to Table 1.

[35669] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2550 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[35670] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2551 (VGAM2551) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[35671] VGAM2551 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2551 was detected is described hereinabove with reference to Figs. 2-8.

[35672] VGAM2551 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rice yellow stunt virus. VGAM2551 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[35673] VGAM2551 gene, herein designated VGAM GENE, encodes a VGAM2551 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2551 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2551 precursor RNA is designated SEQ ID:2537, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2537 is located at position 11536 relative to the genome of Rice yellow stunt virus.

[35674] VGAM2551 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2551 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35675] An enzyme complex designated DICER COMPLEX, dices the VGAM2551 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, into VGAM2551 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 75%) nucleotide sequence of VGAM2551 RNA is designated SEQ ID:5262, and is provided hereinbelow with reference to the sequence listing part.

[35676] VGAM2551 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2551 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2551 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35677] VGAM2551 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2551 host target RNA, herein designated VGAM HOST TARGET RNA. This

complementary binding is due to the fact that the nucleotide sequence of VGAM2551 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2551 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2551 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35678] The complementary binding of VGAM2551 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2551 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2551

host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2551 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[35679] It is appreciated that VGAM2551 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2551 host target genes. The mRNA of each one of this plurality of VGAM2551 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2551 RNA, herein designated VGAM RNA, and which when bound by VGAM2551 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2551 host target proteins.

[35680] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2551 gene, herein designated VGAM GENE, on one or more VGAM2551 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35681] It is yet further appreciated that a function of VGAM2551 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2551 include diagnosis, prevention and treatment of viral infection by Rice yellow stunt virus. Specific functions, and accordingly utilities, of VGAM2551 correlate with, and may be deduced from, the identity of the host target genes which VGAM2551 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[35682] Nucleotide sequences of the VGAM2551 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2551 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2551 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM2551 are further described hereinbelow with reference to Table 1.

[35683] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2551 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[35684] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2552 (VGAM2552) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[35685] VGAM2552 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2552 was detected is described hereinabove with reference to Figs. 2-8.

[35686] VGAM2552 gene, herein designated VGAM GENE, is a viral gene contained in the genome of rice ragged stunt virus. VGAM2552 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[35687] VGAM2552 gene, herein designated VGAM GENE, encodes a VGAM2552 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2552 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2552 precur-

sor RNA is designated SEQ ID:2538, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2538 is located at position 3478 relative to the genome of rice ragged stunt virus.

[35688] VGAM2552 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2552 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35689] An enzyme complex designated DICER COMPLEX, dices the VGAM2552 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2552 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 70%) nucleotide se-

quence of VGAM2552 RNA is designated SEQ ID:5263, and is provided hereinbelow with reference to the sequence listing part.

[35690] VGAM2552 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2552 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2552 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35691] VGAM2552 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2552 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2552 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is ap-

preciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2552 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2552 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35692] The complementary binding of VGAM2552 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2552 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2552 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2552 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[35693] It is appreciated that VGAM2552 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2552 host target genes. The mRNA of

each one of this plurality of VGAM2552 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2552 RNA, herein designated VGAM RNA, and which when bound by VGAM2552 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2552 host target proteins.

[35694] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2552 gene, herein designated VGAM GENE, on one or more VGAM2552 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science

294,779 (2001)).

[35695] It is yet further appreciated that a function of VGAM2552 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2552 include diagnosis, prevention and treatment of viral infection by rice ragged stunt virus. Specific functions, and accordingly utilities, of VGAM2552 correlate with, and may be deduced from, the identity of the host target genes which VGAM2552 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[35696] Nucleotide sequences of the VGAM2552 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2552 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2552 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2552 are further described hereinbelow with reference to Table 1.

[35697] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2552 RNA, herein designated VGAM RNA, are de-

scribed hereinbelow with reference to Table 2.

[35698] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2553 (VGAM2553) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[35699] VGAM2553 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2553 was detected is described hereinabove with reference to Figs. 2-8.

[35700] VGAM2553 gene, herein designated VGAM GENE, is a viral gene contained in the genome of rice ragged stunt virus. VGAM2553 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[35701] VGAM2553 gene, herein designated VGAM GENE, encodes a VGAM2553 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2553 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly

similar to the nucleotide sequence of VGAM2553 precursor RNA is designated SEQ ID:2539, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2539 is located at position 271 relative to the genome of rice ragged stunt virus.

[35702] VGAM2553 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2553 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35703] An enzyme complex designated DICER COMPLEX, dices the VGAM2553 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2553 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2553 RNA is designated SEQ ID:5264, and is provided hereinbelow with reference to the sequence listing part.

[35704] VGAM2553 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2553 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2553 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35705] VGAM2553 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2553 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2553 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I,

BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2553 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2553 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35706] The complementary binding of VGAM2553 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2553 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2553 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2553 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[35707] It is appreciated that VGAM2553 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM2553 host target genes. The mRNA of each one of this plurality of VGAM2553 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2553 RNA, herein designated VGAM RNA, and which when bound by VGAM2553 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2553 host target proteins.

[35708] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2553 gene, herein designated VGAM GENE, on one or more VGAM2553 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35709] It is yet further appreciated that a function of VGAM2553 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2553 include diagnosis, prevention and treatment of viral infection by rice ragged stunt virus. Specific functions, and accordingly utilities, of VGAM2553 correlate with, and may be deduced from, the identity of the host target genes which VGAM2553 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[35710] Nucleotide sequences of the VGAM2553 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2553 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2553 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2553 are further described hereinbelow with reference to Table 1.

[35711] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites

to VGAM2553 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[35712] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2554 (VGAM2554) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[35713] VGAM2554 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2554 was detected is described hereinabove with reference to Figs. 2-8.

[35714] VGAM2554 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Plautia stali intestine virus. VGAM2554 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[35715] VGAM2554 gene, herein designated VGAM GENE, encodes a VGAM2554 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2554 precursor RNA, herein designated VGAM PRECURSOR RNA, does not en-

code a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2554 precursor RNA is designated SEQ ID:2540, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2540 is located at position 685 relative to the genome of Plautia stali intestine virus.

[35716] VGAM2554 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2554 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35717] An enzyme complex designated DICER COMPLEX, dices the VGAM2554 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2554 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 83%) nucleotide sequence of VGAM2554 RNA is designated SEQ ID:5265, and is provided hereinbelow with reference to the sequence listing part.

[35718] VGAM2554 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2554 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2554 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35719] VGAM2554 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2554 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2554 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3

such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2554 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2554 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35720] The complementary binding of VGAM2554 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2554 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2554 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2554 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[35721] It is appreciated that VGAM2554 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2554 host target genes. The mRNA of each one of this plurality of VGAM2554 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2554 RNA, herein designated VGAM RNA, and which when bound by VGAM2554 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2554 host target proteins.

[35722] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2554 gene, herein designated VGAM GENE, on one or more VGAM2554 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35723] It is yet further appreciated that a function of VGAM2554 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2554 include diagnosis, prevention and treatment of viral infection by Plautia stali intestine virus. Specific functions, and accordingly utilities, of VGAM2554 correlate with, and may be deduced from, the identity of the host target genes which VGAM2554 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[35724] Nucleotide sequences of the VGAM2554 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2554 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2554 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2554 are further described hereinbelow with reference to Table 1.

[35725] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the

complementarity of each of these host target binding sites to VGAM2554 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[35726] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2555 (VGAM2555) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[35727] VGAM2555 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2555 was detected is described hereinabove with reference to Figs. 2-8.

[35728] VGAM2555 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Plautia stali intestine virus. VGAM2555 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[35729] VGAM2555 gene, herein designated VGAM GENE, encodes a VGAM2555 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2555 precursor RNA,

herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2555 precursor RNA is designated SEQ ID:2541, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2541 is located at position 3272 relative to the genome of Plautia stali intestine virus.

[35730] VGAM2555 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2555 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35731] An enzyme complex designated DICER COMPLEX, dices the VGAM2555 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2555 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2555 RNA is designated SEQ ID:5266, and is provided hereinbelow with reference to the sequence listing part.

[35732] VGAM2555 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2555 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2555 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35733] VGAM2555 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2555 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2555 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host

target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2555 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2555 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35734] The complementary binding of VGAM2555 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2555 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2555 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2555 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[35735] It is appreciated that VGAM2555 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2555 host target genes. The mRNA of each one of this plurality of VGAM2555 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2555 RNA, herein designated VGAM RNA, and which when bound by VGAM2555 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2555 host target proteins.

[35736] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2555 gene, herein designated VGAM GENE, on one or more VGAM2555 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35737] It is yet further appreciated that a function of VGAM2555 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2555 include diagnosis, prevention and treatment of viral infection by Plautia stali intestine virus. Specific functions, and accordingly utilities, of VGAM2555 correlate with, and may be deduced from, the identity of the host target genes which VGAM2555 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[35738] Nucleotide sequences of the VGAM2555 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2555 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2555 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2555 are further described hereinbelow with reference to Table 1.

[35739] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2555 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[35740] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2556 (VGAM2556) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[35741] VGAM2556 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2556 was detected is described hereinabove with reference to Figs. 2-8.

[35742] VGAM2556 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Plautia stali intestine virus. VGAM2556 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[35743] VGAM2556 gene, herein designated VGAM GENE, encodes a VGAM2556 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and un-

like most ordinary genes, VGAM2556 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2556 precursor RNA is designated SEQ ID:2542, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2542 is located at position 4204 relative to the genome of Plautia stali intestine virus.

[35744] VGAM2556 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2556 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35745] An enzyme complex designated DICER COMPLEX, dices the VGAM2556 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2556 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 48%) nucleotide sequence of VGAM2556 RNA is designated SEQ ID:5267, and is provided hereinbelow with reference to the sequence listing part.

[35746] VGAM2556 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2556 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2556 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35747] VGAM2556 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2556 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2556 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed

sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2556 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2556 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35748] The complementary binding of VGAM2556 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2556 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2556 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2556 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target

protein is therefore outlined by a broken line.

[35749] It is appreciated that VGAM2556 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2556 host target genes. The mRNA of each one of this plurality of VGAM2556 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2556 RNA, herein designated VGAM RNA, and which when bound by VGAM2556 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2556 host target proteins.

[35750] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2556 gene, herein designated VGAM GENE, on one or more VGAM2556 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35751] It is yet further appreciated that a function of VGAM2556 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2556 include diagnosis, prevention and treatment of viral infection by Plautia stali intestine virus. Specific functions, and accordingly utilities, of VGAM2556 correlate with, and may be deduced from, the identity of the host target genes which VGAM2556 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[35752] Nucleotide sequences of the VGAM2556 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2556 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2556 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2556 are further described hereinbelow with reference to Table 1.

[35753] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2556 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[35754] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2557 (VGAM2557) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[35755] VGAM2557 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2557 was detected is described hereinabove with reference to Figs. 2-8.

[35756] VGAM2557 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Himetobi P virus. VGAM2557 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[35757] VGAM2557 gene, herein designated VGAM GENE, encodes a VGAM2557 precursor RNA, herein designated VGAM

PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2557 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2557 precursor RNA is designated SEQ ID:2543, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2543 is located at position 8347 relative to the genome of Himetobi P virus.

[35758] VGAM2557 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2557 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35759] An enzyme complex designated DICER COMPLEX, dices the VGAM2557 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2557 RNA, herein designated VGAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2557 RNA is designated SEQ ID:5268, and is provided hereinbelow with reference to the sequence listing part.

[35760] VGAM2557 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2557 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2557 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35761] VGAM2557 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2557 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2557 RNA, herein designated

VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2557 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2557 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35762] The complementary binding of VGAM2557 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2557 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2557 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2557 host target protein, herein desig-

nated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[35763] It is appreciated that VGAM2557 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2557 host target genes. The mRNA of each one of this plurality of VGAM2557 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2557 RNA, herein designated VGAM RNA, and which when bound by VGAM2557 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2557 host target proteins.

[35764] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2557 gene, herein designated VGAM GENE, on one or more VGAM2557 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35765] It is yet further appreciated that a function of VGAM2557 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2557 include diagnosis, prevention and treatment of viral infection by Himetobi P virus. Specific functions, and accordingly utilities, of VGAM2557 correlate with, and may be deduced from, the identity of the host target genes which VGAM2557 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[35766] Nucleotide sequences of the VGAM2557 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2557 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2557 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2557 are further described hereinbelow with reference to Table 1.

[35767] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2557 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[35768] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2558 (VGAM2558) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[35769] VGAM2558 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2558 was detected is described hereinabove with reference to Figs. 2-8.

[35770] VGAM2558 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Himetobi P virus. VGAM2558 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[35771] VGAM2558 gene, herein designated VGAM GENE, encodes

a VGAM2558 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2558 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2558 precursor RNA is designated SEQ ID:2544, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2544 is located at position 7354 relative to the genome of Himetobi P virus.

[35772] VGAM2558 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2558 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35773] An enzyme complex designated DICER COMPLEX, dices the VGAM2558 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2558 RNA,

herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2558 RNA is designated SEQ ID:5269, and is provided hereinbelow with reference to the sequence listing part.

[35774] VGAM2558 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2558 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2558 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35775] VGAM2558 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2558 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM2558 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2558 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2558 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35776] The complementary binding of VGAM2558 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2558 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2558 host target RNA, herein designated VGAM HOST TARGET

RNA, into VGAM2558 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[35777] It is appreciated that VGAM2558 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2558 host target genes. The mRNA of each one of this plurality of VGAM2558 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2558 RNA, herein designated VGAM RNA, and which when bound by VGAM2558 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2558 host target proteins.

[35778] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2558 gene, herein designated VGAM GENE, on one or more VGAM2558 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35779] It is yet further appreciated that a function of VGAM2558 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2558 include diagnosis, prevention and treatment of viral infection by Himetobi P virus. Specific functions, and accordingly utilities, of VGAM2558 correlate with, and may be deduced from, the identity of the host target genes which VGAM2558 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[35780] Nucleotide sequences of the VGAM2558 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2558 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2558 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2558 are further

described hereinbelow with reference to Table 1.

[35781] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2558 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[35782] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2559 (VGAM2559) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[35783] VGAM2559 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2559 was detected is described hereinabove with reference to Figs. 2-8.

[35784] VGAM2559 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Himetobi P virus. VGAM2559 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[35785] VGAM2559 gene, herein designated VGAM GENE, encodes a VGAM2559 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2559 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2559 precursor RNA is designated SEQ ID:2545, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2545 is located at position 8220 relative to the genome of Himetobi P virus.

[35786] VGAM2559 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2559 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35787] An enzyme complex designated DICER COMPLEX, dices the VGAM2559 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, into VGAM2559 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2559 RNA is designated SEQ ID:5270, and is provided hereinbelow with reference to the sequence listing part.

[35788] VGAM2559 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2559 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2559 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35789] VGAM2559 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2559 host target RNA, herein designated VGAM HOST TARGET RNA. This

complementary binding is due to the fact that the nucleotide sequence of VGAM2559 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2559 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2559 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35790] The complementary binding of VGAM2559 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2559 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2559

host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2559 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[35791] It is appreciated that VGAM2559 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2559 host target genes. The mRNA of each one of this plurality of VGAM2559 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2559 RNA, herein designated VGAM RNA, and which when bound by VGAM2559 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2559 host target proteins.

[35792] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2559 gene, herein designated VGAM GENE, on one or more VGAM2559 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35793] It is yet further appreciated that a function of VGAM2559 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2559 include diagnosis, prevention and treatment of viral infection by Himetobi P virus. Specific functions, and accordingly utilities, of VGAM2559 correlate with, and may be deduced from, the identity of the host target genes which VGAM2559 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[35794] Nucleotide sequences of the VGAM2559 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2559 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2559 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM2559 are further described hereinbelow with reference to Table 1.

[35795] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2559 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[35796] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2560 (VGAM2560) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[35797] VGAM2560 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2560 was detected is described hereinabove with reference to Figs. 2-8.

[35798] VGAM2560 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Himetobi P virus. VGAM2560 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the

human genome.

[35799] VGAM2560 gene, herein designated VGAM GENE, encodes a VGAM2560 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2560 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2560 precursor RNA is designated SEQ ID:2546, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2546 is located at position 8011 relative to the genome of Himetobi P virus.

[35800] VGAM2560 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2560 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35801] An enzyme complex designated DICER COMPLEX, dices

the VGAM2560 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2560 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2560 RNA is designated SEQ ID:5271, and is provided hereinbelow with reference to the sequence listing part.

[35802] VGAM2560 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2560 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2560 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35803] VGAM2560 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2560 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2560 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2560 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2560 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35804] The complementary binding of VGAM2560 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2560 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM2560 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2560 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[35805] It is appreciated that VGAM2560 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2560 host target genes. The mRNA of each one of this plurality of VGAM2560 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2560 RNA, herein designated VGAM RNA, and which when bound by VGAM2560 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2560 host target proteins.

[35806] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2560 gene, herein designated VGAM GENE, on one or more VGAM2560 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35807] It is yet further appreciated that a function of VGAM2560 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2560 include diagnosis, prevention and treatment of viral infection by Himetobi P virus. Specific functions, and accordingly utilities, of VGAM2560 correlate with, and may be deduced from, the identity of the host target genes which VGAM2560 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[35808] Nucleotide sequences of the VGAM2560 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2560 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of

VGAM2560 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2560 are further described hereinbelow with reference to Table 1.

[35809] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2560 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[35810] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2561 (VGAM2561) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[35811] VGAM2561 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2561 was detected is described hereinabove with reference to Figs. 2-8.

[35812] VGAM2561 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Himetobi P virus. VGAM2561 host target gene, herein designated VGAM

HOST TARGET GENE, is a human gene contained in the human genome.

[35813] VGAM2561 gene, herein designated VGAM GENE, encodes a VGAM2561 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2561 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2561 precursor RNA is designated SEQ ID:2547, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2547 is located at position 8473 relative to the genome of Himetobi P virus.

[35814] VGAM2561 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2561 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35815] An enzyme complex designated DICER COMPLEX, dices the VGAM2561 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2561 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2561 RNA is designated SEQ ID:5272, and is provided hereinbelow with reference to the sequence listing part.

[35816] VGAM2561 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2561 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2561 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35817] VGAM2561 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites

located in untranslated regions of VGAM2561 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2561 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2561 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2561 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35818] The complementary binding of VGAM2561 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2561 host target RNA, herein designated VGAM

HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2561 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2561 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[35819] It is appreciated that VGAM2561 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2561 host target genes. The mRNA of each one of this plurality of VGAM2561 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2561 RNA, herein designated VGAM RNA, and which when bound by VGAM2561 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2561 host target proteins.

[35820] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2561 gene, herein designated VGAM GENE, on one or more VGAM2561 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove

with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35821] It is yet further appreciated that a function of VGAM2561 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2561 include diagnosis, prevention and treatment of viral infection by Himetobi P virus. Specific functions, and accordingly utilities, of VGAM2561 correlate with, and may be deduced from, the identity of the host target genes which VGAM2561 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[35822] Nucleotide sequences of the VGAM2561 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2561 RNA, herein designated VGAM RNA, and

a schematic representation of the secondary folding of VGAM2561 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2561 are further described hereinbelow with reference to Table 1.

[35823] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2561 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[35824] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2562 (VGAM2562) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[35825] VGAM2562 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2562 was detected is described hereinabove with reference to Figs. 2-8.

[35826] VGAM2562 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Himetobi P virus.

VGAM2562 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[35827] VGAM2562 gene, herein designated VGAM GENE, encodes a VGAM2562 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2562 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2562 precursor RNA is designated SEQ ID:2548, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2548 is located at position 7594 relative to the genome of Himetobi P virus.

[35828] VGAM2562 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2562 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[35829] An enzyme complex designated DICER COMPLEX, dices the VGAM2562 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2562 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide sequence of VGAM2562 RNA is designated SEQ ID:5273, and is provided hereinbelow with reference to the sequence listing part.

[35830] VGAM2562 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2562 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2562 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35831] VGAM2562 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM2562 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2562 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2562 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2562 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35832] The complementary binding of VGAM2562 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM2562 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2562 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2562 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[35833] It is appreciated that VGAM2562 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2562 host target genes. The mRNA of each one of this plurality of VGAM2562 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2562 RNA, herein designated VGAM RNA, and which when bound by VGAM2562 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2562 host target proteins.

[35834] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2562 gene, herein designated VGAM GENE, on one or more VGAM2562 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35835] It is yet further appreciated that a function of VGAM2562 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2562 include diagnosis, prevention and treatment of viral infection by Himetobi P virus. Specific functions, and accordingly utilities, of VGAM2562 correlate with, and may be deduced from, the identity of the host target genes which VGAM2562 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[35836] Nucleotide sequences of the VGAM2562 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

diced VGAM2562 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2562 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2562 are further described hereinbelow with reference to Table 1.

[35837] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2562 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[35838] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2563 (VGAM2563) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[35839] VGAM2563 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2563 was detected is described hereinabove with reference to Figs. 2-8.

[35840] VGAM2563 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of Himetobi P virus. VGAM2563 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[35841] VGAM2563 gene, herein designated VGAM GENE, encodes a VGAM2563 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2563 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2563 precursor RNA is designated SEQ ID:2549, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2549 is located at position 8878 relative to the genome of Himetobi P virus.

[35842] VGAM2563 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2563 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35843] An enzyme complex designated DICER COMPLEX, dices the VGAM2563 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2563 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2563 RNA is designated SEQ ID:5274, and is provided hereinbelow with reference to the sequence listing part.

[35844] VGAM2563 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2563 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2563 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35845] VGAM2563 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2563 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2563 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2563 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2563 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35846] The complementary binding of VGAM2563 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM2563 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2563 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2563 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[35847] It is appreciated that VGAM2563 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2563 host target genes. The mRNA of each one of this plurality of VGAM2563 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2563 RNA, herein designated VGAM RNA, and which when bound by VGAM2563 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2563 host target proteins.

[35848] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2563 gene, herein designated VGAM GENE, on one or more VGAM2563 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35849] It is yet further appreciated that a function of VGAM2563 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2563 include diagnosis, prevention and treatment of viral infection by Himetobi P virus. Specific functions, and accordingly utilities, of VGAM2563 correlate with, and may be deduced from, the identity of the host target genes which VGAM2563 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[35850] Nucleotide sequences of the VGAM2563 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the diced VGAM2563 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2563 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2563 are further described hereinbelow with reference to Table 1.

[35851] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2563 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[35852] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2564 (VGAM2564) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[35853] VGAM2564 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2564 was detected is described hereinabove with reference to Figs. 2-8.

[35854] VGAM2564 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Triatoma virus. VGAM2564 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[35855] VGAM2564 gene, herein designated VGAM GENE, encodes a VGAM2564 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2564 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2564 precursor RNA is designated SEQ ID:2550, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2550 is located at position 3567 relative to the genome of Triatoma virus.

[35856] VGAM2564 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2564 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35857] An enzyme complex designated DICER COMPLEX, dices the VGAM2564 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2564 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2564 RNA is designated SEQ ID:5275, and is provided hereinbelow with reference to the sequence listing part.

[35858] VGAM2564 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2564 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2564 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN COD-

ING and 3UTR respectively.

[35859] VGAM2564 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2564 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2564 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2564 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2564 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35860] The complementary binding of VGAM2564 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2564 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2564 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2564 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[35861] It is appreciated that VGAM2564 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2564 host target genes. The mRNA of each one of this plurality of VGAM2564 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2564 RNA, herein designated VGAM RNA, and which when bound by VGAM2564 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2564 host target proteins.

[35862] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2564 gene, herein designated VGAM GENE, on one

or more VGAM2564 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35863] It is yet further appreciated that a function of VGAM2564 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2564 include diagnosis, prevention and treatment of viral infection by Triatoma virus. Specific functions, and accordingly utilities, of VGAM2564 correlate with, and may be deduced from, the identity of the host target genes which VGAM2564 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[35864] Nucleotide sequences of the VGAM2564 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2564 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2564 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2564 are further described hereinbelow with reference to Table 1.

[35865] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2564 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[35866] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2565 (VGAM2565) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[35867] VGAM2565 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2565 was detected is de-

scribed hereinabove with reference to Figs. 2-8.

[35868] VGAM2565 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Triatoma virus. VGAM2565 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[35869] VGAM2565 gene, herein designated VGAM GENE, encodes a VGAM2565 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2565 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2565 precursor RNA is designated SEQ ID:2551, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2551 is located at position 1775 relative to the genome of Triatoma virus.

[35870] VGAM2565 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2565 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35871] An enzyme complex designated DICER COMPLEX, dices the VGAM2565 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2565 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2565 RNA is designated SEQ ID:5276, and is provided hereinbelow with reference to the sequence listing part.

[35872] VGAM2565 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2565 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2565 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and

a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35873] VGAM2565 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2565 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2565 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2565 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2565 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both

3UTR and 5UTR regions.

[35874] The complementary binding of VGAM2565 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2565 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2565 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2565 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[35875] It is appreciated that VGAM2565 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2565 host target genes. The mRNA of each one of this plurality of VGAM2565 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2565 RNA, herein designated VGAM RNA, and which when bound by VGAM2565 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2565 host target proteins.

[35876] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM2565 gene, herein designated VGAM GENE, on one or more VGAM2565 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35877] It is yet further appreciated that a function of VGAM2565 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2565 include diagnosis, prevention and treatment of viral infection by Triatoma virus. Specific functions, and accordingly utilities, of VGAM2565 correlate with, and may be deduced from, the identity of the host target genes which VGAM2565 binds and inhibits, and the function of these host target genes, as elaborated

hereinbelow.

[35878] Nucleotide sequences of the VGAM2565 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2565 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2565 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2565 are further described hereinbelow with reference to Table 1.

[35879] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2565 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[35880] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2566 (VGAM2566) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[35881] VGAM2566 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene.

The method by which VGAM2566 was detected is described hereinabove with reference to Figs. 2-8.

[35882] VGAM2566 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Triatoma virus. VGAM2566 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[35883] VGAM2566 gene, herein designated VGAM GENE, encodes a VGAM2566 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2566 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2566 precursor RNA is designated SEQ ID:2552, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2552 is located at position 2022 relative to the genome of Triatoma virus.

[35884] VGAM2566 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2566 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35885] An enzyme complex designated DICER COMPLEX, dices the VGAM2566 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2566 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2566 RNA is designated SEQ ID:5277, and is provided hereinbelow with reference to the sequence listing part.

[35886] VGAM2566 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2566 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2566 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding

gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35887] VGAM2566 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2566 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2566 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2566 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2566 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be lo-

cated in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35888] The complementary binding of VGAM2566 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2566 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2566 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2566 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[35889] It is appreciated that VGAM2566 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2566 host target genes. The mRNA of each one of this plurality of VGAM2566 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2566 RNA, herein designated VGAM RNA, and which when bound by VGAM2566 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2566 host target proteins.

[35890] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM2566 gene, herein designated VGAM GENE, on one or more VGAM2566 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35891] It is yet further appreciated that a function of VGAM2566 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2566 include diagnosis, prevention and treatment of viral infection by Triatoma virus. Specific functions, and accordingly utilities, of VGAM2566 correlate with, and may be deduced from, the identity of the host target genes which VGAM2566 binds and inhibits,

and the function of these host target genes, as elaborated hereinbelow.

[35892] Nucleotide sequences of the VGAM2566 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2566 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2566 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2566 are further described hereinbelow with reference to Table 1.

[35893] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2566 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[35894] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2567 (VGAM2567) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[35895] VGAM2567 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2567 was detected is described hereinabove with reference to Figs. 2-8.

[35896] VGAM2567 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Triatoma virus. VGAM2567 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[35897] VGAM2567 gene, herein designated VGAM GENE, encodes a VGAM2567 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2567 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2567 precursor RNA is designated SEQ ID:2553, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2553 is located at position 3811 relative to the genome of Triatoma virus.

[35898] VGAM2567 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2567 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35899] An enzyme complex designated DICER COMPLEX, dices the VGAM2567 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2567 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 50%) nucleotide sequence of VGAM2567 RNA is designated SEQ ID:5278, and is provided hereinbelow with reference to the sequence listing part.

[35900] VGAM2567 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2567 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2567 host target RNA, herein designated VGAM HOST TARGET RNA, comprises

three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35901] VGAM2567 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2567 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2567 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2567 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2567 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an

example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35902] The complementary binding of VGAM2567 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2567 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2567 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2567 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[35903] It is appreciated that VGAM2567 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2567 host target genes. The mRNA of each one of this plurality of VGAM2567 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2567 RNA, herein designated VGAM RNA, and which when bound by VGAM2567 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2567 host target proteins.

[35904] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2567 gene, herein designated VGAM GENE, on one or more VGAM2567 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35905] It is yet further appreciated that a function of VGAM2567 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2567 include diagnosis, prevention and treatment of viral infection by Triatoma virus. Specific functions, and accordingly utilities, of VGAM2567 correlate with, and may be deduced from, the identity of the

host target genes which VGAM2567 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[35906] Nucleotide sequences of the VGAM2567 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2567 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2567 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2567 are further described hereinbelow with reference to Table 1.

[35907] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2567 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[35908] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2568 (VGAM2568) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[35909] VGAM2568 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2568 was detected is described hereinabove with reference to Figs. 2-8.

[35910] VGAM2568 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Triatoma virus. VGAM2568 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[35911] VGAM2568 gene, herein designated VGAM GENE, encodes a VGAM2568 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2568 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2568 precursor RNA is designated SEQ ID:2554, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2554 is located at position 4293 relative to the genome of Triatoma virus.

[35912] VGAM2568 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2568 folded precursor RNA, herein designated VGAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35913] An enzyme complex designated DICER COMPLEX, dices the VGAM2568 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2568 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 51%) nucleotide sequence of VGAM2568 RNA is designated SEQ ID:5279, and is provided hereinbelow with reference to the sequence listing part.

[35914] VGAM2568 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2568 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2568 host target RNA,

herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35915] VGAM2568 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2568 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2568 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2568 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2568 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host tar-

get binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35916] The complementary binding of VGAM2568 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2568 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2568 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2568 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[35917] It is appreciated that VGAM2568 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2568 host target genes. The mRNA of each one of this plurality of VGAM2568 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2568 RNA, herein designated VGAM RNA, and which when bound by VGAM2568 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2568 host target proteins.

[35918] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2568 gene, herein designated VGAM GENE, on one or more VGAM2568 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35919] It is yet further appreciated that a function of VGAM2568 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2568 include diagnosis, prevention and treatment of viral infection by Triatoma virus. Specific functions, and accordingly utilities, of VGAM2568 corre-

late with, and may be deduced from, the identity of the host target genes which VGAM2568 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[35920] Nucleotide sequences of the VGAM2568 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2568 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2568 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2568 are further described hereinbelow with reference to Table 1.

[35921] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2568 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[35922] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2569 (VGAM2569) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the

art.

[35923] VGAM2569 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2569 was detected is described hereinabove with reference to Figs. 2-8.

[35924] VGAM2569 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Triatoma virus. VGAM2569 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[35925] VGAM2569 gene, herein designated VGAM GENE, encodes a VGAM2569 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2569 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2569 precursor RNA is designated SEQ ID:2555, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2555 is located at position 5389 relative to the genome of Triatoma virus.

[35926] VGAM2569 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2569 folded

precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35927] An enzyme complex designated DICER COMPLEX, dices the VGAM2569 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2569 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2569 RNA is designated SEQ ID:5280, and is provided hereinbelow with reference to the sequence listing part.

[35928] VGAM2569 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2569 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM2569 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35929] VGAM2569 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2569 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2569 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2569 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2569 host target RNA, herein designated VGAM HOST TARGET RNA.

It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35930] The complementary binding of VGAM2569 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2569 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2569 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2569 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[35931] It is appreciated that VGAM2569 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2569 host target genes. The mRNA of each one of this plurality of VGAM2569 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2569 RNA, herein designated VGAM RNA, and which when bound by VGAM2569 RNA, herein designated VGAM RNA, causes inhibition of translation of

respective one or more VGAM2569 host target proteins.

[35932] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2569 gene, herein designated VGAM GENE, on one or more VGAM2569 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35933] It is yet further appreciated that a function of VGAM2569 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2569 include diagnosis, prevention and treatment of viral infection by Triatoma virus. Specific

functions, and accordingly utilities, of VGAM2569 correlate with, and may be deduced from, the identity of the host target genes which VGAM2569 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[35934] Nucleotide sequences of the VGAM2569 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2569 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2569 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2569 are further described hereinbelow with reference to Table 1.

[35935] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2569 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[35936] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2570 (VGAM2570) viral gene, which modulates expression of respective host target genes thereof, the func-

tion and utility of which host target genes is known in the art.

[35937] VGAM2570 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2570 was detected is described hereinabove with reference to Figs. 2-8.

[35938] VGAM2570 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Triatoma virus. VGAM2570 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[35939] VGAM2570 gene, herein designated VGAM GENE, encodes a VGAM2570 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2570 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2570 precursor RNA is designated SEQ ID:2556, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2556 is located at position 5274 relative to the genome of Triatoma virus.

[35940] VGAM2570 precursor RNA, herein designated VGAM PRE-

CURSOR RNA, folds onto itself, forming VGAM2570 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35941] An enzyme complex designated DICER COMPLEX, dices the VGAM2570 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2570 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 72%) nucleotide sequence of VGAM2570 RNA is designated SEQ ID:5281, and is provided hereinbelow with reference to the sequence listing part.

[35942] VGAM2570 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM2570 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2570 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35943] VGAM2570 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2570 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2570 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2570 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2570 host

target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35944] The complementary binding of VGAM2570 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2570 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2570 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2570 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[35945] It is appreciated that VGAM2570 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2570 host target genes. The mRNA of each one of this plurality of VGAM2570 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2570 RNA, herein designated VGAM RNA, and which when bound by VGAM2570 RNA, herein

designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2570 host target proteins.

[35946] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2570 gene, herein designated VGAM GENE, on one or more VGAM2570 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35947] It is yet further appreciated that a function of VGAM2570 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2570 include diagnosis, prevention and

treatment of viral infection by Triatoma virus. Specific functions, and accordingly utilities, of VGAM2570 correlate with, and may be deduced from, the identity of the host target genes which VGAM2570 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[35948] Nucleotide sequences of the VGAM2570 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2570 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2570 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2570 are further described hereinbelow with reference to Table 1.

[35949] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2570 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[35950] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2571 (VGAM2571) viral gene, which modulates ex-

pression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[35951] VGAM2571 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2571 was detected is described hereinabove with reference to Figs. 2-8.

[35952] VGAM2571 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Triatoma virus. VGAM2571 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[35953] VGAM2571 gene, herein designated VGAM GENE, encodes a VGAM2571 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2571 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2571 precursor RNA is designated SEQ ID:2557, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2557 is located at position 5836 relative to the genome of Triatoma virus.

[35954] VGAM2571 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2571 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35955] An enzyme complex designated DICER COMPLEX, dices the VGAM2571 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2571 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2571 RNA is designated SEQ ID:5282, and is provided hereinbelow with reference to the sequence listing part.

[35956] VGAM2571 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2571 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2571 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35957] VGAM2571 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2571 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2571 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2571 RNA, herein designated VGAM RNA, may have a different number of host target

binding sites in untranslated regions of a VGAM2571 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35958] The complementary binding of VGAM2571 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2571 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2571 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2571 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[35959] It is appreciated that VGAM2571 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2571 host target genes. The mRNA of each one of this plurality of VGAM2571 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2571 RNA, herein designated VGAM

RNA, and which when bound by VGAM2571 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2571 host target proteins.

[35960] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2571 gene, herein designated VGAM GENE, on one or more VGAM2571 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35961] It is yet further appreciated that a function of VGAM2571 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM2571 include diagnosis, prevention and treatment of viral infection by Triatoma virus. Specific functions, and accordingly utilities, of VGAM2571 correlate with, and may be deduced from, the identity of the host target genes which VGAM2571 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[35962] Nucleotide sequences of the VGAM2571 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2571 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2571 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2571 are further described hereinbelow with reference to Table 1.

[35963] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2571 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[35964] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Mes-

senger 2572 (VGAM2572) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[35965] VGAM2572 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2572 was detected is described hereinabove with reference to Figs. 2-8.

[35966] VGAM2572 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Triatoma virus. VGAM2572 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[35967] VGAM2572 gene, herein designated VGAM GENE, encodes a VGAM2572 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2572 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2572 precursor RNA is designated SEQ ID:2558, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2558 is located at position 3076

relative to the genome of Triatoma virus.

[35968] VGAM2572 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2572 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35969] An enzyme complex designated DICER COMPLEX, dices the VGAM2572 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2572 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of VGAM2572 RNA is designated SEQ ID:5283, and is provided hereinbelow with reference to the sequence listing part.

[35970] VGAM2572 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2572 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2572 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35971] VGAM2572 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2572 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2572 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2572 RNA, herein designated

VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2572 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35972] The complementary binding of VGAM2572 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2572 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2572 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2572 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[35973] It is appreciated that VGAM2572 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2572 host target genes. The mRNA of each one of this plurality of VGAM2572 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM2572 RNA, herein designated VGAM RNA, and which when bound by VGAM2572 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2572 host target proteins.

[35974] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2572 gene, herein designated VGAM GENE, on one or more VGAM2572 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35975] It is yet further appreciated that a function of VGAM2572 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2572 include diagnosis, prevention and treatment of viral infection by Triatoma virus. Specific functions, and accordingly utilities, of VGAM2572 correlate with, and may be deduced from, the identity of the host target genes which VGAM2572 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[35976] Nucleotide sequences of the VGAM2572 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2572 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2572 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2572 are further described hereinbelow with reference to Table 1.

[35977] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2572 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[35978] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present

invention, referred to here as Viral Genomic Address Messenger 2573 (VGAM2573) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[35979] VGAM2573 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2573 was detected is described hereinabove with reference to Figs. 2-8.

[35980] VGAM2573 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Triatoma virus. VGAM2573 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[35981] VGAM2573 gene, herein designated VGAM GENE, encodes a VGAM2573 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2573 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2573 precursor RNA is designated SEQ ID:2559, and is provided hereinbelow with reference to the sequence listing part. Nu-

cleotide sequence SEQ ID:2559 is located at position 3368 relative to the genome of Triatoma virus.

[35982] VGAM2573 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2573 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35983] An enzyme complex designated DICER COMPLEX, dices the VGAM2573 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2573 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2573 RNA is designated SEQ ID:5284, and is provided hereinbelow with reference to the sequence

listing part.

[35984] VGAM2573 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2573 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2573 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35985] VGAM2573 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2573 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2573 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not

meant to be limiting VGAM2573 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2573 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35986] The complementary binding of VGAM2573 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2573 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2573 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2573 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[35987] It is appreciated that VGAM2573 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2573 host target genes. The mRNA of each one of this plurality of VGAM2573 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2573 RNA, herein designated VGAM RNA, and which when bound by VGAM2573 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2573 host target proteins.

[35988] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2573 gene, herein designated VGAM GENE, on one or more VGAM2573 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35989] It is yet further appreciated that a function of VGAM2573

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2573 include diagnosis, prevention and treatment of viral infection by Triatoma virus. Specific functions, and accordingly utilities, of VGAM2573 correlate with, and may be deduced from, the identity of the host target genes which VGAM2573 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[35990] Nucleotide sequences of the VGAM2573 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2573 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2573 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2573 are further described hereinbelow with reference to Table 1.

[35991] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2573 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[35992] Fig. 1 further provides a conceptual description of another

novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2574 (VGAM2574) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[35993] VGAM2574 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2574 was detected is described hereinabove with reference to Figs. 2-8.

[35994] VGAM2574 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Triatoma virus. VGAM2574 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[35995] VGAM2574 gene, herein designated VGAM GENE, encodes a VGAM2574 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2574 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2574 precursor RNA is designated SEQ ID:2560, and is provided here-

inbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2560 is located at position 2215 relative to the genome of Triatoma virus.

[35996] VGAM2574 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2574 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35997] An enzyme complex designated DICER COMPLEX, dices the VGAM2574 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2574 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 53%) nucleotide sequence of VGAM2574 RNA is designated SEQ ID:5285, and

is provided hereinbelow with reference to the sequence listing part.

[35998] VGAM2574 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2574 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2574 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35999] VGAM2574 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2574 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2574 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites

shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2574 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2574 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36000] The complementary binding of VGAM2574 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2574 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2574 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2574 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[36001] It is appreciated that VGAM2574 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2574 host target genes. The mRNA of each one of this plurality of VGAM2574 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2574 RNA, herein designated VGAM RNA, and which when bound by VGAM2574 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2574 host target proteins.

[36002] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2574 gene, herein designated VGAM GENE, on one or more VGAM2574 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36003] It is yet further appreciated that a function of VGAM2574 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2574 include diagnosis, prevention and treatment of viral infection by Triatoma virus. Specific functions, and accordingly utilities, of VGAM2574 correlate with, and may be deduced from, the identity of the host target genes which VGAM2574 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[36004] Nucleotide sequences of the VGAM2574 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2574 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2574 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2574 are further described hereinbelow with reference to Table 1.

[36005] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2574 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[36006] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2575 (VGAM2575) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[36007] VGAM2575 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2575 was detected is described hereinabove with reference to Figs. 2-8.

[36008] VGAM2575 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Triatoma virus. VGAM2575 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[36009] VGAM2575 gene, herein designated VGAM GENE, encodes a VGAM2575 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2575 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2575 precur-

sor RNA is designated SEQ ID:2561, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2561 is located at position 4661 relative to the genome of Triatoma virus.

[36010] VGAM2575 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2575 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36011] An enzyme complex designated DICER COMPLEX, dices the VGAM2575 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2575 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 48%) nucleotide se-

quence of VGAM2575 RNA is designated SEQ ID:5286, and is provided hereinbelow with reference to the sequence listing part.

[36012] VGAM2575 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2575 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2575 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36013] VGAM2575 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2575 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2575 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is ap-

preciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2575 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2575 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36014] The complementary binding of VGAM2575 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2575 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2575 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2575 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[36015] It is appreciated that VGAM2575 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2575 host target genes. The mRNA of

each one of this plurality of VGAM2575 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2575 RNA, herein designated VGAM RNA, and which when bound by VGAM2575 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2575 host target proteins.

[36016] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2575 gene, herein designated VGAM GENE, on one or more VGAM2575 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science

294,779 (2001)).

[36017] It is yet further appreciated that a function of VGAM2575 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2575 include diagnosis, prevention and treatment of viral infection by Triatoma virus. Specific functions, and accordingly utilities, of VGAM2575 correlate with, and may be deduced from, the identity of the host target genes which VGAM2575 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[36018] Nucleotide sequences of the VGAM2575 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2575 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2575 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2575 are further described hereinbelow with reference to Table 1.

[36019] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2575 RNA, herein designated VGAM RNA, are de-

scribed hereinbelow with reference to Table 2.

[36020] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2576 (VGAM2576) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[36021] VGAM2576 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2576 was detected is described hereinabove with reference to Figs. 2-8.

[36022] VGAM2576 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Triatoma virus. VGAM2576 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[36023] VGAM2576 gene, herein designated VGAM GENE, encodes a VGAM2576 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2576 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly

similar to the nucleotide sequence of VGAM2576 precursor RNA is designated SEQ ID:2562, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2562 is located at position 5068 relative to the genome of Triatoma virus.

[36024] VGAM2576 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2576 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36025] An enzyme complex designated DICER COMPLEX, dices the VGAM2576 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2576 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 90%) nucleotide sequence of VGAM2576 RNA is designated SEQ ID:5287, and is provided hereinbelow with reference to the sequence listing part.

[36026] VGAM2576 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2576 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2576 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36027] VGAM2576 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2576 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2576 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I,

BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2576 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2576 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36028] The complementary binding of VGAM2576 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2576 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2576 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2576 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[36029] It is appreciated that VGAM2576 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM2576 host target genes. The mRNA of each one of this plurality of VGAM2576 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2576 RNA, herein designated VGAM RNA, and which when bound by VGAM2576 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2576 host target proteins.

[36030] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2576 gene, herein designated VGAM GENE, on one or more VGAM2576 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36031] It is yet further appreciated that a function of VGAM2576 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2576 include diagnosis, prevention and treatment of viral infection by Triatoma virus. Specific functions, and accordingly utilities, of VGAM2576 correlate with, and may be deduced from, the identity of the host target genes which VGAM2576 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[36032] Nucleotide sequences of the VGAM2576 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2576 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2576 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2576 are further described hereinbelow with reference to Table 1.

[36033] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites

to VGAM2576 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[36034] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2577 (VGAM2577) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[36035] VGAM2577 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2577 was detected is described hereinabove with reference to Figs. 2-8.

[36036] VGAM2577 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Triatoma virus. VGAM2577 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[36037] VGAM2577 gene, herein designated VGAM GENE, encodes a VGAM2577 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2577 precursor RNA, herein designated VGAM PRECURSOR RNA, does not en-

code a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2577 precursor RNA is designated SEQ ID:2563, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2563 is located at position 985 relative to the genome of Triatoma virus.

[36038] VGAM2577 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2577 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36039] An enzyme complex designated DICER COMPLEX, dices the VGAM2577 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2577 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 78%) nucleotide sequence of VGAM2577 RNA is designated SEQ ID:5288, and is provided hereinbelow with reference to the sequence listing part.

[36040] VGAM2577 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2577 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2577 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36041] VGAM2577 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2577 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2577 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3

such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2577 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2577 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36042] The complementary binding of VGAM2577 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2577 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2577 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2577 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[36043] It is appreciated that VGAM2577 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2577 host target genes. The mRNA of each one of this plurality of VGAM2577 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2577 RNA, herein designated VGAM RNA, and which when bound by VGAM2577 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2577 host target proteins.

[36044] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2577 gene, herein designated VGAM GENE, on one or more VGAM2577 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36045] It is yet further appreciated that a function of VGAM2577 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2577 include diagnosis, prevention and treatment of viral infection by Triatoma virus. Specific functions, and accordingly utilities, of VGAM2577 correlate with, and may be deduced from, the identity of the host target genes which VGAM2577 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[36046] Nucleotide sequences of the VGAM2577 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2577 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2577 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2577 are further described hereinbelow with reference to Table 1.

[36047] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the

complementarity of each of these host target binding sites to VGAM2577 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[36048] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2578 (VGAM2578) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[36049] VGAM2578 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2578 was detected is described hereinabove with reference to Figs. 2-8.

[36050] VGAM2578 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Triatoma virus. VGAM2578 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[36051] VGAM2578 gene, herein designated VGAM GENE, encodes a VGAM2578 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2578 precursor RNA,

herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2578 precursor RNA is designated SEQ ID:2564, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2564 is located at position 849 relative to the genome of Triatoma virus.

[36052] VGAM2578 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2578 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36053] An enzyme complex designated DICER COMPLEX, dices the VGAM2578 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2578 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 56%) nucleotide sequence of VGAM2578 RNA is designated SEQ ID:5289, and is provided hereinbelow with reference to the sequence listing part.

[36054] VGAM2578 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2578 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2578 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36055] VGAM2578 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2578 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2578 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host

target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2578 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2578 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36056] The complementary binding of VGAM2578 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2578 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2578 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2578 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[36057] It is appreciated that VGAM2578 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2578 host target genes. The mRNA of each one of this plurality of VGAM2578 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2578 RNA, herein designated VGAM RNA, and which when bound by VGAM2578 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2578 host target proteins.

[36058] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2578 gene, herein designated VGAM GENE, on one or more VGAM2578 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36059] It is yet further appreciated that a function of VGAM2578 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2578 include diagnosis, prevention and treatment of viral infection by Triatoma virus. Specific functions, and accordingly utilities, of VGAM2578 correlate with, and may be deduced from, the identity of the host target genes which VGAM2578 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[36060] Nucleotide sequences of the VGAM2578 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2578 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2578 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2578 are further described hereinbelow with reference to Table 1.

[36061] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2578 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[36062] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2579 (VGAM2579) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[36063] VGAM2579 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2579 was detected is described hereinabove with reference to Figs. 2-8.

[36064] VGAM2579 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Triatoma virus. VGAM2579 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[36065] VGAM2579 gene, herein designated VGAM GENE, encodes a VGAM2579 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and un-

like most ordinary genes, VGAM2579 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2579 precursor RNA is designated SEQ ID:2565, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2565 is located at position 7412 relative to the genome of Triatoma virus.

[36066] VGAM2579 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2579 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36067] An enzyme complex designated DICER COMPLEX, dices the VGAM2579 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2579 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 63%) nucleotide sequence of VGAM2579 RNA is designated SEQ ID:5290, and is provided hereinbelow with reference to the sequence listing part.

[36068] VGAM2579 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2579 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2579 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36069] VGAM2579 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2579 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2579 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed

sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2579 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2579 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36070] The complementary binding of VGAM2579 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2579 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2579 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2579 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target

protein is therefore outlined by a broken line.

[36071] It is appreciated that VGAM2579 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2579 host target genes. The mRNA of each one of this plurality of VGAM2579 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2579 RNA, herein designated VGAM RNA, and which when bound by VGAM2579 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2579 host target proteins.

[36072] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2579 gene, herein designated VGAM GENE, on one or more VGAM2579 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36073] It is yet further appreciated that a function of VGAM2579 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2579 include diagnosis, prevention and treatment of viral infection by Triatoma virus. Specific functions, and accordingly utilities, of VGAM2579 correlate with, and may be deduced from, the identity of the host target genes which VGAM2579 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[36074] Nucleotide sequences of the VGAM2579 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2579 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2579 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2579 are further described hereinbelow with reference to Table 1.

[36075] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2579 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[36076] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2580 (VGAM2580) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[36077] VGAM2580 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2580 was detected is described hereinabove with reference to Figs. 2-8.

[36078] VGAM2580 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Triatoma virus. VGAM2580 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[36079] VGAM2580 gene, herein designated VGAM GENE, encodes a VGAM2580 precursor RNA, herein designated VGAM

PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2580 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2580 precursor RNA is designated SEQ ID:2566, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2566 is located at position 7916 relative to the genome of Triatoma virus.

[36080] VGAM2580 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2580 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36081] An enzyme complex designated DICER COMPLEX, dices the VGAM2580 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2580 RNA, herein designated VGAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide sequence of VGAM2580 RNA is designated SEQ ID:5291, and is provided hereinbelow with reference to the sequence listing part.

[36082] VGAM2580 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2580 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2580 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36083] VGAM2580 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2580 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2580 RNA, herein designated

VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2580 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2580 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36084] The complementary binding of VGAM2580 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2580 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2580 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2580 host target protein, herein desig-

nated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[36085] It is appreciated that VGAM2580 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2580 host target genes. The mRNA of each one of this plurality of VGAM2580 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2580 RNA, herein designated VGAM RNA, and which when bound by VGAM2580 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2580 host target proteins.

[36086] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2580 gene, herein designated VGAM GENE, on one or more VGAM2580 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36087] It is yet further appreciated that a function of VGAM2580 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2580 include diagnosis, prevention and treatment of viral infection by Triatoma virus. Specific functions, and accordingly utilities, of VGAM2580 correlate with, and may be deduced from, the identity of the host target genes which VGAM2580 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[36088] Nucleotide sequences of the VGAM2580 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2580 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2580 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2580 are further described hereinbelow with reference to Table 1.

[36089] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2580 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[36090] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2581 (VGAM2581) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[36091] VGAM2581 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2581 was detected is described hereinabove with reference to Figs. 2-8.

[36092] VGAM2581 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Triatoma virus.
VGAM2581 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[36093] VGAM2581 gene, herein designated VGAM GENE, encodes

a VGAM2581 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2581 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2581 precursor RNA is designated SEQ ID:2567, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2567 is located at position 6465 relative to the genome of Triatoma virus.

[36094] VGAM2581 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2581 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36095] An enzyme complex designated DICER COMPLEX, dices the VGAM2581 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2581 RNA,

herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 66%) nucleotide sequence of VGAM2581 RNA is designated SEQ ID:5292, and is provided hereinbelow with reference to the sequence listing part.

[36096] VGAM2581 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2581 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2581 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36097] VGAM2581 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2581 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM2581 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2581 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2581 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36098] The complementary binding of VGAM2581 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2581 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2581 host target RNA, herein designated VGAM HOST TARGET

RNA, into VGAM2581 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[36099] It is appreciated that VGAM2581 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2581 host target genes. The mRNA of each one of this plurality of VGAM2581 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2581 RNA, herein designated VGAM RNA, and which when bound by VGAM2581 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2581 host target proteins.

[36100] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2581 gene, herein designated VGAM GENE, on one or more VGAM2581 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36101] It is yet further appreciated that a function of VGAM2581 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2581 include diagnosis, prevention and treatment of viral infection by Triatoma virus. Specific functions, and accordingly utilities, of VGAM2581 correlate with, and may be deduced from, the identity of the host target genes which VGAM2581 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[36102] Nucleotide sequences of the VGAM2581 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2581 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2581 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2581 are further

described hereinbelow with reference to Table 1.

[36103] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2581 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[36104] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2582 (VGAM2582) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[36105] VGAM2582 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2582 was detected is described hereinabove with reference to Figs. 2-8.

[36106] VGAM2582 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Triatoma virus. VGAM2582 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[36107] VGAM2582 gene, herein designated VGAM GENE, encodes a VGAM2582 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2582 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2582 precursor RNA is designated SEQ ID:2568, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2568 is located at position 8016 relative to the genome of Triatoma virus.

[36108] VGAM2582 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2582 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36109] An enzyme complex designated DICER COMPLEX, dices the VGAM2582 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, into VGAM2582 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2582 RNA is designated SEQ ID:5293, and is provided hereinbelow with reference to the sequence listing part.

[36110] VGAM2582 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2582 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2582 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36111] VGAM2582 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2582 host target RNA, herein designated VGAM HOST TARGET RNA. This

complementary binding is due to the fact that the nucleotide sequence of VGAM2582 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2582 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2582 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36112] The complementary binding of VGAM2582 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2582 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2582

host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2582 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[36113] It is appreciated that VGAM2582 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2582 host target genes. The mRNA of each one of this plurality of VGAM2582 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2582 RNA, herein designated VGAM RNA, and which when bound by VGAM2582 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2582 host target proteins.

[36114] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2582 gene, herein designated VGAM GENE, on one or more VGAM2582 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36115] It is yet further appreciated that a function of VGAM2582 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2582 include diagnosis, prevention and treatment of viral infection by Triatoma virus. Specific functions, and accordingly utilities, of VGAM2582 correlate with, and may be deduced from, the identity of the host target genes which VGAM2582 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[36116] Nucleotide sequences of the VGAM2582 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2582 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2582 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM2582 are further described hereinbelow with reference to Table 1.

[36117] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2582 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[36118] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2583 (VGAM2583) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[36119] VGAM2583 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2583 was detected is described hereinabove with reference to Figs. 2-8.

[36120] VGAM2583 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Triatoma virus. VGAM2583 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the

human genome.

[36121] VGAM2583 gene, herein designated VGAM GENE, encodes a VGAM2583 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2583 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2583 precursor RNA is designated SEQ ID:2569, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2569 is located at position 7137 relative to the genome of Triatoma virus.

[36122] VGAM2583 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2583 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36123] An enzyme complex designated DICER COMPLEX, dices

the VGAM2583 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2583 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2583 RNA is designated SEQ ID:5294, and is provided hereinbelow with reference to the sequence listing part.

[36124] VGAM2583 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2583 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2583 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36125] VGAM2583 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2583 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2583 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2583 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2583 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36126] The complementary binding of VGAM2583 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2583 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM2583 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2583 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[36127] It is appreciated that VGAM2583 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2583 host target genes. The mRNA of each one of this plurality of VGAM2583 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2583 RNA, herein designated VGAM RNA, and which when bound by VGAM2583 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2583 host target proteins.

[36128] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2583 gene, herein designated VGAM GENE, on one or more VGAM2583 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36129] It is yet further appreciated that a function of VGAM2583 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2583 include diagnosis, prevention and treatment of viral infection by Triatoma virus. Specific functions, and accordingly utilities, of VGAM2583 correlate with, and may be deduced from, the identity of the host target genes which VGAM2583 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[36130] Nucleotide sequences of the VGAM2583 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2583 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of

VGAM2583 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2583 are further described hereinbelow with reference to Table 1.

[36131] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2583 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[36132] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2584 (VGAM2584) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[36133] VGAM2584 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2584 was detected is described hereinabove with reference to Figs. 2-8.

[36134] VGAM2584 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Satsuma dwarf virus. VGAM2584 host target gene, herein designated VGAM

HOST TARGET GENE, is a human gene contained in the human genome.

[36135] VGAM2584 gene, herein designated VGAM GENE, encodes a VGAM2584 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2584 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2584 precursor RNA is designated SEQ ID:2570, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2570 is located at position 2340 relative to the genome of Satsuma dwarf virus.

[36136] VGAM2584 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2584 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36137] An enzyme complex designated DICER COMPLEX, dices the VGAM2584 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2584 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2584 RNA is designated SEQ ID:5295, and is provided hereinbelow with reference to the sequence listing part.

[36138] VGAM2584 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2584 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2584 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36139] VGAM2584 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites

located in untranslated regions of VGAM2584 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2584 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2584 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2584 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36140] The complementary binding of VGAM2584 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2584 host target RNA, herein designated VGAM

HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2584 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2584 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[36141] It is appreciated that VGAM2584 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2584 host target genes. The mRNA of each one of this plurality of VGAM2584 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2584 RNA, herein designated VGAM RNA, and which when bound by VGAM2584 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2584 host target proteins.

[36142] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2584 gene, herein designated VGAM GENE, on one or more VGAM2584 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove

with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36143] It is yet further appreciated that a function of VGAM2584 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2584 include diagnosis, prevention and treatment of viral infection by Satsuma dwarf virus. Specific functions, and accordingly utilities, of VGAM2584 correlate with, and may be deduced from, the identity of the host target genes which VGAM2584 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[36144] Nucleotide sequences of the VGAM2584 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2584 RNA, herein designated VGAM RNA, and

a schematic representation of the secondary folding of VGAM2584 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2584 are further described hereinbelow with reference to Table 1.

[36145] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2584 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[36146] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2585 (VGAM2585) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[36147] VGAM2585 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2585 was detected is described hereinabove with reference to Figs. 2-8.

[36148] VGAM2585 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Satsuma dwarf virus.

VGAM2585 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[36149] VGAM2585 gene, herein designated VGAM GENE, encodes a VGAM2585 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2585 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2585 precursor RNA is designated SEQ ID:2571, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2571 is located at position 5960 relative to the genome of Satsuma dwarf virus.

[36150] VGAM2585 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2585 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[36151] An enzyme complex designated DICER COMPLEX, dices the VGAM2585 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2585 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2585 RNA is designated SEQ ID:5296, and is provided hereinbelow with reference to the sequence listing part.

[36152] VGAM2585 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2585 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2585 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36153] VGAM2585 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM2585 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2585 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2585 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2585 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36154] The complementary binding of VGAM2585 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM2585 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2585 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2585 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[36155] It is appreciated that VGAM2585 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2585 host target genes. The mRNA of each one of this plurality of VGAM2585 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2585 RNA, herein designated VGAM RNA, and which when bound by VGAM2585 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2585 host target proteins.

[36156] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2585 gene, herein designated VGAM GENE, on one or more VGAM2585 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36157] It is yet further appreciated that a function of VGAM2585 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2585 include diagnosis, prevention and treatment of viral infection by Satsuma dwarf virus. Specific functions, and accordingly utilities, of VGAM2585 correlate with, and may be deduced from, the identity of the host target genes which VGAM2585 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[36158] Nucleotide sequences of the VGAM2585 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

diced VGAM2585 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2585 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2585 are further described hereinbelow with reference to Table 1.

[36159] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2585 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[36160] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2586 (VGAM2586) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[36161] VGAM2586 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2586 was detected is described hereinabove with reference to Figs. 2-8.

[36162] VGAM2586 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of Satsuma dwarf virus. VGAM2586 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[36163] VGAM2586 gene, herein designated VGAM GENE, encodes a VGAM2586 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2586 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2586 precursor RNA is designated SEQ ID:2572, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2572 is located at position 5834 relative to the genome of Satsuma dwarf virus.

[36164] VGAM2586 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2586 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36165] An enzyme complex designated DICER COMPLEX, dices the VGAM2586 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2586 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 53%) nucleotide sequence of VGAM2586 RNA is designated SEQ ID:5297, and is provided hereinbelow with reference to the sequence listing part.

[36166] VGAM2586 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2586 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2586 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36167] VGAM2586 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2586 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2586 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2586 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2586 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36168] The complementary binding of VGAM2586 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM2586 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2586 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2586 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[36169] It is appreciated that VGAM2586 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2586 host target genes. The mRNA of each one of this plurality of VGAM2586 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2586 RNA, herein designated VGAM RNA, and which when bound by VGAM2586 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2586 host target proteins.

[36170] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2586 gene, herein designated VGAM GENE, on one or more VGAM2586 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36171] It is yet further appreciated that a function of VGAM2586 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2586 include diagnosis, prevention and treatment of viral infection by Satsuma dwarf virus. Specific functions, and accordingly utilities, of VGAM2586 correlate with, and may be deduced from, the identity of the host target genes which VGAM2586 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[36172] Nucleotide sequences of the VGAM2586 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the diced VGAM2586 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2586 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2586 are further described hereinbelow with reference to Table 1.

[36173] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2586 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[36174] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2587 (VGAM2587) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[36175] VGAM2587 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2587 was detected is described hereinabove with reference to Figs. 2-8.

[36176] VGAM2587 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Satsuma dwarf virus. VGAM2587 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[36177] VGAM2587 gene, herein designated VGAM GENE, encodes a VGAM2587 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2587 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2587 precursor RNA is designated SEQ ID:2573, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2573 is located at position 4499 relative to the genome of Satsuma dwarf virus.

[36178] VGAM2587 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2587 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36179] An enzyme complex designated DICER COMPLEX, dices the VGAM2587 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2587 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2587 RNA is designated SEQ ID:5298, and is provided hereinbelow with reference to the sequence listing part.

[36180] VGAM2587 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2587 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2587 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN COD-

ING and 3UTR respectively.

[36181] VGAM2587 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2587 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2587 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2587 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2587 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36182] The complementary binding of VGAM2587 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2587 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2587 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2587 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[36183] It is appreciated that VGAM2587 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2587 host target genes. The mRNA of each one of this plurality of VGAM2587 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2587 RNA, herein designated VGAM RNA, and which when bound by VGAM2587 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2587 host target proteins.

[36184] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2587 gene, herein designated VGAM GENE, on one

or more VGAM2587 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36185] It is yet further appreciated that a function of VGAM2587 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2587 include diagnosis, prevention and treatment of viral infection by Satsuma dwarf virus. Specific functions, and accordingly utilities, of VGAM2587 correlate with, and may be deduced from, the identity of the host target genes which VGAM2587 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[36186] Nucleotide sequences of the VGAM2587 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2587 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2587 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2587 are further described hereinbelow with reference to Table 1.

[36187] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2587 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[36188] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2588 (VGAM2588) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[36189] VGAM2588 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2588 was detected is de-

scribed hereinabove with reference to Figs. 2-8.

[36190] VGAM2588 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Satsuma dwarf virus. VGAM2588 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[36191] VGAM2588 gene, herein designated VGAM GENE, encodes a VGAM2588 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2588 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2588 precursor RNA is designated SEQ ID:2574, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2574 is located at position 1651 relative to the genome of Satsuma dwarf virus.

[36192] VGAM2588 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2588 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36193] An enzyme complex designated DICER COMPLEX, dices the VGAM2588 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2588 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2588 RNA is designated SEQ ID:5299, and is provided hereinbelow with reference to the sequence listing part.

[36194] VGAM2588 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2588 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2588 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and

a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36195] VGAM2588 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2588 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2588 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2588 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2588 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both

3UTR and 5UTR regions.

[36196] The complementary binding of VGAM2588 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2588 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2588 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2588 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[36197] It is appreciated that VGAM2588 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2588 host target genes. The mRNA of each one of this plurality of VGAM2588 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2588 RNA, herein designated VGAM RNA, and which when bound by VGAM2588 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2588 host target proteins.

[36198] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM2588 gene, herein designated VGAM GENE, on one or more VGAM2588 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36199] It is yet further appreciated that a function of VGAM2588 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2588 include diagnosis, prevention and treatment of viral infection by Satsuma dwarf virus. Specific functions, and accordingly utilities, of VGAM2588 correlate with, and may be deduced from, the identity of the host target genes which VGAM2588 binds and inhibits, and the function of these host target genes, as

elaborated hereinbelow.

[36200] Nucleotide sequences of the VGAM2588 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2588 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2588 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2588 are further described hereinbelow with reference to Table 1.

[36201] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2588 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[36202] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2589 (VGAM2589) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[36203] VGAM2589 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene.

The method by which VGAM2589 was detected is described hereinabove with reference to Figs. 2-8.

[36204] VGAM2589 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Apple latent spherical virus. VGAM2589 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[36205] VGAM2589 gene, herein designated VGAM GENE, encodes a VGAM2589 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2589 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2589 precursor RNA is designated SEQ ID:2575, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2575 is located at position 1180 relative to the genome of Apple latent spherical virus.

[36206] VGAM2589 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2589 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36207] An enzyme complex designated DICER COMPLEX, dices the VGAM2589 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2589 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2589 RNA is designated SEQ ID:5300, and is provided hereinbelow with reference to the sequence listing part.

[36208] VGAM2589 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2589 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2589 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding

gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36209] VGAM2589 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2589 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2589 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2589 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2589 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be lo-

cated in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36210] The complementary binding of VGAM2589 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2589 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2589 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2589 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[36211] It is appreciated that VGAM2589 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2589 host target genes. The mRNA of each one of this plurality of VGAM2589 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2589 RNA, herein designated VGAM RNA, and which when bound by VGAM2589 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2589 host target proteins.

[36212] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM2589 gene, herein designated VGAM GENE, on one or more VGAM2589 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36213] It is yet further appreciated that a function of VGAM2589 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2589 include diagnosis, prevention and treatment of viral infection by Apple latent spherical virus. Specific functions, and accordingly utilities, of VGAM2589 correlate with, and may be deduced from, the identity of the host target genes which VGAM2589 binds and in-

hibits, and the function of these host target genes, as elaborated hereinbelow.

[36214] Nucleotide sequences of the VGAM2589 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2589 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2589 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2589 are further described hereinbelow with reference to Table 1.

[36215] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2589 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[36216] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2590 (VGAM2590) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[36217] VGAM2590 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2590 was detected is described hereinabove with reference to Figs. 2-8.

[36218] VGAM2590 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Apple latent spherical virus. VGAM2590 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[36219] VGAM2590 gene, herein designated VGAM GENE, encodes a VGAM2590 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2590 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2590 precursor RNA is designated SEQ ID:2576, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2576 is located at position 2408 relative to the genome of Apple latent spherical virus.

[36220] VGAM2590 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2590 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36221] An enzyme complex designated DICER COMPLEX, dices the VGAM2590 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2590 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 73%) nucleotide sequence of VGAM2590 RNA is designated SEQ ID:5301, and is provided hereinbelow with reference to the sequence listing part.

[36222] VGAM2590 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2590 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2590 host target RNA, herein designated VGAM HOST TARGET RNA, comprises

three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36223] VGAM2590 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2590 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2590 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2590 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2590 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an

example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36224] The complementary binding of VGAM2590 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2590 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2590 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2590 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[36225] It is appreciated that VGAM2590 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2590 host target genes. The mRNA of each one of this plurality of VGAM2590 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2590 RNA, herein designated VGAM RNA, and which when bound by VGAM2590 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2590 host target proteins.

[36226] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2590 gene, herein designated VGAM GENE, on one or more VGAM2590 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36227] It is yet further appreciated that a function of VGAM2590 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2590 include diagnosis, prevention and treatment of viral infection by Apple latent spherical virus. Specific functions, and accordingly utilities, of VGAM2590 correlate with, and may be deduced from, the identity of

the host target genes which VGAM2590 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[36228] Nucleotide sequences of the VGAM2590 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2590 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2590 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2590 are further described hereinbelow with reference to Table 1.

[36229] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2590 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[36230] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2591 (VGAM2591) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[36231] VGAM2591 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2591 was detected is described hereinabove with reference to Figs. 2-8.

[36232] VGAM2591 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Apple latent spherical virus. VGAM2591 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[36233] VGAM2591 gene, herein designated VGAM GENE, encodes a VGAM2591 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2591 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2591 precursor RNA is designated SEQ ID:2577, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2577 is located at position 6309 relative to the genome of Apple latent spherical virus.

[36234] VGAM2591 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2591 folded precursor RNA, herein designated VGAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36235] An enzyme complex designated DICER COMPLEX, dices the VGAM2591 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2591 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 62%) nucleotide sequence of VGAM2591 RNA is designated SEQ ID:5302, and is provided hereinbelow with reference to the sequence listing part.

[36236] VGAM2591 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2591 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2591 host target RNA,

herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36237] VGAM2591 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2591 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2591 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2591 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2591 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host tar-

get binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36238] The complementary binding of VGAM2591 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2591 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2591 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2591 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[36239] It is appreciated that VGAM2591 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2591 host target genes. The mRNA of each one of this plurality of VGAM2591 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2591 RNA, herein designated VGAM RNA, and which when bound by VGAM2591 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2591 host target proteins.

[36240] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2591 gene, herein designated VGAM GENE, on one or more VGAM2591 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36241] It is yet further appreciated that a function of VGAM2591 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2591 include diagnosis, prevention and treatment of viral infection by Apple latent spherical virus. Specific functions, and accordingly utilities, of VGAM2591

correlate with, and may be deduced from, the identity of the host target genes which VGAM2591 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[36242] Nucleotide sequences of the VGAM2591 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2591 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2591 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2591 are further described hereinbelow with reference to Table 1.

[36243] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2591 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[36244] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2592 (VGAM2592) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the

art.

[36245] VGAM2592 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2592 was detected is described hereinabove with reference to Figs. 2-8.

[36246] VGAM2592 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Apple latent spherical virus. VGAM2592 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[36247] VGAM2592 gene, herein designated VGAM GENE, encodes a VGAM2592 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2592 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2592 precursor RNA is designated SEQ ID:2578, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2578 is located at position 1588 relative to the genome of Apple latent spherical virus.

[36248] VGAM2592 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2592 folded

precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36249] An enzyme complex designated DICER COMPLEX, dices the VGAM2592 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2592 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2592 RNA is designated SEQ ID:5303, and is provided hereinbelow with reference to the sequence listing part.

[36250] VGAM2592 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2592 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM2592 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36251] VGAM2592 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2592 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2592 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2592 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2592 host target RNA, herein designated VGAM HOST TARGET RNA.

It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36252] The complementary binding of VGAM2592 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2592 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2592 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2592 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[36253] It is appreciated that VGAM2592 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2592 host target genes. The mRNA of each one of this plurality of VGAM2592 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2592 RNA, herein designated VGAM RNA, and which when bound by VGAM2592 RNA, herein designated VGAM RNA, causes inhibition of translation of

respective one or more VGAM2592 host target proteins.

[36254] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2592 gene, herein designated VGAM GENE, on one or more VGAM2592 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36255] It is yet further appreciated that a function of VGAM2592 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2592 include diagnosis, prevention and treatment of viral infection by Apple latent spherical virus.

Specific functions, and accordingly utilities, of VGAM2592 correlate with, and may be deduced from, the identity of the host target genes which VGAM2592 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[36256] Nucleotide sequences of the VGAM2592 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2592 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2592 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2592 are further described hereinbelow with reference to Table 1.

[36257] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2592 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[36258] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2593 (VGAM2593) viral gene, which modulates expression of respective host target genes thereof, the func-

tion and utility of which host target genes is known in the art.

[36259] VGAM2593 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2593 was detected is described hereinabove with reference to Figs. 2-8.

[36260] VGAM2593 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Apple latent spherical virus. VGAM2593 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[36261] VGAM2593 gene, herein designated VGAM GENE, encodes a VGAM2593 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2593 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2593 precursor RNA is designated SEQ ID:2579, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2579 is located at position 5091 relative to the genome of Apple latent spherical virus.

[36262] VGAM2593 precursor RNA, herein designated VGAM PRE-

CURSOR RNA, folds onto itself, forming VGAM2593 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36263] An enzyme complex designated DICER COMPLEX, dices the VGAM2593 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2593 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 71%) nucleotide sequence of VGAM2593 RNA is designated SEQ ID:5304, and is provided hereinbelow with reference to the sequence listing part.

[36264] VGAM2593 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM2593 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2593 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36265] VGAM2593 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2593 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2593 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2593 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2593 host

target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36266] The complementary binding of VGAM2593 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2593 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2593 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2593 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[36267] It is appreciated that VGAM2593 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2593 host target genes. The mRNA of each one of this plurality of VGAM2593 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2593 RNA, herein designated VGAM RNA, and which when bound by VGAM2593 RNA, herein

designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2593 host target proteins.

[36268] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2593 gene, herein designated VGAM GENE, on one or more VGAM2593 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36269] It is yet further appreciated that a function of VGAM2593 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2593 include diagnosis, prevention and

treatment of viral infection by Apple latent spherical virus. Specific functions, and accordingly utilities, of VGAM2593 correlate with, and may be deduced from, the identity of the host target genes which VGAM2593 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[36270] Nucleotide sequences of the VGAM2593 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2593 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2593 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2593 are further described hereinbelow with reference to Table 1.

[36271] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2593 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[36272] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2594 (VGAM2594) viral gene, which modulates ex-

pression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[36273] VGAM2594 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2594 was detected is described hereinabove with reference to Figs. 2-8.

[36274] VGAM2594 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Apple latent spherical virus. VGAM2594 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[36275] VGAM2594 gene, herein designated VGAM GENE, encodes a VGAM2594 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2594 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2594 precursor RNA is designated SEQ ID:2580, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2580 is located at position 1452 relative to the genome of Apple latent spherical virus.

[36276] VGAM2594 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2594 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36277] An enzyme complex designated DICER COMPLEX, dices the VGAM2594 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2594 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2594 RNA is designated SEQ ID:5305, and is provided hereinbelow with reference to the sequence listing part.

[36278] VGAM2594 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2594 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2594 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36279] VGAM2594 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2594 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2594 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2594 RNA, herein designated VGAM RNA, may have a different number of host target

binding sites in untranslated regions of a VGAM2594 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36280] The complementary binding of VGAM2594 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2594 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2594 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2594 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[36281] It is appreciated that VGAM2594 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2594 host target genes. The mRNA of each one of this plurality of VGAM2594 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2594 RNA, herein designated VGAM

RNA, and which when bound by VGAM2594 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2594 host target proteins.

[36282] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2594 gene, herein designated VGAM GENE, on one or more VGAM2594 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36283] It is yet further appreciated that a function of VGAM2594 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM2594 include diagnosis, prevention and treatment of viral infection by Apple latent spherical virus. Specific functions, and accordingly utilities, of VGAM2594 correlate with, and may be deduced from, the identity of the host target genes which VGAM2594 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[36284] Nucleotide sequences of the VGAM2594 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2594 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2594 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2594 are further described hereinbelow with reference to Table 1.

[36285] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2594 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[36286] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Mes-

senger 2595 (VGAM2595) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[36287] VGAM2595 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2595 was detected is described hereinabove with reference to Figs. 2-8.

[36288] VGAM2595 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Apple latent spherical virus. VGAM2595 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[36289] VGAM2595 gene, herein designated VGAM GENE, encodes a VGAM2595 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2595 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2595 precursor RNA is designated SEQ ID:2581, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2581 is located at position 6486

relative to the genome of Apple latent spherical virus.

[36290] VGAM2595 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2595 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36291] An enzyme complex designated DICER COMPLEX, dices the VGAM2595 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2595 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 47%) nucleotide sequence of VGAM2595 RNA is designated SEQ ID:5306, and is provided hereinbelow with reference to the sequence listing part.

[36292] VGAM2595 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2595 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2595 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36293] VGAM2595 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2595 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2595 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2595 RNA, herein designated

VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2595 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36294] The complementary binding of VGAM2595 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2595 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2595 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2595 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[36295] It is appreciated that VGAM2595 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2595 host target genes. The mRNA of each one of this plurality of VGAM2595 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM2595 RNA, herein designated VGAM RNA, and which when bound by VGAM2595 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2595 host target proteins.

[36296] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2595 gene, herein designated VGAM GENE, on one or more VGAM2595 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36297] It is yet further appreciated that a function of VGAM2595 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2595 include diagnosis, prevention and treatment of viral infection by Apple latent spherical virus. Specific functions, and accordingly utilities, of VGAM2595 correlate with, and may be deduced from, the identity of the host target genes which VGAM2595 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[36298] Nucleotide sequences of the VGAM2595 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2595 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2595 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2595 are further described hereinbelow with reference to Table 1.

[36299] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2595 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[36300] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present

invention, referred to here as Viral Genomic Address Messenger 2596 (VGAM2596) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[36301] VGAM2596 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2596 was detected is described hereinabove with reference to Figs. 2-8.

[36302] VGAM2596 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Tobacco rattle virus. VGAM2596 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[36303] VGAM2596 gene, herein designated VGAM GENE, encodes a VGAM2596 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2596 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2596 precursor RNA is designated SEQ ID:2582, and is provided hereinbelow with reference to the sequence listing part. Nu-

cleotide sequence SEQ ID:2582 is located at position 3368 relative to the genome of Tobacco rattle virus.

[36304] VGAM2596 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2596 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36305] An enzyme complex designated DICER COMPLEX, dices the VGAM2596 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2596 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide sequence of VGAM2596 RNA is designated SEQ ID:5307, and is provided hereinbelow with reference to the sequence

listing part.

[36306] VGAM2596 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2596 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2596 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36307] VGAM2596 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2596 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2596 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not

meant to be limiting VGAM2596 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2596 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36308] The complementary binding of VGAM2596 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2596 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2596 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2596 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[36309] It is appreciated that VGAM2596 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2596 host target genes. The mRNA of each one of this plurality of VGAM2596 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2596 RNA, herein designated VGAM RNA, and which when bound by VGAM2596 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2596 host target proteins.

[36310] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2596 gene, herein designated VGAM GENE, on one or more VGAM2596 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36311] It is yet further appreciated that a function of VGAM2596

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2596 include diagnosis, prevention and treatment of viral infection by Tobacco rattle virus. Specific functions, and accordingly utilities, of VGAM2596 correlate with, and may be deduced from, the identity of the host target genes which VGAM2596 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[36312] Nucleotide sequences of the VGAM2596 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2596 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2596 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2596 are further described hereinbelow with reference to Table 1.

[36313] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2596 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[36314] Fig. 1 further provides a conceptual description of another

novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2597 (VGAM2597) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[36315] VGAM2597 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2597 was detected is described hereinabove with reference to Figs. 2-8.

[36316] VGAM2597 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Tobacco rattle virus. VGAM2597 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[36317] VGAM2597 gene, herein designated VGAM GENE, encodes a VGAM2597 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2597 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2597 precursor RNA is designated SEQ ID:2583, and is provided here-

inbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2583 is located at position 1854 relative to the genome of Tobacco rattle virus.

[36318] VGAM2597 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2597 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36319] An enzyme complex designated DICER COMPLEX, dices the VGAM2597 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2597 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 64%) nucleotide sequence of VGAM2597 RNA is designated SEQ ID:5308, and

is provided hereinbelow with reference to the sequence listing part.

[36320] VGAM2597 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2597 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2597 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36321] VGAM2597 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2597 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2597 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites

shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2597 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2597 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36322] The complementary binding of VGAM2597 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2597 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2597 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2597 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[36323] It is appreciated that VGAM2597 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2597 host target genes. The mRNA of each one of this plurality of VGAM2597 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2597 RNA, herein designated VGAM RNA, and which when bound by VGAM2597 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2597 host target proteins.

[36324] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2597 gene, herein designated VGAM GENE, on one or more VGAM2597 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36325] It is yet further appreciated that a function of VGAM2597 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2597 include diagnosis, prevention and treatment of viral infection by Tobacco rattle virus. Specific functions, and accordingly utilities, of VGAM2597 correlate with, and may be deduced from, the identity of the host target genes which VGAM2597 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[36326] Nucleotide sequences of the VGAM2597 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2597 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2597 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2597 are further described hereinbelow with reference to Table 1.

[36327] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2597 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[36328] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2598 (VGAM2598) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[36329] VGAM2598 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2598 was detected is described hereinabove with reference to Figs. 2-8.

[36330] VGAM2598 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Tobacco rattle virus. VGAM2598 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[36331] VGAM2598 gene, herein designated VGAM GENE, encodes a VGAM2598 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2598 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2598 precur-

sor RNA is designated SEQ ID:2584, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2584 is located at position 1327 relative to the genome of Tobacco rattle virus.

[36332] VGAM2598 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2598 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36333] An enzyme complex designated DICER COMPLEX, dices the VGAM2598 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2598 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide se-

quence of VGAM2598 RNA is designated SEQ ID:5309, and is provided hereinbelow with reference to the sequence listing part.

[36334] VGAM2598 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2598 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2598 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36335] VGAM2598 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2598 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2598 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is ap-

preciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2598 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2598 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36336] The complementary binding of VGAM2598 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2598 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2598 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2598 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[36337] It is appreciated that VGAM2598 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2598 host target genes. The mRNA of

each one of this plurality of VGAM2598 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2598 RNA, herein designated VGAM RNA, and which when bound by VGAM2598 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2598 host target proteins.

[36338] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2598 gene, herein designated VGAM GENE, on one or more VGAM2598 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science

294,779 (2001)).

[36339] It is yet further appreciated that a function of VGAM2598 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2598 include diagnosis, prevention and treatment of viral infection by Tobacco rattle virus. Specific functions, and accordingly utilities, of VGAM2598 correlate with, and may be deduced from, the identity of the host target genes which VGAM2598 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[36340] Nucleotide sequences of the VGAM2598 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2598 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2598 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2598 are further described hereinbelow with reference to Table 1.

[36341] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2598 RNA, herein designated VGAM RNA, are de-

scribed hereinbelow with reference to Table 2.

[36342] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2599 (VGAM2599) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[36343] VGAM2599 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2599 was detected is described hereinabove with reference to Figs. 2-8.

[36344] VGAM2599 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Obuda pepper virus. VGAM2599 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[36345] VGAM2599 gene, herein designated VGAM GENE, encodes a VGAM2599 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2599 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly

similar to the nucleotide sequence of VGAM2599 precursor RNA is designated SEQ ID:2585, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2585 is located at position 2974 relative to the genome of Obuda pepper virus.

[36346] VGAM2599 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2599 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36347] An enzyme complex designated DICER COMPLEX, dices the VGAM2599 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2599 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 56%) nucleotide sequence of VGAM2599 RNA is designated SEQ ID:5310, and is provided hereinbelow with reference to the sequence listing part.

[36348] VGAM2599 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2599 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2599 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36349] VGAM2599 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2599 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2599 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I,

BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2599 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2599 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36350] The complementary binding of VGAM2599 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2599 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2599 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2599 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[36351] It is appreciated that VGAM2599 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM2599 host target genes. The mRNA of each one of this plurality of VGAM2599 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2599 RNA, herein designated VGAM RNA, and which when bound by VGAM2599 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2599 host target proteins.

[36352] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2599 gene, herein designated VGAM GENE, on one or more VGAM2599 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36353] It is yet further appreciated that a function of VGAM2599 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2599 include diagnosis, prevention and treatment of viral infection by Obuda pepper virus. Specific functions, and accordingly utilities, of VGAM2599 correlate with, and may be deduced from, the identity of the host target genes which VGAM2599 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[36354] Nucleotide sequences of the VGAM2599 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2599 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2599 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2599 are further described hereinbelow with reference to Table 1.

[36355] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites

to VGAM2599 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[36356] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2600 (VGAM2600) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[36357] VGAM2600 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2600 was detected is described hereinabove with reference to Figs. 2-8.

[36358] VGAM2600 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Obuda pepper virus. VGAM2600 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[36359] VGAM2600 gene, herein designated VGAM GENE, encodes a VGAM2600 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2600 precursor RNA, herein designated VGAM PRECURSOR RNA, does not en-

code a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2600 precursor RNA is designated SEQ ID:2586, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2586 is located at position 1275 relative to the genome of Obuda pepper virus.

[36360] VGAM2600 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2600 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36361] An enzyme complex designated DICER COMPLEX, dices the VGAM2600 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2600 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2600 RNA is designated SEQ ID:5311, and is provided hereinbelow with reference to the sequence listing part.

[36362] VGAM2600 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2600 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2600 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36363] VGAM2600 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2600 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2600 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3

such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2600 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2600 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36364] The complementary binding of VGAM2600 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2600 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2600 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2600 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[36365] It is appreciated that VGAM2600 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2600 host target genes. The mRNA of each one of this plurality of VGAM2600 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2600 RNA, herein designated VGAM RNA, and which when bound by VGAM2600 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2600 host target proteins.

[36366] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2600 gene, herein designated VGAM GENE, on one or more VGAM2600 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36367] It is yet further appreciated that a function of VGAM2600 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2600 include diagnosis, prevention and treatment of viral infection by Obuda pepper virus. Specific functions, and accordingly utilities, of VGAM2600 correlate with, and may be deduced from, the identity of the host target genes which VGAM2600 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[36368] Nucleotide sequences of the VGAM2600 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2600 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2600 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2600 are further described hereinbelow with reference to Table 1.

[36369] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the

complementarity of each of these host target binding sites to VGAM2600 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[36370] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2601 (VGAM2601) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[36371] VGAM2601 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2601 was detected is described hereinabove with reference to Figs. 2-8.

[36372] VGAM2601 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Obuda pepper virus. VGAM2601 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[36373] VGAM2601 gene, herein designated VGAM GENE, encodes a VGAM2601 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2601 precursor RNA,

herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2601 precursor RNA is designated SEQ ID:2587, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2587 is located at position 589 relative to the genome of Obuda pepper virus.

[36374] VGAM2601 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2601 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36375] An enzyme complex designated DICER COMPLEX, dices the VGAM2601 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2601 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 92%) nucleotide sequence of VGAM2601 RNA is designated SEQ ID:5312, and is provided hereinbelow with reference to the sequence listing part.

[36376] VGAM2601 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2601 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2601 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36377] VGAM2601 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2601 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2601 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host

target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2601 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2601 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36378] The complementary binding of VGAM2601 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2601 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2601 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2601 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[36379] It is appreciated that VGAM2601 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2601 host target genes. The mRNA of each one of this plurality of VGAM2601 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2601 RNA, herein designated VGAM RNA, and which when bound by VGAM2601 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2601 host target proteins.

[36380] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2601 gene, herein designated VGAM GENE, on one or more VGAM2601 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36381] It is yet further appreciated that a function of VGAM2601 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2601 include diagnosis, prevention and treatment of viral infection by Obuda pepper virus. Specific functions, and accordingly utilities, of VGAM2601 correlate with, and may be deduced from, the identity of the host target genes which VGAM2601 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[36382] Nucleotide sequences of the VGAM2601 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2601 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2601 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2601 are further described hereinbelow with reference to Table 1.

[36383] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2601 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[36384] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2602 (VGAM2602) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[36385] VGAM2602 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2602 was detected is described hereinabove with reference to Figs. 2-8.

[36386] VGAM2602 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Obuda pepper virus. VGAM2602 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[36387] VGAM2602 gene, herein designated VGAM GENE, encodes a VGAM2602 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and un-

like most ordinary genes, VGAM2602 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2602 precursor RNA is designated SEQ ID:2588, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2588 is located at position 2115 relative to the genome of Obuda pepper virus.

[36388] VGAM2602 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2602 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36389] An enzyme complex designated DICER COMPLEX, dices the VGAM2602 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2602 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2602 RNA is designated SEQ ID:5313, and is provided hereinbelow with reference to the sequence listing part.

[36390] VGAM2602 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2602 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2602 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36391] VGAM2602 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2602 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2602 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed

sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2602 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2602 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36392] The complementary binding of VGAM2602 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2602 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2602 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2602 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target

protein is therefore outlined by a broken line.

[36393] It is appreciated that VGAM2602 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2602 host target genes. The mRNA of each one of this plurality of VGAM2602 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2602 RNA, herein designated VGAM RNA, and which when bound by VGAM2602 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2602 host target proteins.

[36394] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2602 gene, herein designated VGAM GENE, on one or more VGAM2602 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36395] It is yet further appreciated that a function of VGAM2602 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2602 include diagnosis, prevention and treatment of viral infection by Obuda pepper virus. Specific functions, and accordingly utilities, of VGAM2602 correlate with, and may be deduced from, the identity of the host target genes which VGAM2602 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[36396] Nucleotide sequences of the VGAM2602 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2602 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2602 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2602 are further described hereinbelow with reference to Table 1.

[36397] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2602 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[36398] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2603 (VGAM2603) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[36399] VGAM2603 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2603 was detected is described hereinabove with reference to Figs. 2-8.

[36400] VGAM2603 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Sugarcane striate mosaic associated virus. VGAM2603 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[36401] VGAM2603 gene, herein designated VGAM GENE, encodes a VGAM2603 precursor RNA, herein designated VGAM

PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2603 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2603 precursor RNA is designated SEQ ID:2589, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2589 is located at position 5796 relative to the genome of Sugarcane striate mosaic associated virus.

[36402] VGAM2603 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2603 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36403] An enzyme complex designated DICER COMPLEX, dices the VGAM2603 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2603 RNA,

herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 73%) nucleotide sequence of VGAM2603 RNA is designated SEQ ID:5314, and is provided hereinbelow with reference to the sequence listing part.

[36404] VGAM2603 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2603 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2603 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36405] VGAM2603 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2603 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM2603 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2603 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2603 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36406] The complementary binding of VGAM2603 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2603 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2603 host target RNA, herein designated VGAM HOST TARGET

RNA, into VGAM2603 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[36407] It is appreciated that VGAM2603 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2603 host target genes. The mRNA of each one of this plurality of VGAM2603 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2603 RNA, herein designated VGAM RNA, and which when bound by VGAM2603 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2603 host target proteins.

[36408] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2603 gene, herein designated VGAM GENE, on one or more VGAM2603 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36409] It is yet further appreciated that a function of VGAM2603 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2603 include diagnosis, prevention and treatment of viral infection by Sugarcane striate mosaic associated virus. Specific functions, and accordingly utilities, of VGAM2603 correlate with, and may be deduced from, the identity of the host target genes which VGAM2603 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[36410] Nucleotide sequences of the VGAM2603 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2603 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2603 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2603 are further

described hereinbelow with reference to Table 1.

[36411] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2603 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[36412] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2604 (VGAM2604) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[36413] VGAM2604 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2604 was detected is described hereinabove with reference to Figs. 2-8.

[36414] VGAM2604 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Sugarcane striate mosaic associated virus. VGAM2604 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[36415] VGAM2604 gene, herein designated VGAM GENE, encodes a VGAM2604 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2604 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2604 precursor RNA is designated SEQ ID:2590, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2590 is located at position 3074 relative to the genome of Sugarcane striate mosaic associated virus.

[36416] VGAM2604 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2604 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36417] An enzyme complex designated DICER COMPLEX, dices

the VGAM2604 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2604 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2604 RNA is designated SEQ ID:5315, and is provided hereinbelow with reference to the sequence listing part.

[36418] VGAM2604 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2604 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2604 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36419] VGAM2604 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2604 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2604 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2604 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2604 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36420] The complementary binding of VGAM2604 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2604 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM2604 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2604 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[36421] It is appreciated that VGAM2604 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2604 host target genes. The mRNA of each one of this plurality of VGAM2604 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2604 RNA, herein designated VGAM RNA, and which when bound by VGAM2604 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2604 host target proteins.

[36422] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2604 gene, herein designated VGAM GENE, on one or more VGAM2604 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36423] It is yet further appreciated that a function of VGAM2604 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2604 include diagnosis, prevention and treatment of viral infection by Sugarcane striate mosaic associated virus. Specific functions, and accordingly utilities, of VGAM2604 correlate with, and may be deduced from, the identity of the host target genes which VGAM2604 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[36424] Nucleotide sequences of the VGAM2604 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2604 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of

VGAM2604 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2604 are further described hereinbelow with reference to Table 1.

[36425] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2604 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[36426] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2605 (VGAM2605) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[36427] VGAM2605 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2605 was detected is described hereinabove with reference to Figs. 2-8.

[36428] VGAM2605 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Salmon pancreas disease virus. VGAM2605 host target gene, herein designated

VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[36429] VGAM2605 gene, herein designated VGAM GENE, encodes a VGAM2605 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2605 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2605 precursor RNA is designated SEQ ID:2591, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2591 is located at position 9457 relative to the genome of Salmon pancreas disease virus.

[36430] VGAM2605 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2605 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36431] An enzyme complex designated DICER COMPLEX, dices the VGAM2605 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2605 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2605 RNA is designated SEQ ID:5316, and is provided hereinbelow with reference to the sequence listing part.

[36432] VGAM2605 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2605 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2605 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36433] VGAM2605 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites

located in untranslated regions of VGAM2605 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2605 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2605 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2605 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36434] The complementary binding of VGAM2605 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2605 host target RNA, herein designated VGAM

HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2605 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2605 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[36435] It is appreciated that VGAM2605 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2605 host target genes. The mRNA of each one of this plurality of VGAM2605 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2605 RNA, herein designated VGAM RNA, and which when bound by VGAM2605 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2605 host target proteins.

[36436] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2605 gene, herein designated VGAM GENE, on one or more VGAM2605 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove

with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36437] It is yet further appreciated that a function of VGAM2605 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2605 include diagnosis, prevention and treatment of viral infection by Salmon pancreas disease virus. Specific functions, and accordingly utilities, of VGAM2605 correlate with, and may be deduced from, the identity of the host target genes which VGAM2605 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[36438] Nucleotide sequences of the VGAM2605 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2605 RNA, herein designated VGAM RNA, and

a schematic representation of the secondary folding of VGAM2605 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2605 are further described hereinbelow with reference to Table 1.

[36439] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2605 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[36440] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2606 (VGAM2606) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[36441] VGAM2606 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2606 was detected is described hereinabove with reference to Figs. 2-8.

[36442] VGAM2606 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Salmon pancreas disease

virus. VGAM2606 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[36443] VGAM2606 gene, herein designated VGAM GENE, encodes a VGAM2606 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2606 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2606 precursor RNA is designated SEQ ID:2592, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2592 is located at position 11312 relative to the genome of Salmon pancreas disease virus.

[36444] VGAM2606 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2606 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36445] An enzyme complex designated DICER COMPLEX, dices the VGAM2606 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2606 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2606 RNA is designated SEQ ID:5317, and is provided hereinbelow with reference to the sequence listing part.

[36446] VGAM2606 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2606 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2606 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36447] VGAM2606 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2606 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2606 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2606 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2606 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36448] The complementary binding of VGAM2606 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM2606 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2606 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2606 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[36449] It is appreciated that VGAM2606 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2606 host target genes. The mRNA of each one of this plurality of VGAM2606 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2606 RNA, herein designated VGAM RNA, and which when bound by VGAM2606 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2606 host target proteins.

[36450] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2606 gene, herein designated VGAM GENE, on one or more VGAM2606 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36451] It is yet further appreciated that a function of VGAM2606 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2606 include diagnosis, prevention and treatment of viral infection by Salmon pancreas disease virus. Specific functions, and accordingly utilities, of VGAM2606 correlate with, and may be deduced from, the identity of the host target genes which VGAM2606 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[36452] Nucleotide sequences of the VGAM2606 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the diced VGAM2606 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2606 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2606 are further described hereinbelow with reference to Table 1.

[36453] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2606 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[36454] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2607 (VGAM2607) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[36455] VGAM2607 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2607 was detected is described hereinabove with reference to Figs. 2-8.

[36456] VGAM2607 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ljungan virus. VGAM2607 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[36457] VGAM2607 gene, herein designated VGAM GENE, encodes a VGAM2607 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2607 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2607 precursor RNA is designated SEQ ID:2593, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2593 is located at position 7425 relative to the genome of Ljungan virus.

[36458] VGAM2607 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2607 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36459] An enzyme complex designated DICER COMPLEX, dices the VGAM2607 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2607 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2607 RNA is designated SEQ ID:5318, and is provided hereinbelow with reference to the sequence listing part.

[36460] VGAM2607 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2607 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2607 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN COD-

ING and 3UTR respectively.

[36461] VGAM2607 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2607 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2607 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2607 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2607 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36462] The complementary binding of VGAM2607 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2607 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2607 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2607 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[36463] It is appreciated that VGAM2607 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2607 host target genes. The mRNA of each one of this plurality of VGAM2607 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2607 RNA, herein designated VGAM RNA, and which when bound by VGAM2607 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2607 host target proteins.

[36464] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2607 gene, herein designated VGAM GENE, on one

or more VGAM2607 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36465] It is yet further appreciated that a function of VGAM2607 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2607 include diagnosis, prevention and treatment of viral infection by Ljungan virus. Specific functions, and accordingly utilities, of VGAM2607 correlate with, and may be deduced from, the identity of the host target genes which VGAM2607 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[36466] Nucleotide sequences of the VGAM2607 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2607 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2607 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2607 are further described hereinbelow with reference to Table 1.

[36467] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2607 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[36468] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2608 (VGAM2608) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[36469] VGAM2608 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2608 was detected is de-

scribed hereinabove with reference to Figs. 2-8.

[36470] VGAM2608 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ljungan virus. VGAM2608 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[36471] VGAM2608 gene, herein designated VGAM GENE, encodes a VGAM2608 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2608 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2608 precursor RNA is designated SEQ ID:2594, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2594 is located at position 6824 relative to the genome of Ljungan virus.

[36472] VGAM2608 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2608 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36473] An enzyme complex designated DICER COMPLEX, dices the VGAM2608 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2608 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 87%) nucleotide sequence of VGAM2608 RNA is designated SEQ ID:5319, and is provided hereinbelow with reference to the sequence listing part.

[36474] VGAM2608 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2608 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2608 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and

a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36475] VGAM2608 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2608 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2608 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2608 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2608 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both

3UTR and 5UTR regions.

[36476] The complementary binding of VGAM2608 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2608 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2608 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2608 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[36477] It is appreciated that VGAM2608 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2608 host target genes. The mRNA of each one of this plurality of VGAM2608 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2608 RNA, herein designated VGAM RNA, and which when bound by VGAM2608 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2608 host target proteins.

[36478] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM2608 gene, herein designated VGAM GENE, on one or more VGAM2608 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36479] It is yet further appreciated that a function of VGAM2608 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2608 include diagnosis, prevention and treatment of viral infection by Ljungan virus. Specific functions, and accordingly utilities, of VGAM2608 correlate with, and may be deduced from, the identity of the host target genes which VGAM2608 binds and inhibits, and the function of these host target genes, as elaborated

hereinbelow.

[36480] Nucleotide sequences of the VGAM2608 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2608 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2608 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2608 are further described hereinbelow with reference to Table 1.

[36481] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2608 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[36482] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2609 (VGAM2609) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[36483] VGAM2609 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene.

The method by which VGAM2609 was detected is described hereinabove with reference to Figs. 2-8.

[36484] VGAM2609 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ljungan virus. VGAM2609 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[36485] VGAM2609 gene, herein designated VGAM GENE, encodes a VGAM2609 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2609 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2609 precursor RNA is designated SEQ ID:2595, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2595 is located at position 2766 relative to the genome of Ljungan virus.

[36486] VGAM2609 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2609 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36487] An enzyme complex designated DICER COMPLEX, dices the VGAM2609 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2609 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 57%) nucleotide sequence of VGAM2609 RNA is designated SEQ ID:5320, and is provided hereinbelow with reference to the sequence listing part.

[36488] VGAM2609 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2609 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2609 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding

gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36489] VGAM2609 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2609 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2609 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2609 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2609 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be lo-

cated in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36490] The complementary binding of VGAM2609 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2609 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2609 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2609 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[36491] It is appreciated that VGAM2609 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2609 host target genes. The mRNA of each one of this plurality of VGAM2609 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2609 RNA, herein designated VGAM RNA, and which when bound by VGAM2609 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2609 host target proteins.

[36492] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM2609 gene, herein designated VGAM GENE, on one or more VGAM2609 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36493] It is yet further appreciated that a function of VGAM2609 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2609 include diagnosis, prevention and treatment of viral infection by Ljungan virus. Specific functions, and accordingly utilities, of VGAM2609 correlate with, and may be deduced from, the identity of the host target genes which VGAM2609 binds and inhibits,

and the function of these host target genes, as elaborated hereinbelow.

[36494] Nucleotide sequences of the VGAM2609 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2609 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2609 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2609 are further described hereinbelow with reference to Table 1.

[36495] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2609 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[36496] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2610 (VGAM2610) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[36497] VGAM2610 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2610 was detected is described hereinabove with reference to Figs. 2-8.

[36498] VGAM2610 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ljungan virus. VGAM2610 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[36499] VGAM2610 gene, herein designated VGAM GENE, encodes a VGAM2610 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2610 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2610 precursor RNA is designated SEQ ID:2596, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2596 is located at position 7099 relative to the genome of Ljungan virus.

[36500] VGAM2610 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2610 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36501] An enzyme complex designated DICER COMPLEX, dices the VGAM2610 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2610 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2610 RNA is designated SEQ ID:5321, and is provided hereinbelow with reference to the sequence listing part.

[36502] VGAM2610 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2610 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2610 host target RNA, herein designated VGAM HOST TARGET RNA, comprises

three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36503] VGAM2610 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2610 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2610 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2610 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2610 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an

example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36504] The complementary binding of VGAM2610 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2610 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2610 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2610 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[36505] It is appreciated that VGAM2610 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2610 host target genes. The mRNA of each one of this plurality of VGAM2610 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2610 RNA, herein designated VGAM RNA, and which when bound by VGAM2610 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2610 host target proteins.

[36506] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2610 gene, herein designated VGAM GENE, on one or more VGAM2610 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36507] It is yet further appreciated that a function of VGAM2610 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2610 include diagnosis, prevention and treatment of viral infection by Ljungan virus. Specific functions, and accordingly utilities, of VGAM2610 correlate with, and may be deduced from, the identity of the

host target genes which VGAM2610 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[36508] Nucleotide sequences of the VGAM2610 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2610 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2610 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2610 are further described hereinbelow with reference to Table 1.

[36509] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2610 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[36510] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2611 (VGAM2611) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[36511] VGAM2611 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2611 was detected is described hereinabove with reference to Figs. 2-8.

[36512] VGAM2611 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine rhinitis A virus. VGAM2611 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[36513] VGAM2611 gene, herein designated VGAM GENE, encodes a VGAM2611 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2611 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2611 precursor RNA is designated SEQ ID:2597, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2597 is located at position 3057 relative to the genome of Equine rhinitis A virus.

[36514] VGAM2611 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2611 folded precursor RNA, herein designated VGAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36515] An enzyme complex designated DICER COMPLEX, dices the VGAM2611 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2611 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 70%) nucleotide sequence of VGAM2611 RNA is designated SEQ ID:5322, and is provided hereinbelow with reference to the sequence listing part.

[36516] VGAM2611 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2611 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2611 host target RNA,

herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36517] VGAM2611 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2611 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2611 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2611 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2611 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host tar-

get binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36518] The complementary binding of VGAM2611 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2611 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2611 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2611 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[36519] It is appreciated that VGAM2611 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2611 host target genes. The mRNA of each one of this plurality of VGAM2611 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2611 RNA, herein designated VGAM RNA, and which when bound by VGAM2611 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2611 host target proteins.

[36520] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2611 gene, herein designated VGAM GENE, on one or more VGAM2611 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36521] It is yet further appreciated that a function of VGAM2611 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2611 include diagnosis, prevention and treatment of viral infection by Equine rhinitis A virus. Specific functions, and accordingly utilities, of VGAM2611

correlate with, and may be deduced from, the identity of the host target genes which VGAM2611 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[36522] Nucleotide sequences of the VGAM2611 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2611 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2611 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2611 are further described hereinbelow with reference to Table 1.

[36523] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2611 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[36524] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2612 (VGAM2612) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the

art.

[36525] VGAM2612 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2612 was detected is described hereinabove with reference to Figs. 2-8.

[36526] VGAM2612 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine rhinitis A virus. VGAM2612 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[36527] VGAM2612 gene, herein designated VGAM GENE, encodes a VGAM2612 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2612 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2612 precursor RNA is designated SEQ ID:2598, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2598 is located at position 2734 relative to the genome of Equine rhinitis A virus.

[36528] VGAM2612 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2612 folded

precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36529] An enzyme complex designated DICER COMPLEX, dices the VGAM2612 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2612 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2612 RNA is designated SEQ ID:5323, and is provided hereinbelow with reference to the sequence listing part.

[36530] VGAM2612 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2612 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM2612 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36531] VGAM2612 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2612 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2612 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2612 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2612 host target RNA, herein designated VGAM HOST TARGET RNA.

It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36532] The complementary binding of VGAM2612 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2612 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2612 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2612 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[36533] It is appreciated that VGAM2612 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2612 host target genes. The mRNA of each one of this plurality of VGAM2612 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2612 RNA, herein designated VGAM RNA, and which when bound by VGAM2612 RNA, herein designated VGAM RNA, causes inhibition of translation of

respective one or more VGAM2612 host target proteins.

[36534] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2612 gene, herein designated VGAM GENE, on one or more VGAM2612 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36535] It is yet further appreciated that a function of VGAM2612 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2612 include diagnosis, prevention and treatment of viral infection by Equine rhinitis A virus. Spe-

cific functions, and accordingly utilities, of VGAM2612 correlate with, and may be deduced from, the identity of the host target genes which VGAM2612 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[36536] Nucleotide sequences of the VGAM2612 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2612 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2612 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2612 are further described hereinbelow with reference to Table 1.

[36537] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2612 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[36538] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2613 (VGAM2613) viral gene, which modulates expression of respective host target genes thereof, the func-

tion and utility of which host target genes is known in the art.

[36539] VGAM2613 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2613 was detected is described hereinabove with reference to Figs. 2-8.

[36540] VGAM2613 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine rhinitis A virus. VGAM2613 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[36541] VGAM2613 gene, herein designated VGAM GENE, encodes a VGAM2613 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2613 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2613 precursor RNA is designated SEQ ID:2599, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2599 is located at position 5479 relative to the genome of Equine rhinitis A virus.

[36542] VGAM2613 precursor RNA, herein designated VGAM PRE-

CURSOR RNA, folds onto itself, forming VGAM2613 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36543] An enzyme complex designated DICER COMPLEX, dices the VGAM2613 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2613 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 75%) nucleotide sequence of VGAM2613 RNA is designated SEQ ID:5324, and is provided hereinbelow with reference to the sequence listing part.

[36544] VGAM2613 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM2613 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2613 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36545] VGAM2613 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2613 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2613 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2613 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2613 host

target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36546] The complementary binding of VGAM2613 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2613 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2613 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2613 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[36547] It is appreciated that VGAM2613 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2613 host target genes. The mRNA of each one of this plurality of VGAM2613 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2613 RNA, herein designated VGAM RNA, and which when bound by VGAM2613 RNA, herein

designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2613 host target proteins.

[36548] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2613 gene, herein designated VGAM GENE, on one or more VGAM2613 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36549] It is yet further appreciated that a function of VGAM2613 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2613 include diagnosis, prevention and

treatment of viral infection by Equine rhinitis A virus. Specific functions, and accordingly utilities, of VGAM2613 correlate with, and may be deduced from, the identity of the host target genes which VGAM2613 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[36550] Nucleotide sequences of the VGAM2613 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2613 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2613 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2613 are further described hereinbelow with reference to Table 1.

[36551] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2613 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[36552] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2614 (VGAM2614) viral gene, which modulates ex-

pression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[36553] VGAM2614 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2614 was detected is described hereinabove with reference to Figs. 2-8.

[36554] VGAM2614 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine rhinitis B virus. VGAM2614 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[36555] VGAM2614 gene, herein designated VGAM GENE, encodes a VGAM2614 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2614 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2614 precursor RNA is designated SEQ ID:2600, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2600 is located at position 6330 relative to the genome of Equine rhinitis B virus.

[36556] VGAM2614 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2614 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36557] An enzyme complex designated DICER COMPLEX, dices the VGAM2614 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2614 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2614 RNA is designated SEQ ID:5325, and is provided hereinbelow with reference to the sequence listing part.

[36558] VGAM2614 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2614 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2614 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36559] VGAM2614 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2614 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2614 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2614 RNA, herein designated VGAM RNA, may have a different number of host target

binding sites in untranslated regions of a VGAM2614 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36560] The complementary binding of VGAM2614 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2614 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2614 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2614 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[36561] It is appreciated that VGAM2614 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2614 host target genes. The mRNA of each one of this plurality of VGAM2614 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2614 RNA, herein designated VGAM

RNA, and which when bound by VGAM2614 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2614 host target proteins.

[36562] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2614 gene, herein designated VGAM GENE, on one or more VGAM2614 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36563] It is yet further appreciated that a function of VGAM2614 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM2614 include diagnosis, prevention and treatment of viral infection by Equine rhinitis B virus. Specific functions, and accordingly utilities, of VGAM2614 correlate with, and may be deduced from, the identity of the host target genes which VGAM2614 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[36564] Nucleotide sequences of the VGAM2614 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2614 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2614 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2614 are further described hereinbelow with reference to Table 1.

[36565] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2614 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[36566] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Mes-

senger 2615 (VGAM2615) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[36567] VGAM2615 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2615 was detected is described hereinabove with reference to Figs. 2-8.

[36568] VGAM2615 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine rhinitis B virus. VGAM2615 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[36569] VGAM2615 gene, herein designated VGAM GENE, encodes a VGAM2615 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2615 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2615 precursor RNA is designated SEQ ID:2601, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2601 is located at position 2100

relative to the genome of Equine rhinitis B virus.

[36570] VGAM2615 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2615 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36571] An enzyme complex designated DICER COMPLEX, dices the VGAM2615 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2615 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2615 RNA is designated SEQ ID:5326, and is provided hereinbelow with reference to the sequence listing part.

[36572] VGAM2615 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2615 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2615 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36573] VGAM2615 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2615 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2615 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2615 RNA, herein designated

VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2615 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36574] The complementary binding of VGAM2615 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2615 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2615 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2615 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[36575] It is appreciated that VGAM2615 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2615 host target genes. The mRNA of each one of this plurality of VGAM2615 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM2615 RNA, herein designated VGAM RNA, and which when bound by VGAM2615 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2615 host target proteins.

[36576] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2615 gene, herein designated VGAM GENE, on one or more VGAM2615 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36577] It is yet further appreciated that a function of VGAM2615 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2615 include diagnosis, prevention and treatment of viral infection by Equine rhinitis B virus. Specific functions, and accordingly utilities, of VGAM2615 correlate with, and may be deduced from, the identity of the host target genes which VGAM2615 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[36578] Nucleotide sequences of the VGAM2615 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2615 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2615 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2615 are further described hereinbelow with reference to Table 1.

[36579] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2615 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[36580] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present

invention, referred to here as Viral Genomic Address Messenger 2616 (VGAM2616) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[36581] VGAM2616 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2616 was detected is described hereinabove with reference to Figs. 2-8.

[36582] VGAM2616 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine rhinitis B virus. VGAM2616 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[36583] VGAM2616 gene, herein designated VGAM GENE, encodes a VGAM2616 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2616 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2616 precursor RNA is designated SEQ ID:2602, and is provided hereinbelow with reference to the sequence listing part. Nu-

cleotide sequence SEQ ID:2602 is located at position 4799 relative to the genome of Equine rhinitis B virus.

[36584] VGAM2616 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2616 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36585] An enzyme complex designated DICER COMPLEX, dices the VGAM2616 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2616 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2616 RNA is designated SEQ ID:5327, and is provided hereinbelow with reference to the sequence

listing part.

[36586] VGAM2616 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2616 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2616 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36587] VGAM2616 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2616 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2616 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not

meant to be limiting VGAM2616 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2616 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36588] The complementary binding of VGAM2616 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2616 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2616 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2616 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[36589] It is appreciated that VGAM2616 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2616 host target genes. The mRNA of each one of this plurality of VGAM2616 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2616 RNA, herein designated VGAM RNA, and which when bound by VGAM2616 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2616 host target proteins.

[36590] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2616 gene, herein designated VGAM GENE, on one or more VGAM2616 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36591] It is yet further appreciated that a function of VGAM2616

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2616 include diagnosis, prevention and treatment of viral infection by Equine rhinitis B virus. Specific functions, and accordingly utilities, of VGAM2616 correlate with, and may be deduced from, the identity of the host target genes which VGAM2616 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[36592] Nucleotide sequences of the VGAM2616 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2616 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2616 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2616 are further described hereinbelow with reference to Table 1.

[36593] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2616 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[36594] Fig. 1 further provides a conceptual description of another

novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2617 (VGAM2617) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[36595] VGAM2617 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2617 was detected is described hereinabove with reference to Figs. 2-8.

[36596] VGAM2617 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine rhinitis B virus. VGAM2617 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[36597] VGAM2617 gene, herein designated VGAM GENE, encodes a VGAM2617 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2617 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2617 precursor RNA is designated SEQ ID:2603, and is provided here-

inbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2603 is located at position 8196 relative to the genome of Equine rhinitis B virus.

[36598] VGAM2617 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2617 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36599] An enzyme complex designated DICER COMPLEX, dices the VGAM2617 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2617 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2617 RNA is designated SEQ ID:5328, and

is provided hereinbelow with reference to the sequence listing part.

[36600] VGAM2617 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2617 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2617 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36601] VGAM2617 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2617 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2617 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites

shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2617 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2617 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36602] The complementary binding of VGAM2617 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2617 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2617 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2617 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[36603] It is appreciated that VGAM2617 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2617 host target genes. The mRNA of each one of this plurality of VGAM2617 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2617 RNA, herein designated VGAM RNA, and which when bound by VGAM2617 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2617 host target proteins.

[36604] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2617 gene, herein designated VGAM GENE, on one or more VGAM2617 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36605] It is yet further appreciated that a function of VGAM2617 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2617 include diagnosis, prevention and treatment of viral infection by Equine rhinitis B virus. Specific functions, and accordingly utilities, of VGAM2617 correlate with, and may be deduced from, the identity of the host target genes which VGAM2617 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[36606] Nucleotide sequences of the VGAM2617 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2617 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2617 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2617 are further described hereinbelow with reference to Table 1.

[36607] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2617 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[36608] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2618 (VGAM2618) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[36609] VGAM2618 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2618 was detected is described hereinabove with reference to Figs. 2-8.

[36610] VGAM2618 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine rhinitis B virus. VGAM2618 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[36611] VGAM2618 gene, herein designated VGAM GENE, encodes a VGAM2618 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2618 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2618 precur-

sor RNA is designated SEQ ID:2604, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2604 is located at position 6170 relative to the genome of Equine rhinitis B virus.

[36612] VGAM2618 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2618 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36613] An enzyme complex designated DICER COMPLEX, dices the VGAM2618 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2618 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 81%) nucleotide se-

quence of VGAM2618 RNA is designated SEQ ID:5329, and is provided hereinbelow with reference to the sequence listing part.

[36614] VGAM2618 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2618 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2618 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36615] VGAM2618 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2618 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2618 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is ap-

preciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2618 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2618 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36616] The complementary binding of VGAM2618 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2618 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2618 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2618 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[36617] It is appreciated that VGAM2618 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2618 host target genes. The mRNA of

each one of this plurality of VGAM2618 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2618 RNA, herein designated VGAM RNA, and which when bound by VGAM2618 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2618 host target proteins.

[36618] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2618 gene, herein designated VGAM GENE, on one or more VGAM2618 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science

294,779 (2001)).

[36619] It is yet further appreciated that a function of VGAM2618 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2618 include diagnosis, prevention and treatment of viral infection by Equine rhinitis B virus. Specific functions, and accordingly utilities, of VGAM2618 correlate with, and may be deduced from, the identity of the host target genes which VGAM2618 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[36620] Nucleotide sequences of the VGAM2618 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2618 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2618 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2618 are further described hereinbelow with reference to Table 1.

[36621] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2618 RNA, herein designated VGAM RNA, are de-

scribed hereinbelow with reference to Table 2.

[36622] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2619 (VGAM2619) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[36623] VGAM2619 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2619 was detected is described hereinabove with reference to Figs. 2-8.

[36624] VGAM2619 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine rhinitis B virus. VGAM2619 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[36625] VGAM2619 gene, herein designated VGAM GENE, encodes a VGAM2619 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2619 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly

similar to the nucleotide sequence of VGAM2619 precursor RNA is designated SEQ ID:2605, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2605 is located at position 4452 relative to the genome of Equine rhinitis B virus.

[36626] VGAM2619 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2619 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36627] An enzyme complex designated DICER COMPLEX, dices the VGAM2619 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2619 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2619 RNA is designated SEQ ID:5330, and is provided hereinbelow with reference to the sequence listing part.

[36628] VGAM2619 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2619 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2619 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36629] VGAM2619 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2619 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2619 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I,

BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2619 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2619 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36630] The complementary binding of VGAM2619 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2619 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2619 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2619 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[36631] It is appreciated that VGAM2619 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM2619 host target genes. The mRNA of each one of this plurality of VGAM2619 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2619 RNA, herein designated VGAM RNA, and which when bound by VGAM2619 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2619 host target proteins.

[36632] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2619 gene, herein designated VGAM GENE, on one or more VGAM2619 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36633] It is yet further appreciated that a function of VGAM2619 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2619 include diagnosis, prevention and treatment of viral infection by Equine rhinitis B virus. Specific functions, and accordingly utilities, of VGAM2619 correlate with, and may be deduced from, the identity of the host target genes which VGAM2619 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[36634] Nucleotide sequences of the VGAM2619 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2619 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2619 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2619 are further described hereinbelow with reference to Table 1.

[36635] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites

to VGAM2619 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[36636] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2620 (VGAM2620) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[36637] VGAM2620 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2620 was detected is described hereinabove with reference to Figs. 2-8.

[36638] VGAM2620 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Porcine enterovirus A (PEV8). VGAM2620 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[36639] VGAM2620 gene, herein designated VGAM GENE, encodes a VGAM2620 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2620 precursor RNA, herein designated VGAM PRECURSOR RNA, does not en-

code a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2620 precursor RNA is designated SEQ ID:2606, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2606 is located at position 2601 relative to the genome of Porcine enterovirus A (PEV8).

[36640] VGAM2620 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2620 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36641] An enzyme complex designated DICER COMPLEX, dices the VGAM2620 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2620 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 76%) nucleotide sequence of VGAM2620 RNA is designated SEQ ID:5331, and is provided hereinbelow with reference to the sequence listing part.

[36642] VGAM2620 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2620 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2620 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36643] VGAM2620 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2620 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2620 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3

such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2620 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2620 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36644] The complementary binding of VGAM2620 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2620 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2620 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2620 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[36645] It is appreciated that VGAM2620 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2620 host target genes. The mRNA of each one of this plurality of VGAM2620 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2620 RNA, herein designated VGAM RNA, and which when bound by VGAM2620 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2620 host target proteins.

[36646] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2620 gene, herein designated VGAM GENE, on one or more VGAM2620 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36647] It is yet further appreciated that a function of VGAM2620 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2620 include diagnosis, prevention and treatment of viral infection by Porcine enterovirus A (PEV8). Specific functions, and accordingly utilities, of VGAM2620 correlate with, and may be deduced from, the identity of the host target genes which VGAM2620 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[36648] Nucleotide sequences of the VGAM2620 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2620 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2620 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2620 are further described hereinbelow with reference to Table 1.

[36649] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the

complementarity of each of these host target binding sites to VGAM2620 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[36650] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2621 (VGAM2621) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[36651] VGAM2621 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2621 was detected is described hereinabove with reference to Figs. 2-8.

[36652] VGAM2621 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Porcine enterovirus A (PEV8). VGAM2621 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[36653] VGAM2621 gene, herein designated VGAM GENE, encodes a VGAM2621 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2621 precursor RNA,

herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2621 precursor RNA is designated SEQ ID:2607, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2607 is located at position 6168 relative to the genome of Porcine enterovirus A (PEV8).

[36654] VGAM2621 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2621 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36655] An enzyme complex designated DICER COMPLEX, dices the VGAM2621 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2621 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2621 RNA is designated SEQ ID:5332, and is provided hereinbelow with reference to the sequence listing part.

[36656] VGAM2621 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2621 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2621 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36657] VGAM2621 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2621 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2621 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host

target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2621 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2621 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36658] The complementary binding of VGAM2621 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2621 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2621 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2621 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[36659] It is appreciated that VGAM2621 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2621 host target genes. The mRNA of each one of this plurality of VGAM2621 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2621 RNA, herein designated VGAM RNA, and which when bound by VGAM2621 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2621 host target proteins.

[36660] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2621 gene, herein designated VGAM GENE, on one or more VGAM2621 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36661] It is yet further appreciated that a function of VGAM2621 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2621 include diagnosis, prevention and treatment of viral infection by Porcine enterovirus A (PEV8). Specific functions, and accordingly utilities, of VGAM2621 correlate with, and may be deduced from, the identity of the host target genes which VGAM2621 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[36662] Nucleotide sequences of the VGAM2621 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2621 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2621 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2621 are further described hereinbelow with reference to Table 1.

[36663] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2621 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[36664] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2622 (VGAM2622) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[36665] VGAM2622 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2622 was detected is described hereinabove with reference to Figs. 2-8.

[36666] VGAM2622 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Porcine enterovirus A (PEV8). VGAM2622 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[36667] VGAM2622 gene, herein designated VGAM GENE, encodes a VGAM2622 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and un-

like most ordinary genes, VGAM2622 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2622 precursor RNA is designated SEQ ID:2608, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2608 is located at position 3608 relative to the genome of Porcine enterovirus A (PEV8).

[36668] VGAM2622 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2622 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36669] An enzyme complex designated DICER COMPLEX, dices the VGAM2622 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2622 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2622 RNA is designated SEQ ID:5333, and is provided hereinbelow with reference to the sequence listing part.

[36670] VGAM2622 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2622 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2622 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36671] VGAM2622 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2622 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2622 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed

sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2622 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2622 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36672] The complementary binding of VGAM2622 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2622 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2622 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2622 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target

protein is therefore outlined by a broken line.

[36673] It is appreciated that VGAM2622 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2622 host target genes. The mRNA of each one of this plurality of VGAM2622 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2622 RNA, herein designated VGAM RNA, and which when bound by VGAM2622 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2622 host target proteins.

[36674] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2622 gene, herein designated VGAM GENE, on one or more VGAM2622 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36675] It is yet further appreciated that a function of VGAM2622 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2622 include diagnosis, prevention and treatment of viral infection by Porcine enterovirus A (PEV8). Specific functions, and accordingly utilities, of VGAM2622 correlate with, and may be deduced from, the identity of the host target genes which VGAM2622 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[36676] Nucleotide sequences of the VGAM2622 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2622 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2622 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2622 are further described hereinbelow with reference to Table 1.

[36677] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2622 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[36678] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2623 (VGAM2623) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[36679] VGAM2623 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2623 was detected is described hereinabove with reference to Figs. 2-8.

[36680] VGAM2623 gene, herein designated VGAM GENE, is a viral gene contained in the genome of A-2 plaque virus. VGAM2623 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[36681] VGAM2623 gene, herein designated VGAM GENE, encodes a VGAM2623 precursor RNA, herein designated VGAM

PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2623 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2623 precursor RNA is designated SEQ ID:2609, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2609 is located at position 4786 relative to the genome of A-2 plaque virus.

[36682] VGAM2623 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2623 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36683] An enzyme complex designated DICER COMPLEX, dices the VGAM2623 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2623 RNA, herein designated VGAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 56%) nucleotide sequence of VGAM2623 RNA is designated SEQ ID:5334, and is provided hereinbelow with reference to the sequence listing part.

[36684] VGAM2623 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2623 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2623 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36685] VGAM2623 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2623 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2623 RNA, herein designated

VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2623 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2623 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36686] The complementary binding of VGAM2623 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2623 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2623 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2623 host target protein, herein desig-

nated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[36687] It is appreciated that VGAM2623 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2623 host target genes. The mRNA of each one of this plurality of VGAM2623 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2623 RNA, herein designated VGAM RNA, and which when bound by VGAM2623 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2623 host target proteins.

[36688] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2623 gene, herein designated VGAM GENE, on one or more VGAM2623 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36689] It is yet further appreciated that a function of VGAM2623 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2623 include diagnosis, prevention and treatment of viral infection by A-2 plaque virus. Specific functions, and accordingly utilities, of VGAM2623 correlate with, and may be deduced from, the identity of the host target genes which VGAM2623 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[36690] Nucleotide sequences of the VGAM2623 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2623 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2623 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2623 are further described hereinbelow with reference to Table 1.

[36691] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2623 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[36692] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2624 (VGAM2624) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[36693] VGAM2624 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2624 was detected is described hereinabove with reference to Figs. 2-8.

[36694] VGAM2624 gene, herein designated VGAM GENE, is a viral gene contained in the genome of A-2 plaque virus. VGAM2624 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[36695] VGAM2624 gene, herein designated VGAM GENE, encodes

a VGAM2624 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2624 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2624 precursor RNA is designated SEQ ID:2610, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2610 is located at position 5482 relative to the genome of A-2 plaque virus.

[36696] VGAM2624 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2624 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36697] An enzyme complex designated DICER COMPLEX, dices the VGAM2624 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2624 RNA,

herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2624 RNA is designated SEQ ID:5335, and is provided hereinbelow with reference to the sequence listing part.

[36698] VGAM2624 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2624 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2624 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36699] VGAM2624 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2624 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM2624 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2624 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2624 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36700] The complementary binding of VGAM2624 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2624 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2624 host target RNA, herein designated VGAM HOST TARGET

RNA, into VGAM2624 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[36701] It is appreciated that VGAM2624 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2624 host target genes. The mRNA of each one of this plurality of VGAM2624 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2624 RNA, herein designated VGAM RNA, and which when bound by VGAM2624 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2624 host target proteins.

[36702] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2624 gene, herein designated VGAM GENE, on one or more VGAM2624 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36703] It is yet further appreciated that a function of VGAM2624 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2624 include diagnosis, prevention and treatment of viral infection by A-2 plaque virus. Specific functions, and accordingly utilities, of VGAM2624 correlate with, and may be deduced from, the identity of the host target genes which VGAM2624 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[36704] Nucleotide sequences of the VGAM2624 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2624 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2624 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2624 are further described hereinbelow with reference to Table 1.

[36705] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2624 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[36706] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2625 (VGAM2625) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[36707] VGAM2625 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2625 was detected is described hereinabove with reference to Figs. 2-8.

[36708] VGAM2625 gene, herein designated VGAM GENE, is a viral gene contained in the genome of A-2 plaque virus. VGAM2625 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[36709] VGAM2625 gene, herein designated VGAM GENE, encodes a VGAM2625 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2625 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2625 precur-

sor RNA is designated SEQ ID:2611, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2611 is located at position 6077 relative to the genome of A-2 plaque virus.

[36710] VGAM2625 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2625 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36711] An enzyme complex designated DICER COMPLEX, dices the VGAM2625 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2625 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide se-

quence of VGAM2625 RNA is designated SEQ ID:5336, and is provided hereinbelow with reference to the sequence listing part.

[36712] VGAM2625 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2625 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2625 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36713] VGAM2625 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2625 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2625 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is ap-

preciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2625 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2625 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36714] The complementary binding of VGAM2625 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2625 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2625 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2625 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[36715] It is appreciated that VGAM2625 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2625 host target genes. The mRNA of

each one of this plurality of VGAM2625 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2625 RNA, herein designated VGAM RNA, and which when bound by VGAM2625 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2625 host target proteins.

[36716] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2625 gene, herein designated VGAM GENE, on one or more VGAM2625 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science

294,779 (2001)).

[36717] It is yet further appreciated that a function of VGAM2625 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2625 include diagnosis, prevention and treatment of viral infection by A-2 plaque virus. Specific functions, and accordingly utilities, of VGAM2625 correlate with, and may be deduced from, the identity of the host target genes which VGAM2625 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[36718] Nucleotide sequences of the VGAM2625 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2625 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2625 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2625 are further described hereinbelow with reference to Table 1.

[36719] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2625 RNA, herein designated VGAM RNA, are de-

scribed hereinbelow with reference to Table 2.

[36720] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2626 (VGAM2626) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[36721] VGAM2626 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2626 was detected is described hereinabove with reference to Figs. 2-8.

[36722] VGAM2626 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Avian encephalomyelitis virus. VGAM2626 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[36723] VGAM2626 gene, herein designated VGAM GENE, encodes a VGAM2626 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2626 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly

similar to the nucleotide sequence of VGAM2626 precursor RNA is designated SEQ ID:2612, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2612 is located at position 6595 relative to the genome of Avian encephalomyelitis virus.

[36724] VGAM2626 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2626 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36725] An enzyme complex designated DICER COMPLEX, dices the VGAM2626 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2626 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 48%) nucleotide sequence of VGAM2626 RNA is designated SEQ ID:5337, and is provided hereinbelow with reference to the sequence listing part.

[36726] VGAM2626 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2626 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2626 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36727] VGAM2626 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2626 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2626 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I,

BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2626 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2626 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36728] The complementary binding of VGAM2626 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2626 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2626 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2626 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[36729] It is appreciated that VGAM2626 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM2626 host target genes. The mRNA of each one of this plurality of VGAM2626 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2626 RNA, herein designated VGAM RNA, and which when bound by VGAM2626 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2626 host target proteins.

[36730] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2626 gene, herein designated VGAM GENE, on one or more VGAM2626 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36731] It is yet further appreciated that a function of VGAM2626 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2626 include diagnosis, prevention and treatment of viral infection by Avian encephalomyelitis virus. Specific functions, and accordingly utilities, of VGAM2626 correlate with, and may be deduced from, the identity of the host target genes which VGAM2626 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[36732] Nucleotide sequences of the VGAM2626 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2626 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2626 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2626 are further described hereinbelow with reference to Table 1.

[36733] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites

to VGAM2626 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[36734] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2627 (VGAM2627) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[36735] VGAM2627 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2627 was detected is described hereinabove with reference to Figs. 2-8.

[36736] VGAM2627 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Avian encephalomyelitis virus. VGAM2627 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[36737] VGAM2627 gene, herein designated VGAM GENE, encodes a VGAM2627 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2627 precursor RNA, herein designated VGAM PRECURSOR RNA, does not en-

code a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2627 precursor RNA is designated SEQ ID:2613, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2613 is located at position 5436 relative to the genome of Avian encephalomyelitis virus.

[36738] VGAM2627 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2627 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36739] An enzyme complex designated DICER COMPLEX, dices the VGAM2627 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2627 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of VGAM2627 RNA is designated SEQ ID:5338, and is provided hereinbelow with reference to the sequence listing part.

[36740] VGAM2627 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2627 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2627 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36741] VGAM2627 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2627 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2627 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3

such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2627 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2627 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36742] The complementary binding of VGAM2627 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2627 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2627 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2627 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[36743] It is appreciated that VGAM2627 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2627 host target genes. The mRNA of each one of this plurality of VGAM2627 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2627 RNA, herein designated VGAM RNA, and which when bound by VGAM2627 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2627 host target proteins.

[36744] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2627 gene, herein designated VGAM GENE, on one or more VGAM2627 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36745] It is yet further appreciated that a function of VGAM2627 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2627 include diagnosis, prevention and treatment of viral infection by Avian encephalomyelitis virus. Specific functions, and accordingly utilities, of VGAM2627 correlate with, and may be deduced from, the identity of the host target genes which VGAM2627 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[36746] Nucleotide sequences of the VGAM2627 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2627 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2627 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2627 are further described hereinbelow with reference to Table 1.

[36747] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the

complementarity of each of these host target binding sites to VGAM2627 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[36748] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2628 (VGAM2628) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[36749] VGAM2628 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2628 was detected is described hereinabove with reference to Figs. 2-8.

[36750] VGAM2628 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Avian encephalomyelitis virus. VGAM2628 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[36751] VGAM2628 gene, herein designated VGAM GENE, encodes a VGAM2628 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2628 precursor RNA,

herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2628 precursor RNA is designated SEQ ID:2614, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2614 is located at position 4961 relative to the genome of Avian encephalomyelitis virus.

[36752] VGAM2628 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2628 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36753] An enzyme complex designated DICER COMPLEX, dices the VGAM2628 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2628 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2628 RNA is designated SEQ ID:5339, and is provided hereinbelow with reference to the sequence listing part.

[36754] VGAM2628 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2628 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2628 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36755] VGAM2628 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2628 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2628 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host

target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2628 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2628 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36756] The complementary binding of VGAM2628 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2628 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2628 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2628 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[36757] It is appreciated that VGAM2628 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2628 host target genes. The mRNA of each one of this plurality of VGAM2628 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2628 RNA, herein designated VGAM RNA, and which when bound by VGAM2628 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2628 host target proteins.

[36758] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2628 gene, herein designated VGAM GENE, on one or more VGAM2628 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36759] It is yet further appreciated that a function of VGAM2628 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2628 include diagnosis, prevention and treatment of viral infection by Avian encephalomyelitis virus. Specific functions, and accordingly utilities, of VGAM2628 correlate with, and may be deduced from, the identity of the host target genes which VGAM2628 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[36760] Nucleotide sequences of the VGAM2628 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2628 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2628 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2628 are further described hereinbelow with reference to Table 1.

[36761] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2628 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[36762] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2629 (VGAM2629) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[36763] VGAM2629 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2629 was detected is described hereinabove with reference to Figs. 2-8.

[36764] VGAM2629 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Avian encephalomyelitis virus. VGAM2629 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[36765] VGAM2629 gene, herein designated VGAM GENE, encodes a VGAM2629 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and un-

like most ordinary genes, VGAM2629 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2629 precursor RNA is designated SEQ ID:2615, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2615 is located at position 2698 relative to the genome of Avian encephalomyelitis virus.

[36766] VGAM2629 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2629 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36767] An enzyme complex designated DICER COMPLEX, dices the VGAM2629 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2629 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2629 RNA is designated SEQ ID:5340, and is provided hereinbelow with reference to the sequence listing part.

[36768] VGAM2629 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2629 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2629 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36769] VGAM2629 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2629 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2629 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed

sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2629 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2629 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36770] The complementary binding of VGAM2629 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2629 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2629 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2629 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target

protein is therefore outlined by a broken line.

[36771] It is appreciated that VGAM2629 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2629 host target genes. The mRNA of each one of this plurality of VGAM2629 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2629 RNA, herein designated VGAM RNA, and which when bound by VGAM2629 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2629 host target proteins.

[36772] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2629 gene, herein designated VGAM GENE, on one or more VGAM2629 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36773] It is yet further appreciated that a function of VGAM2629 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2629 include diagnosis, prevention and treatment of viral infection by Avian encephalomyelitis virus. Specific functions, and accordingly utilities, of VGAM2629 correlate with, and may be deduced from, the identity of the host target genes which VGAM2629 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[36774] Nucleotide sequences of the VGAM2629 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2629 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2629 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2629 are further described hereinbelow with reference to Table 1.

[36775] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2629 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[36776] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2630 (VGAM2630) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[36777] VGAM2630 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2630 was detected is described hereinabove with reference to Figs. 2-8.

[36778] VGAM2630 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Tamana bat virus. VGAM2630 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[36779] VGAM2630 gene, herein designated VGAM GENE, encodes a VGAM2630 precursor RNA, herein designated VGAM

PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2630 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2630 precursor RNA is designated SEQ ID:2616, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2616 is located at position 2276 relative to the genome of Tamana bat virus.

[36780] VGAM2630 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2630 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36781] An enzyme complex designated DICER COMPLEX, dices the VGAM2630 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2630 RNA, herein designated VGAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 83%) nucleotide sequence of VGAM2630 RNA is designated SEQ ID:5341, and is provided hereinbelow with reference to the sequence listing part.

[36782] VGAM2630 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2630 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2630 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36783] VGAM2630 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2630 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2630 RNA, herein designated

VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2630 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2630 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36784] The complementary binding of VGAM2630 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2630 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2630 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2630 host target protein, herein desig-

nated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[36785] It is appreciated that VGAM2630 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2630 host target genes. The mRNA of each one of this plurality of VGAM2630 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2630 RNA, herein designated VGAM RNA, and which when bound by VGAM2630 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2630 host target proteins.

[36786] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2630 gene, herein designated VGAM GENE, on one or more VGAM2630 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36787] It is yet further appreciated that a function of VGAM2630 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2630 include diagnosis, prevention and treatment of viral infection by Tamana bat virus. Specific functions, and accordingly utilities, of VGAM2630 correlate with, and may be deduced from, the identity of the host target genes which VGAM2630 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[36788] Nucleotide sequences of the VGAM2630 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2630 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2630 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2630 are further described hereinbelow with reference to Table 1.

[36789] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2630 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[36790] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2631 (VGAM2631) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[36791] VGAM2631 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2631 was detected is described hereinabove with reference to Figs. 2-8.

[36792] VGAM2631 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Tamana bat virus. VGAM2631 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[36793] VGAM2631 gene, herein designated VGAM GENE, encodes

a VGAM2631 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2631 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2631 precursor RNA is designated SEQ ID:2617, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2617 is located at position 9727 relative to the genome of Tamana bat virus.

[36794] VGAM2631 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2631 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36795] An enzyme complex designated DICER COMPLEX, dices the VGAM2631 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2631 RNA,

herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 84%) nucleotide sequence of VGAM2631 RNA is designated SEQ ID:5342, and is provided hereinbelow with reference to the sequence listing part.

[36796] VGAM2631 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2631 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2631 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36797] VGAM2631 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2631 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM2631 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2631 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2631 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36798] The complementary binding of VGAM2631 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2631 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2631 host target RNA, herein designated VGAM HOST TARGET

RNA, into VGAM2631 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[36799] It is appreciated that VGAM2631 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2631 host target genes. The mRNA of each one of this plurality of VGAM2631 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2631 RNA, herein designated VGAM RNA, and which when bound by VGAM2631 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2631 host target proteins.

[36800] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2631 gene, herein designated VGAM GENE, on one or more VGAM2631 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36801] It is yet further appreciated that a function of VGAM2631 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2631 include diagnosis, prevention and treatment of viral infection by Tamana bat virus. Specific functions, and accordingly utilities, of VGAM2631 correlate with, and may be deduced from, the identity of the host target genes which VGAM2631 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[36802] Nucleotide sequences of the VGAM2631 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2631 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2631 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2631 are further

described hereinbelow with reference to Table 1.

[36803] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2631 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[36804] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2632 (VGAM2632) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[36805] VGAM2632 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2632 was detected is described hereinabove with reference to Figs. 2-8.

[36806] VGAM2632 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Tamana bat virus. VGAM2632 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[36807] VGAM2632 gene, herein designated VGAM GENE, encodes a VGAM2632 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2632 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2632 precursor RNA is designated SEQ ID:2618, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2618 is located at position 1113 relative to the genome of Tamana bat virus.

[36808] VGAM2632 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2632 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36809] An enzyme complex designated DICER COMPLEX, dices the VGAM2632 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, into VGAM2632 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2632 RNA is designated SEQ ID:5343, and is provided hereinbelow with reference to the sequence listing part.

[36810] VGAM2632 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2632 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2632 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36811] VGAM2632 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2632 host target RNA, herein designated VGAM HOST TARGET RNA. This

complementary binding is due to the fact that the nucleotide sequence of VGAM2632 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2632 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2632 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36812] The complementary binding of VGAM2632 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2632 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2632

host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2632 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[36813] It is appreciated that VGAM2632 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2632 host target genes. The mRNA of each one of this plurality of VGAM2632 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2632 RNA, herein designated VGAM RNA, and which when bound by VGAM2632 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2632 host target proteins.

[36814] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2632 gene, herein designated VGAM GENE, on one or more VGAM2632 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36815] It is yet further appreciated that a function of VGAM2632 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2632 include diagnosis, prevention and treatment of viral infection by Tamana bat virus. Specific functions, and accordingly utilities, of VGAM2632 correlate with, and may be deduced from, the identity of the host target genes which VGAM2632 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[36816] Nucleotide sequences of the VGAM2632 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2632 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2632 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM2632 are further described hereinbelow with reference to Table 1.

[36817] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2632 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[36818] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2633 (VGAM2633) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[36819] VGAM2633 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2633 was detected is described hereinabove with reference to Figs. 2-8.

[36820] VGAM2633 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Tamana bat virus. VGAM2633 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the

human genome.

[36821] VGAM2633 gene, herein designated VGAM GENE, encodes a VGAM2633 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2633 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2633 precursor RNA is designated SEQ ID:2619, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2619 is located at position 3876 relative to the genome of Tamana bat virus.

[36822] VGAM2633 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2633 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36823] An enzyme complex designated DICER COMPLEX, dices

the VGAM2633 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2633 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2633 RNA is designated SEQ ID:5344, and is provided hereinbelow with reference to the sequence listing part.

[36824] VGAM2633 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2633 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2633 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36825] VGAM2633 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2633 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2633 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2633 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2633 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36826] The complementary binding of VGAM2633 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2633 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM2633 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2633 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[36827] It is appreciated that VGAM2633 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2633 host target genes. The mRNA of each one of this plurality of VGAM2633 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2633 RNA, herein designated VGAM RNA, and which when bound by VGAM2633 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2633 host target proteins.

[36828] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2633 gene, herein designated VGAM GENE, on one or more VGAM2633 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36829] It is yet further appreciated that a function of VGAM2633 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2633 include diagnosis, prevention and treatment of viral infection by Tamana bat virus. Specific functions, and accordingly utilities, of VGAM2633 correlate with, and may be deduced from, the identity of the host target genes which VGAM2633 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[36830] Nucleotide sequences of the VGAM2633 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2633 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of

VGAM2633 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2633 are further described hereinbelow with reference to Table 1.

[36831] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2633 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[36832] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2634 (VGAM2634) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[36833] VGAM2634 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2634 was detected is described hereinabove with reference to Figs. 2-8.

[36834] VGAM2634 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Tamana bat virus. VGAM2634 host target gene, herein designated VGAM

HOST TARGET GENE, is a human gene contained in the human genome.

[36835] VGAM2634 gene, herein designated VGAM GENE, encodes a VGAM2634 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2634 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2634 precursor RNA is designated SEQ ID:2620, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2620 is located at position 3523 relative to the genome of Tamana bat virus.

[36836] VGAM2634 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2634 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36837] An enzyme complex designated DICER COMPLEX, dices the VGAM2634 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2634 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2634 RNA is designated SEQ ID:5345, and is provided hereinbelow with reference to the sequence listing part.

[36838] VGAM2634 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2634 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2634 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36839] VGAM2634 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites

located in untranslated regions of VGAM2634 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2634 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2634 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2634 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36840] The complementary binding of VGAM2634 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2634 host target RNA, herein designated VGAM

HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2634 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2634 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[36841] It is appreciated that VGAM2634 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2634 host target genes. The mRNA of each one of this plurality of VGAM2634 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2634 RNA, herein designated VGAM RNA, and which when bound by VGAM2634 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2634 host target proteins.

[36842] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2634 gene, herein designated VGAM GENE, on one or more VGAM2634 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove

with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36843] It is yet further appreciated that a function of VGAM2634 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2634 include diagnosis, prevention and treatment of viral infection by Tamana bat virus. Specific functions, and accordingly utilities, of VGAM2634 correlate with, and may be deduced from, the identity of the host target genes which VGAM2634 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[36844] Nucleotide sequences of the VGAM2634 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2634 RNA, herein designated VGAM RNA, and

a schematic representation of the secondary folding of VGAM2634 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2634 are further described hereinbelow with reference to Table 1.

[36845] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2634 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[36846] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2635 (VGAM2635) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[36847] VGAM2635 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2635 was detected is described hereinabove with reference to Figs. 2-8.

[36848] VGAM2635 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Tamana bat virus.

VGAM2635 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[36849] VGAM2635 gene, herein designated VGAM GENE, encodes a VGAM2635 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2635 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2635 precursor RNA is designated SEQ ID:2621, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2621 is located at position 2105 relative to the genome of Tamana bat virus.

[36850] VGAM2635 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2635 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[36851] An enzyme complex designated DICER COMPLEX, dices the VGAM2635 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2635 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2635 RNA is designated SEQ ID:5346, and is provided hereinbelow with reference to the sequence listing part.

[36852] VGAM2635 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2635 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2635 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36853] VGAM2635 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM2635 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2635 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2635 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2635 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36854] The complementary binding of VGAM2635 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM2635 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2635 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2635 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[36855] It is appreciated that VGAM2635 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2635 host target genes. The mRNA of each one of this plurality of VGAM2635 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2635 RNA, herein designated VGAM RNA, and which when bound by VGAM2635 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2635 host target proteins.

[36856] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2635 gene, herein designated VGAM GENE, on one or more VGAM2635 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36857] It is yet further appreciated that a function of VGAM2635 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2635 include diagnosis, prevention and treatment of viral infection by Tamana bat virus. Specific functions, and accordingly utilities, of VGAM2635 correlate with, and may be deduced from, the identity of the host target genes which VGAM2635 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[36858] Nucleotide sequences of the VGAM2635 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

diced VGAM2635 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2635 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2635 are further described hereinbelow with reference to Table 1.

[36859] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2635 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[36860] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2636 (VGAM2636) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[36861] VGAM2636 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2636 was detected is described hereinabove with reference to Figs. 2-8.

[36862] VGAM2636 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of sheeppox virus. VGAM2636 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[36863] VGAM2636 gene, herein designated VGAM GENE, encodes a VGAM2636 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2636 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2636 precursor RNA is designated SEQ ID:2622, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2622 is located at position 25048 relative to the genome of sheeppox virus.

[36864] VGAM2636 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2636 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36865] An enzyme complex designated DICER COMPLEX, dices the VGAM2636 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2636 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2636 RNA is designated SEQ ID:5347, and is provided hereinbelow with reference to the sequence listing part.

[36866] VGAM2636 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2636 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2636 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36867] VGAM2636 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2636 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2636 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2636 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2636 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36868] The complementary binding of VGAM2636 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM2636 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2636 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2636 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[36869] It is appreciated that VGAM2636 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2636 host target genes. The mRNA of each one of this plurality of VGAM2636 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2636 RNA, herein designated VGAM RNA, and which when bound by VGAM2636 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2636 host target proteins.

[36870] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2636 gene, herein designated VGAM GENE, on one or more VGAM2636 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36871] It is yet further appreciated that a function of VGAM2636 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2636 include diagnosis, prevention and treatment of viral infection by sheeppox virus. Specific functions, and accordingly utilities, of VGAM2636 correlate with, and may be deduced from, the identity of the host target genes which VGAM2636 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[36872] Nucleotide sequences of the VGAM2636 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the diced VGAM2636 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2636 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2636 are further described hereinbelow with reference to Table 1.

[36873] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2636 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[36874] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2637 (VGAM2637) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[36875] VGAM2637 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2637 was detected is described hereinabove with reference to Figs. 2-8.

[36876] VGAM2637 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox virus. VGAM2637 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[36877] VGAM2637 gene, herein designated VGAM GENE, encodes a VGAM2637 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2637 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2637 precursor RNA is designated SEQ ID:2623, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2623 is located at position 24739 relative to the genome of Goatpox virus.

[36878] VGAM2637 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2637 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36879] An enzyme complex designated DICER COMPLEX, dices the VGAM2637 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2637 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 70%) nucleotide sequence of VGAM2637 RNA is designated SEQ ID:5348, and is provided hereinbelow with reference to the sequence listing part.

[36880] VGAM2637 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2637 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2637 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN COD-

ING and 3UTR respectively.

[36881] VGAM2637 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2637 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2637 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2637 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2637 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36882] The complementary binding of VGAM2637 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2637 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2637 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2637 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[36883] It is appreciated that VGAM2637 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2637 host target genes. The mRNA of each one of this plurality of VGAM2637 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2637 RNA, herein designated VGAM RNA, and which when bound by VGAM2637 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2637 host target proteins.

[36884] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2637 gene, herein designated VGAM GENE, on one

or more VGAM2637 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36885] It is yet further appreciated that a function of VGAM2637 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2637 include diagnosis, prevention and treatment of viral infection by Goatpox virus. Specific functions, and accordingly utilities, of VGAM2637 correlate with, and may be deduced from, the identity of the host target genes which VGAM2637 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[36886] Nucleotide sequences of the VGAM2637 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2637 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2637 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2637 are further described hereinbelow with reference to Table 1.

[36887] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2637 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[36888] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2638 (VGAM2638) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[36889] VGAM2638 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2638 was detected is de-

scribed hereinabove with reference to Figs. 2-8.

[36890] VGAM2638 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Foot-and-mouth disease virus O. VGAM2638 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[36891] VGAM2638 gene, herein designated VGAM GENE, encodes a VGAM2638 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2638 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2638 precursor RNA is designated SEQ ID:2624, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2624 is located at position 3143 relative to the genome of Foot-and-mouth disease virus O.

[36892] VGAM2638 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2638 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36893] An enzyme complex designated DICER COMPLEX, dices the VGAM2638 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2638 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 53%) nucleotide sequence of VGAM2638 RNA is designated SEQ ID:5349, and is provided hereinbelow with reference to the sequence listing part.

[36894] VGAM2638 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2638 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2638 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding

gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36895] VGAM2638 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2638 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2638 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2638 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2638 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be lo-

cated in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36896] The complementary binding of VGAM2638 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2638 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2638 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2638 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[36897] It is appreciated that VGAM2638 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2638 host target genes. The mRNA of each one of this plurality of VGAM2638 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2638 RNA, herein designated VGAM RNA, and which when bound by VGAM2638 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2638 host target proteins.

[36898] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM2638 gene, herein designated VGAM GENE, on one or more VGAM2638 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36899] It is yet further appreciated that a function of VGAM2638 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2638 include diagnosis, prevention and treatment of viral infection by Foot-and-mouth disease virus O. Specific functions, and accordingly utilities, of VGAM2638 correlate with, and may be deduced from, the identity of the host target genes which VGAM2638 binds

and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[36900] Nucleotide sequences of the VGAM2638 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2638 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2638 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2638 are further described hereinbelow with reference to Table 1.

[36901] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2638 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[36902] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2639 (VGAM2639) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[36903] VGAM2639 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2639 was detected is described hereinabove with reference to Figs. 2-8.

[36904] VGAM2639 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Foot-and-mouth disease virus O. VGAM2639 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[36905] VGAM2639 gene, herein designated VGAM GENE, encodes a VGAM2639 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2639 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2639 precursor RNA is designated SEQ ID:2625, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2625 is located at position 2526 relative to the genome of Foot-and-mouth disease virus O.

[36906] VGAM2639 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2639 folded precursor RNA, herein designated VGAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36907] An enzyme complex designated DICER COMPLEX, dices the VGAM2639 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2639 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2639 RNA is designated SEQ ID:5350, and is provided hereinbelow with reference to the sequence listing part.

[36908] VGAM2639 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2639 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2639 host target RNA,

herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36909] VGAM2639 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2639 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2639 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2639 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2639 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host tar-

get binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36910] The complementary binding of VGAM2639 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2639 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2639 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2639 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[36911] It is appreciated that VGAM2639 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2639 host target genes. The mRNA of each one of this plurality of VGAM2639 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2639 RNA, herein designated VGAM RNA, and which when bound by VGAM2639 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2639 host target proteins.

[36912] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2639 gene, herein designated VGAM GENE, on one or more VGAM2639 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36913] It is yet further appreciated that a function of VGAM2639 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2639 include diagnosis, prevention and treatment of viral infection by Foot-and-mouth disease virus O. Specific functions, and accordingly utilities, of

VGAM2639 correlate with, and may be deduced from, the identity of the host target genes which VGAM2639 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[36914] Nucleotide sequences of the VGAM2639 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2639 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2639 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2639 are further described hereinbelow with reference to Table 1.

[36915] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2639 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[36916] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2640 (VGAM2640) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the

art.

[36917] VGAM2640 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2640 was detected is described hereinabove with reference to Figs. 2-8.

[36918] VGAM2640 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Foot-and-mouth disease virus O. VGAM2640 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[36919] VGAM2640 gene, herein designated VGAM GENE, encodes a VGAM2640 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2640 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2640 precursor RNA is designated SEQ ID:2626, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2626 is located at position 4136 relative to the genome of Foot-and-mouth disease virus O.

[36920] VGAM2640 precursor RNA, herein designated VGAM PRE-

CURSOR RNA, folds onto itself, forming VGAM2640 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36921] An enzyme complex designated DICER COMPLEX, dices the VGAM2640 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2640 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 54%) nucleotide sequence of VGAM2640 RNA is designated SEQ ID:5351, and is provided hereinbelow with reference to the sequence listing part.

[36922] VGAM2640 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM2640 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2640 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36923] VGAM2640 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2640 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2640 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2640 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2640 host

target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36924] The complementary binding of VGAM2640 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2640 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2640 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2640 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[36925] It is appreciated that VGAM2640 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2640 host target genes. The mRNA of each one of this plurality of VGAM2640 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2640 RNA, herein designated VGAM RNA, and which when bound by VGAM2640 RNA, herein

designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2640 host target proteins.

[36926] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2640 gene, herein designated VGAM GENE, on one or more VGAM2640 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36927] It is yet further appreciated that a function of VGAM2640 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2640 include diagnosis, prevention and

treatment of viral infection by Foot-and-mouth disease virus O. Specific functions, and accordingly utilities, of VGAM2640 correlate with, and may be deduced from, the identity of the host target genes which VGAM2640 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[36928] Nucleotide sequences of the VGAM2640 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2640 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2640 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2640 are further described hereinbelow with reference to Table 1.

[36929] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2640 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[36930] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2641 (VGAM2641) viral gene, which modulates ex-

pression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[36931] VGAM2641 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2641 was detected is described hereinabove with reference to Figs. 2-8.

[36932] VGAM2641 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Foot-and-mouth disease virus O. VGAM2641 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[36933] VGAM2641 gene, herein designated VGAM GENE, encodes a VGAM2641 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2641 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2641 precursor RNA is designated SEQ ID:2627, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2627 is located at position 1368 relative to the genome of Foot-and-mouth disease virus

O.

[36934] VGAM2641 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2641 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36935] An enzyme complex designated DICER COMPLEX, dices the VGAM2641 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2641 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 63%) nucleotide sequence of VGAM2641 RNA is designated SEQ ID:5352, and is provided hereinbelow with reference to the sequence listing part.

[36936] VGAM2641 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2641 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2641 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36937] VGAM2641 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2641 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2641 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2641 RNA, herein designated

VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2641 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36938] The complementary binding of VGAM2641 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2641 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2641 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2641 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[36939] It is appreciated that VGAM2641 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2641 host target genes. The mRNA of each one of this plurality of VGAM2641 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM2641 RNA, herein designated VGAM RNA, and which when bound by VGAM2641 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2641 host target proteins.

[36940] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2641 gene, herein designated VGAM GENE, on one or more VGAM2641 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36941] It is yet further appreciated that a function of VGAM2641 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2641 include diagnosis, prevention and treatment of viral infection by Foot-and-mouth disease virus O. Specific functions, and accordingly utilities, of VGAM2641 correlate with, and may be deduced from, the identity of the host target genes which VGAM2641 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[36942] Nucleotide sequences of the VGAM2641 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2641 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2641 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2641 are further described hereinbelow with reference to Table 1.

[36943] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2641 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[36944] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present

invention, referred to here as Viral Genomic Address Messenger 2642 (VGAM2642) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[36945] VGAM2642 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2642 was detected is described hereinabove with reference to Figs. 2-8.

[36946] VGAM2642 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Foot-and-mouth disease virus O. VGAM2642 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[36947] VGAM2642 gene, herein designated VGAM GENE, encodes a VGAM2642 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2642 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2642 precursor RNA is designated SEQ ID:2628, and is provided hereinbelow with reference to the sequence listing part. Nu-

cleotide sequence SEQ ID:2628 is located at position 1959 relative to the genome of Foot-and-mouth disease virus O.

[36948] VGAM2642 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2642 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36949] An enzyme complex designated DICER COMPLEX, dices the VGAM2642 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2642 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 87%) nucleotide sequence of VGAM2642 RNA is designated SEQ ID:5353, and

is provided hereinbelow with reference to the sequence listing part.

[36950] VGAM2642 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2642 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2642 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36951] VGAM2642 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2642 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2642 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites

shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2642 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2642 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36952] The complementary binding of VGAM2642 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2642 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2642 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2642 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[36953] It is appreciated that VGAM2642 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2642 host target genes. The mRNA of each one of this plurality of VGAM2642 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2642 RNA, herein designated VGAM RNA, and which when bound by VGAM2642 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2642 host target proteins.

[36954] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2642 gene, herein designated VGAM GENE, on one or more VGAM2642 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36955] It is yet further appreciated that a function of VGAM2642 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2642 include diagnosis, prevention and treatment of viral infection by Foot-and-mouth disease virus O. Specific functions, and accordingly utilities, of VGAM2642 correlate with, and may be deduced from, the identity of the host target genes which VGAM2642 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[36956] Nucleotide sequences of the VGAM2642 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2642 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2642 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2642 are further described hereinbelow with reference to Table 1.

[36957] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2642 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[36958] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2643 (VGAM2643) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[36959] VGAM2643 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2643 was detected is described hereinabove with reference to Figs. 2-8.

[36960] VGAM2643 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cowpea aphid-borne mosaic virus. VGAM2643 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[36961] VGAM2643 gene, herein designated VGAM GENE, encodes a VGAM2643 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2643 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2643 precur-

sor RNA is designated SEQ ID:2629, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2629 is located at position 4628 relative to the genome of Cowpea aphid-borne mosaic virus.

[36962] VGAM2643 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2643 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36963] An enzyme complex designated DICER COMPLEX, dices the VGAM2643 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2643 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 53%) nucleotide sequence of VGAM2643 RNA is designated SEQ ID:5354, and is provided hereinbelow with reference to the sequence listing part.

[36964] VGAM2643 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2643 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2643 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36965] VGAM2643 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2643 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2643 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I,

BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2643 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2643 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36966] The complementary binding of VGAM2643 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2643 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2643 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2643 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[36967] It is appreciated that VGAM2643 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM2643 host target genes. The mRNA of each one of this plurality of VGAM2643 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2643 RNA, herein designated VGAM RNA, and which when bound by VGAM2643 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2643 host target proteins.

[36968] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2643 gene, herein designated VGAM GENE, on one or more VGAM2643 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36969] It is yet further appreciated that a function of VGAM2643 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2643 include diagnosis, prevention and treatment of viral infection by Cowpea aphid-borne mosaic virus. Specific functions, and accordingly utilities, of VGAM2643 correlate with, and may be deduced from, the identity of the host target genes which VGAM2643 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[36970] Nucleotide sequences of the VGAM2643 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2643 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2643 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2643 are further described hereinbelow with reference to Table 1.

[36971] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites

to VGAM2643 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[36972] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2644 (VGAM2644) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[36973] VGAM2644 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2644 was detected is described hereinabove with reference to Figs. 2-8.

[36974] VGAM2644 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cowpea aphid-borne mosaic virus. VGAM2644 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[36975] VGAM2644 gene, herein designated VGAM GENE, encodes a VGAM2644 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2644 precursor RNA, herein designated VGAM PRECURSOR RNA, does not en-

code a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2644 precursor RNA is designated SEQ ID:2630, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2630 is located at position 5711 relative to the genome of Cowpea aphid-borne mosaic virus.

[36976] VGAM2644 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2644 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36977] An enzyme complex designated DICER COMPLEX, dices the VGAM2644 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2644 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2644 RNA is designated SEQ ID:5355, and is provided hereinbelow with reference to the sequence listing part.

[36978] VGAM2644 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2644 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2644 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36979] VGAM2644 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2644 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2644 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host

target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2644 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2644 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36980] The complementary binding of VGAM2644 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2644 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2644 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2644 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[36981] It is appreciated that VGAM2644 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2644 host target genes. The mRNA of each one of this plurality of VGAM2644 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2644 RNA, herein designated VGAM RNA, and which when bound by VGAM2644 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2644 host target proteins.

[36982] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2644 gene, herein designated VGAM GENE, on one or more VGAM2644 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36983] It is yet further appreciated that a function of VGAM2644 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2644 include diagnosis, prevention and treatment of viral infection by Cowpea aphid-borne mosaic virus. Specific functions, and accordingly utilities, of VGAM2644 correlate with, and may be deduced from, the identity of the host target genes which VGAM2644 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[36984] Nucleotide sequences of the VGAM2644 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2644 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2644 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2644 are further described hereinbelow with reference to Table 1.

[36985] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2644 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[36986] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2645 (VGAM2645) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[36987] VGAM2645 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2645 was detected is described hereinabove with reference to Figs. 2-8.

[36988] VGAM2645 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cowpea aphid-borne mosaic virus. VGAM2645 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[36989] VGAM2645 gene, herein designated VGAM GENE, encodes a VGAM2645 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and un-

like most ordinary genes, VGAM2645 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2645 precursor RNA is designated SEQ ID:2631, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2631 is located at position 2957 relative to the genome of Cowpea aphid-borne mosaic virus.

[36990] VGAM2645 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2645 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36991] An enzyme complex designated DICER COMPLEX, dices the VGAM2645 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2645 RNA, herein designated VGAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of VGAM2645 RNA is designated SEQ ID:5356, and is provided hereinbelow with reference to the sequence listing part.

[36992] VGAM2645 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2645 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2645 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36993] VGAM2645 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2645 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2645 RNA, herein designated

VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2645 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2645 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36994] The complementary binding of VGAM2645 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2645 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2645 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2645 host target protein, herein desig-

nated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[36995] It is appreciated that VGAM2645 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2645 host target genes. The mRNA of each one of this plurality of VGAM2645 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2645 RNA, herein designated VGAM RNA, and which when bound by VGAM2645 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2645 host target proteins.

[36996] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2645 gene, herein designated VGAM GENE, on one or more VGAM2645 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36997] It is yet further appreciated that a function of VGAM2645 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2645 include diagnosis, prevention and treatment of viral infection by Cowpea aphid-borne mosaic virus. Specific functions, and accordingly utilities, of VGAM2645 correlate with, and may be deduced from, the identity of the host target genes which VGAM2645 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[36998] Nucleotide sequences of the VGAM2645 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2645 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2645 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2645 are further described hereinbelow with reference to Table 1.

[36999] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2645 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[37000] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2646 (VGAM2646) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[37001] VGAM2646 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2646 was detected is described hereinabove with reference to Figs. 2-8.

[37002] VGAM2646 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cowpea aphid-borne mosaic virus. VGAM2646 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[37003] VGAM2646 gene, herein designated VGAM GENE, encodes

a VGAM2646 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2646 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2646 precursor RNA is designated SEQ ID:2632, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2632 is located at position 1728 relative to the genome of Cowpea aphid-borne mosaic virus.

[37004] VGAM2646 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2646 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[37005] An enzyme complex designated DICER COMPLEX, dices the VGAM2646 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, into VGAM2646 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 63%) nucleotide sequence of VGAM2646 RNA is designated SEQ ID:5357, and is provided hereinbelow with reference to the sequence listing part.

[37006] VGAM2646 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2646 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2646 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[37007] VGAM2646 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2646 host target RNA, herein designated VGAM HOST TARGET RNA. This

complementary binding is due to the fact that the nucleotide sequence of VGAM2646 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2646 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2646 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[37008] The complementary binding of VGAM2646 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2646 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2646

host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2646 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[37009] It is appreciated that VGAM2646 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2646 host target genes. The mRNA of each one of this plurality of VGAM2646 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2646 RNA, herein designated VGAM RNA, and which when bound by VGAM2646 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2646 host target proteins.

[37010] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2646 gene, herein designated VGAM GENE, on one or more VGAM2646 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[37011] It is yet further appreciated that a function of VGAM2646 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2646 include diagnosis, prevention and treatment of viral infection by Cowpea aphid-borne mosaic virus. Specific functions, and accordingly utilities, of VGAM2646 correlate with, and may be deduced from, the identity of the host target genes which VGAM2646 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[37012] Nucleotide sequences of the VGAM2646 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2646 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2646 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM2646 are further described hereinbelow with reference to Table 1.

[37013] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2646 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[37014] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2647 (VGAM2647) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[37015] VGAM2647 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2647 was detected is described hereinabove with reference to Figs. 2-8.

[37016] VGAM2647 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cowpea aphid-borne mosaic virus. VGAM2647 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene con-

tained in the human genome.

[37017] VGAM2647 gene, herein designated VGAM GENE, encodes a VGAM2647 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2647 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2647 precursor RNA is designated SEQ ID:2633, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2633 is located at position 7881 relative to the genome of Cowpea aphid-borne mosaic virus.

[37018] VGAM2647 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2647 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[37019] An enzyme complex designated DICER COMPLEX, dices the VGAM2647 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2647 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 58%) nucleotide sequence of VGAM2647 RNA is designated SEQ ID:5358, and is provided hereinbelow with reference to the sequence listing part.

[37020] VGAM2647 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2647 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2647 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[37021] VGAM2647 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites

located in untranslated regions of VGAM2647 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2647 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2647 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2647 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[37022] The complementary binding of VGAM2647 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2647 host target RNA, herein designated VGAM

HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2647 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2647 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[37023] It is appreciated that VGAM2647 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2647 host target genes. The mRNA of each one of this plurality of VGAM2647 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2647 RNA, herein designated VGAM RNA, and which when bound by VGAM2647 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2647 host target proteins.

[37024] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2647 gene, herein designated VGAM GENE, on one or more VGAM2647 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove

with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[37025] It is yet further appreciated that a function of VGAM2647 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2647 include diagnosis, prevention and treatment of viral infection by Cowpea aphid-borne mosaic virus. Specific functions, and accordingly utilities, of VGAM2647 correlate with, and may be deduced from, the identity of the host target genes which VGAM2647 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[37026] Nucleotide sequences of the VGAM2647 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2647 RNA, herein designated VGAM RNA, and

a schematic representation of the secondary folding of VGAM2647 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2647 are further described hereinbelow with reference to Table 1.

[37027] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2647 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[37028] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2648 (VGAM2648) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[37029] VGAM2648 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2648 was detected is described hereinabove with reference to Figs. 2-8.

[37030] VGAM2648 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cowpea aphid-borne

mosaic virus. VGAM2648 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[37031] VGAM2648 gene, herein designated VGAM GENE, encodes a VGAM2648 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2648 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2648 precursor RNA is designated SEQ ID:2634, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2634 is located at position 7656 relative to the genome of Cowpea aphid-borne mosaic virus.

[37032] VGAM2648 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2648 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[37033] An enzyme complex designated DICER COMPLEX, dices the VGAM2648 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2648 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of VGAM2648 RNA is designated SEQ ID:5359, and is provided hereinbelow with reference to the sequence listing part.

[37034] VGAM2648 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2648 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2648 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[37035] VGAM2648 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2648 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2648 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2648 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2648 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[37036] The complementary binding of VGAM2648 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM2648 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2648 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2648 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[37037] It is appreciated that VGAM2648 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2648 host target genes. The mRNA of each one of this plurality of VGAM2648 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2648 RNA, herein designated VGAM RNA, and which when bound by VGAM2648 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2648 host target proteins.

[37038] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2648 gene, herein designated VGAM GENE, on one or more VGAM2648 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[37039] It is yet further appreciated that a function of VGAM2648 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2648 include diagnosis, prevention and treatment of viral infection by Cowpea aphid-borne mosaic virus. Specific functions, and accordingly utilities, of VGAM2648 correlate with, and may be deduced from, the identity of the host target genes which VGAM2648 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[37040] Nucleotide sequences of the VGAM2648 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the diced VGAM2648 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2648 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2648 are further described hereinbelow with reference to Table 1.

[37041] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2648 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[37042] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2649 (VGAM2649) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[37043] VGAM2649 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2649 was detected is described hereinabove with reference to Figs. 2-8.

[37044] VGAM2649 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cowpea aphid-borne mosaic virus. VGAM2649 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[37045] VGAM2649 gene, herein designated VGAM GENE, encodes a VGAM2649 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2649 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2649 precursor RNA is designated SEQ ID:2635, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2635 is located at position 2803 relative to the genome of Cowpea aphid-borne mosaic virus.

[37046] VGAM2649 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2649 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[37047] An enzyme complex designated DICER COMPLEX, dices the VGAM2649 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2649 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2649 RNA is designated SEQ ID:5360, and is provided hereinbelow with reference to the sequence listing part.

[37048] VGAM2649 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2649 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2649 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and

a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[37049] VGAM2649 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2649 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2649 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2649 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2649 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both

3UTR and 5UTR regions.

[37050] The complementary binding of VGAM2649 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2649 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2649 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2649 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[37051] It is appreciated that VGAM2649 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2649 host target genes. The mRNA of each one of this plurality of VGAM2649 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2649 RNA, herein designated VGAM RNA, and which when bound by VGAM2649 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2649 host target proteins.

[37052] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM2649 gene, herein designated VGAM GENE, on one or more VGAM2649 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[37053] It is yet further appreciated that a function of VGAM2649 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2649 include diagnosis, prevention and treatment of viral infection by Cowpea aphid-borne mosaic virus. Specific functions, and accordingly utilities, of VGAM2649 correlate with, and may be deduced from, the identity of the host target genes which VGAM2649 binds and inhibits, and the function of these host target genes,

as elaborated hereinbelow.

[37054] Nucleotide sequences of the VGAM2649 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2649 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2649 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2649 are further described hereinbelow with reference to Table 1.

[37055] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2649 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[37056] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2650 (VGAM2650) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[37057] VGAM2650 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene.

The method by which VGAM2650 was detected is described hereinabove with reference to Figs. 2-8.

[37058] VGAM2650 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Trichomonas vaginalis virus 3. VGAM2650 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[37059] VGAM2650 gene, herein designated VGAM GENE, encodes a VGAM2650 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2650 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2650 precursor RNA is designated SEQ ID:2636, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2636 is located at position 2782 relative to the genome of Trichomonas vaginalis virus 3.

[37060] VGAM2650 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2650 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[37061] An enzyme complex designated DICER COMPLEX, dices the VGAM2650 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2650 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2650 RNA is designated SEQ ID:5361, and is provided hereinbelow with reference to the sequence listing part.

[37062] VGAM2650 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2650 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2650 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding

gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[37063] VGAM2650 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2650 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2650 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2650 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2650 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be lo-

cated in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[37064] The complementary binding of VGAM2650 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2650 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2650 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2650 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[37065] It is appreciated that VGAM2650 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2650 host target genes. The mRNA of each one of this plurality of VGAM2650 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2650 RNA, herein designated VGAM RNA, and which when bound by VGAM2650 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2650 host target proteins.

[37066] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM2650 gene, herein designated VGAM GENE, on one or more VGAM2650 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[37067] It is yet further appreciated that a function of VGAM2650 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2650 include diagnosis, prevention and treatment of viral infection by Trichomonas vaginalis virus 3. Specific functions, and accordingly utilities, of VGAM2650 correlate with, and may be deduced from, the identity of the host target genes which VGAM2650 binds

and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[37068] Nucleotide sequences of the VGAM2650 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2650 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2650 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2650 are further described hereinbelow with reference to Table 1.

[37069] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2650 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[37070] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2651 (VGAM2651) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[37071] VGAM2651 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2651 was detected is described hereinabove with reference to Figs. 2-8.

[37072] VGAM2651 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Trichomonas vaginalis virus 3. VGAM2651 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[37073] VGAM2651 gene, herein designated VGAM GENE, encodes a VGAM2651 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2651 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2651 precursor RNA is designated SEQ ID:2637, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2637 is located at position 3926 relative to the genome of Trichomonas vaginalis virus 3.

[37074] VGAM2651 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2651 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[37075] An enzyme complex designated DICER COMPLEX, dices the VGAM2651 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2651 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of VGAM2651 RNA is designated SEQ ID:5362, and is provided hereinbelow with reference to the sequence listing part.

[37076] VGAM2651 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2651 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2651 host target RNA, herein designated VGAM HOST TARGET RNA, comprises

three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[37077] VGAM2651 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2651 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2651 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2651 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2651 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an

example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[37078] The complementary binding of VGAM2651 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2651 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2651 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2651 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[37079] It is appreciated that VGAM2651 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2651 host target genes. The mRNA of each one of this plurality of VGAM2651 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2651 RNA, herein designated VGAM RNA, and which when bound by VGAM2651 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2651 host target proteins.

[37080] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2651 gene, herein designated VGAM GENE, on one or more VGAM2651 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[37081] It is yet further appreciated that a function of VGAM2651 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2651 include diagnosis, prevention and treatment of viral infection by Trichomonas vaginalis virus 3. Specific functions, and accordingly utilities, of VGAM2651 correlate with, and may be deduced from, the

identity of the host target genes which VGAM2651 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[37082] Nucleotide sequences of the VGAM2651 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2651 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2651 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2651 are further described hereinbelow with reference to Table 1.

[37083] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2651 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[37084] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2652 (VGAM2652) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[37085] VGAM2652 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2652 was detected is described hereinabove with reference to Figs. 2-8.

[37086] VGAM2652 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Sorghum mosaic virus. VGAM2652 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[37087] VGAM2652 gene, herein designated VGAM GENE, encodes a VGAM2652 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2652 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2652 precursor RNA is designated SEQ ID:2638, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2638 is located at position 6180 relative to the genome of Sorghum mosaic virus.

[37088] VGAM2652 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2652 folded precursor RNA, herein designated VGAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[37089] An enzyme complex designated DICER COMPLEX, dices the VGAM2652 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2652 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2652 RNA is designated SEQ ID:5363, and is provided hereinbelow with reference to the sequence listing part.

[37090] VGAM2652 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2652 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2652 host target RNA,

herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[37091] VGAM2652 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2652 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2652 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2652 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host tar-

get binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[37092] The complementary binding of VGAM2652 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2652 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2652 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2652 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[37093] It is appreciated that VGAM2652 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2652 host target genes. The mRNA of each one of this plurality of VGAM2652 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2652 RNA, herein designated VGAM RNA, and which when bound by VGAM2652 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2652 host target proteins.

[37094] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2652 gene, herein designated VGAM GENE, on one or more VGAM2652 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[37095] It is yet further appreciated that a function of VGAM2652 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of viral infection by Sorghum mosaic virus. Specific functions, and accordingly utilities, of VGAM2652

correlate with, and may be deduced from, the identity of the host target genes which VGAM2652 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[37096] Nucleotide sequences of the VGAM2652 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2652 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2652 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2652 are further described hereinbelow with reference to Table 1.

[37097] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2652 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[37098] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2653 (VGAM2653) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the

art.

[37099] VGAM2653 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2653 was detected is described hereinabove with reference to Figs. 2-8.

[37100] VGAM2653 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Sorghum mosaic virus. VGAM2653 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[37101] VGAM2653 gene, herein designated VGAM GENE, encodes a VGAM2653 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2653 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2653 precursor RNA is designated SEQ ID:2639, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2639 is located at position 9158 relative to the genome of Sorghum mosaic virus.

[37102] VGAM2653 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2653 folded

precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[37103] An enzyme complex designated DICER COMPLEX, dices the VGAM2653 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2653 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2653 RNA is designated SEQ ID:5364, and is provided hereinbelow with reference to the sequence listing part.

[37104] VGAM2653 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2653 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM2653 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[37105] VGAM2653 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2653 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2653 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2653 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2653 host target RNA, herein designated VGAM HOST TARGET RNA.

It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[37106] The complementary binding of VGAM2653 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2653 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2653 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2653 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[37107] It is appreciated that VGAM2653 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2653 host target genes. The mRNA of each one of this plurality of VGAM2653 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2653 RNA, herein designated VGAM RNA, and which when bound by VGAM2653 RNA, herein designated VGAM RNA, causes inhibition of translation of

respective one or more VGAM2653 host target proteins.

[37108] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2653 gene, herein designated VGAM GENE, on one or more VGAM2653 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[37109] It is yet further appreciated that a function of VGAM2653 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2653 include diagnosis, prevention and treatment of viral infection by Sorghum mosaic virus. Spe-

cific functions, and accordingly utilities, of VGAM2653 correlate with, and may be deduced from, the identity of the host target genes which VGAM2653 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[37110] Nucleotide sequences of the VGAM2653 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2653 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2653 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2653 are further described hereinbelow with reference to Table 1.

[37111] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2653 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[37112] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2654 (VGAM2654) viral gene, which modulates expression of respective host target genes thereof, the func-

tion and utility of which host target genes is known in the art.

[37113] VGAM2654 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2654 was detected is described hereinabove with reference to Figs. 2-8.

[37114] VGAM2654 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Sorghum mosaic virus. VGAM2654 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[37115] VGAM2654 gene, herein designated VGAM GENE, encodes a VGAM2654 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2654 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2654 precursor RNA is designated SEQ ID:2640, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2640 is located at position 2508 relative to the genome of Sorghum mosaic virus.

[37116] VGAM2654 precursor RNA, herein designated VGAM PRE-

CURSOR RNA, folds onto itself, forming VGAM2654 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[37117] An enzyme complex designated DICER COMPLEX, dices the VGAM2654 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2654 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 47%) nucleotide sequence of VGAM2654 RNA is designated SEQ ID:5365, and is provided hereinbelow with reference to the sequence listing part.

[37118] VGAM2654 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM2654 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2654 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[37119] VGAM2654 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2654 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2654 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2654 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2654 host

target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[37120] The complementary binding of VGAM2654 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2654 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2654 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2654 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[37121] It is appreciated that VGAM2654 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2654 host target genes. The mRNA of each one of this plurality of VGAM2654 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2654 RNA, herein designated VGAM RNA, and which when bound by VGAM2654 RNA, herein

designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2654 host target proteins.

[37122] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2654 gene, herein designated VGAM GENE, on one or more VGAM2654 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[37123] It is yet further appreciated that a function of VGAM2654 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2654 include diagnosis, prevention and

treatment of viral infection by Sorghum mosaic virus. Specific functions, and accordingly utilities, of VGAM2654 correlate with, and may be deduced from, the identity of the host target genes which VGAM2654 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[37124] Nucleotide sequences of the VGAM2654 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2654 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2654 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2654 are further described hereinbelow with reference to Table 1.

[37125] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2654 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[37126] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2655 (VGAM2655) viral gene, which modulates ex-

pression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[37127] VGAM2655 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2655 was detected is described hereinabove with reference to Figs. 2-8.

[37128] VGAM2655 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Sorghum mosaic virus. VGAM2655 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[37129] VGAM2655 gene, herein designated VGAM GENE, encodes a VGAM2655 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2655 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2655 precursor RNA is designated SEQ ID:2641, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2641 is located at position 8865 relative to the genome of Sorghum mosaic virus.

[37130] VGAM2655 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2655 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[37131] An enzyme complex designated DICER COMPLEX, dices the VGAM2655 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2655 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 74%) nucleotide sequence of VGAM2655 RNA is designated SEQ ID:5366, and is provided hereinbelow with reference to the sequence listing part.

[37132] VGAM2655 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2655 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2655 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[37133] VGAM2655 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2655 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2655 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2655 RNA, herein designated VGAM RNA, may have a different number of host target

binding sites in untranslated regions of a VGAM2655 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[37134] The complementary binding of VGAM2655 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2655 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2655 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2655 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[37135] It is appreciated that VGAM2655 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2655 host target genes. The mRNA of each one of this plurality of VGAM2655 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2655 RNA, herein designated VGAM

RNA, and which when bound by VGAM2655 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2655 host target proteins.

[37136] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2655 gene, herein designated VGAM GENE, on one or more VGAM2655 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[37137] It is yet further appreciated that a function of VGAM2655 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM2655 include diagnosis, prevention and treatment of viral infection by Sorghum mosaic virus. Specific functions, and accordingly utilities, of VGAM2655 correlate with, and may be deduced from, the identity of the host target genes which VGAM2655 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[37138] Nucleotide sequences of the VGAM2655 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2655 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2655 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2655 are further described hereinbelow with reference to Table 1.

[37139] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2655 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[37140] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Mes-

senger 2656 (VGAM2656) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[37141] VGAM2656 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2656 was detected is described hereinabove with reference to Figs. 2-8.

[37142] VGAM2656 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Potato virus A. VGAM2656 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[37143] VGAM2656 gene, herein designated VGAM GENE, encodes a VGAM2656 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2656 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2656 precursor RNA is designated SEQ ID:2642, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2642 is located at position 5538

relative to the genome of Potato virus A.

[37144] VGAM2656 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2656 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[37145] An enzyme complex designated DICER COMPLEX, dices the VGAM2656 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2656 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2656 RNA is designated SEQ ID:5367, and is provided hereinbelow with reference to the sequence listing part.

[37146] VGAM2656 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2656 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2656 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[37147] VGAM2656 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2656 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2656 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2656 RNA, herein designated

VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2656 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[37148] The complementary binding of VGAM2656 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2656 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2656 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2656 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[37149] It is appreciated that VGAM2656 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2656 host target genes. The mRNA of each one of this plurality of VGAM2656 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM2656 RNA, herein designated VGAM RNA, and which when bound by VGAM2656 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2656 host target proteins.

[37150] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2656 gene, herein designated VGAM GENE, on one or more VGAM2656 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[37151] It is yet further appreciated that a function of VGAM2656 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2656 include diagnosis, prevention and treatment of viral infection by Potato virus A. Specific functions, and accordingly utilities, of VGAM2656 correlate with, and may be deduced from, the identity of the host target genes which VGAM2656 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[37152] Nucleotide sequences of the VGAM2656 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2656 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2656 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2656 are further described hereinbelow with reference to Table 1.

[37153] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2656 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[37154] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present

invention, referred to here as Viral Genomic Address Messenger 2657 (VGAM2657) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[37155] VGAM2657 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2657 was detected is described hereinabove with reference to Figs. 2-8.

[37156] VGAM2657 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Potato virus A. VGAM2657 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[37157] VGAM2657 gene, herein designated VGAM GENE, encodes a VGAM2657 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2657 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2657 precursor RNA is designated SEQ ID:2643, and is provided hereinbelow with reference to the sequence listing part. Nu-

cleotide sequence SEQ ID:2643 is located at position 7993 relative to the genome of Potato virus A.

[37158] VGAM2657 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2657 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[37159] An enzyme complex designated DICER COMPLEX, dices the VGAM2657 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2657 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2657 RNA is designated SEQ ID:5368, and is provided hereinbelow with reference to the sequence

listing part.

[37160] VGAM2657 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2657 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2657 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[37161] VGAM2657 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2657 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2657 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not

meant to be limiting VGAM2657 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2657 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[37162] The complementary binding of VGAM2657 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2657 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2657 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2657 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[37163] It is appreciated that VGAM2657 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2657 host target genes. The mRNA of each one of this plurality of VGAM2657 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2657 RNA, herein designated VGAM RNA, and which when bound by VGAM2657 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2657 host target proteins.

[37164] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2657 gene, herein designated VGAM GENE, on one or more VGAM2657 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[37165] It is yet further appreciated that a function of VGAM2657

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2657 include diagnosis, prevention and treatment of viral infection by Potato virus A. Specific functions, and accordingly utilities, of VGAM2657 correlate with, and may be deduced from, the identity of the host target genes which VGAM2657 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[37166] Nucleotide sequences of the VGAM2657 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2657 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2657 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2657 are further described hereinbelow with reference to Table 1.

[37167] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2657 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[37168] Fig. 1 further provides a conceptual description of another

novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2658 (VGAM2658) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[37169] VGAM2658 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2658 was detected is described hereinabove with reference to Figs. 2-8.

[37170] VGAM2658 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Potato virus A. VGAM2658 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[37171] VGAM2658 gene, herein designated VGAM GENE, encodes a VGAM2658 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2658 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2658 precursor RNA is designated SEQ ID:2644, and is provided here-

inbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2644 is located at position 8772 relative to the genome of Potato virus A.

[37172] VGAM2658 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2658 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[37173] An enzyme complex designated DICER COMPLEX, dices the VGAM2658 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2658 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 55%) nucleotide sequence of VGAM2658 RNA is designated SEQ ID:5369, and

is provided hereinbelow with reference to the sequence listing part.

[37174] VGAM2658 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2658 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2658 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[37175] VGAM2658 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2658 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2658 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites

shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2658 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2658 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[37176] The complementary binding of VGAM2658 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2658 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2658 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2658 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[37177] It is appreciated that VGAM2658 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2658 host target genes. The mRNA of each one of this plurality of VGAM2658 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2658 RNA, herein designated VGAM RNA, and which when bound by VGAM2658 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2658 host target proteins.

[37178] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2658 gene, herein designated VGAM GENE, on one or more VGAM2658 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[37179] It is yet further appreciated that a function of VGAM2658 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2658 include diagnosis, prevention and treatment of viral infection by Potato virus A. Specific functions, and accordingly utilities, of VGAM2658 correlate with, and may be deduced from, the identity of the host target genes which VGAM2658 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[37180] Nucleotide sequences of the VGAM2658 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2658 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2658 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2658 are further described hereinbelow with reference to Table 1.

[37181] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2658 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[37182] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2659 (VGAM2659) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[37183] VGAM2659 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2659 was detected is described hereinabove with reference to Figs. 2-8.

[37184] VGAM2659 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Potato virus A. VGAM2659 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[37185] VGAM2659 gene, herein designated VGAM GENE, encodes a VGAM2659 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2659 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2659 precur-

sor RNA is designated SEQ ID:2645, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2645 is located at position 3436 relative to the genome of Potato virus A.

[37186] VGAM2659 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2659 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[37187] An enzyme complex designated DICER COMPLEX, dices the VGAM2659 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2659 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide se-

quence of VGAM2659 RNA is designated SEQ ID:5370, and is provided hereinbelow with reference to the sequence listing part.

[37188] VGAM2659 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2659 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2659 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[37189] VGAM2659 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2659 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2659 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is ap-

preciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2659 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2659 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[37190] The complementary binding of VGAM2659 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2659 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2659 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2659 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[37191] It is appreciated that VGAM2659 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2659 host target genes. The mRNA of

each one of this plurality of VGAM2659 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2659 RNA, herein designated VGAM RNA, and which when bound by VGAM2659 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2659 host target proteins.

[37192] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2659 gene, herein designated VGAM GENE, on one or more VGAM2659 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science

294,779 (2001)).

[37193] It is yet further appreciated that a function of VGAM2659 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2659 include diagnosis, prevention and treatment of viral infection by Potato virus A. Specific functions, and accordingly utilities, of VGAM2659 correlate with, and may be deduced from, the identity of the host target genes which VGAM2659 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[37194] Nucleotide sequences of the VGAM2659 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2659 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2659 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2659 are further described hereinbelow with reference to Table 1.

[37195] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2659 RNA, herein designated VGAM RNA, are de-

scribed hereinbelow with reference to Table 2.

[37196] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2660 (VGAM2660) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[37197] VGAM2660 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2660 was detected is described hereinabove with reference to Figs. 2-8.

[37198] VGAM2660 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Potato virus A. VGAM2660 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[37199] VGAM2660 gene, herein designated VGAM GENE, encodes a VGAM2660 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2660 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly

similar to the nucleotide sequence of VGAM2660 precursor RNA is designated SEQ ID:2646, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2646 is located at position 4281 relative to the genome of Potato virus A.

[37200] VGAM2660 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2660 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[37201] An enzyme complex designated DICER COMPLEX, dices the VGAM2660 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2660 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2660 RNA is designated SEQ ID:5371, and is provided hereinbelow with reference to the sequence listing part.

[37202] VGAM2660 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2660 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2660 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[37203] VGAM2660 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2660 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2660 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I,

BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2660 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2660 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[37204] The complementary binding of VGAM2660 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2660 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2660 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2660 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[37205] It is appreciated that VGAM2660 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM2660 host target genes. The mRNA of each one of this plurality of VGAM2660 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2660 RNA, herein designated VGAM RNA, and which when bound by VGAM2660 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2660 host target proteins.

[37206] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2660 gene, herein designated VGAM GENE, on one or more VGAM2660 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[37207] It is yet further appreciated that a function of VGAM2660 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2660 include diagnosis, prevention and treatment of viral infection by Potato virus A. Specific functions, and accordingly utilities, of VGAM2660 correlate with, and may be deduced from, the identity of the host target genes which VGAM2660 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[37208] Nucleotide sequences of the VGAM2660 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2660 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2660 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2660 are further described hereinbelow with reference to Table 1.

[37209] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites

to VGAM2660 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[37210] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2661 (VGAM2661) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[37211] VGAM2661 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2661 was detected is described hereinabove with reference to Figs. 2-8.

[37212] VGAM2661 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Potato virus A. VGAM2661 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[37213] VGAM2661 gene, herein designated VGAM GENE, encodes a VGAM2661 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2661 precursor RNA, herein designated VGAM PRECURSOR RNA, does not en-

code a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2661 precursor RNA is designated SEQ ID:2647, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2647 is located at position 2878 relative to the genome of Potato virus A.

[37214] VGAM2661 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2661 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[37215] An enzyme complex designated DICER COMPLEX, dices the VGAM2661 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2661 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2661 RNA is designated SEQ ID:5372, and is provided hereinbelow with reference to the sequence listing part.

[37216] VGAM2661 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2661 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2661 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[37217] VGAM2661 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2661 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2661 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3

such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2661 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2661 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[37218] The complementary binding of VGAM2661 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2661 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2661 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2661 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[37219] It is appreciated that VGAM2661 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2661 host target genes. The mRNA of each one of this plurality of VGAM2661 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2661 RNA, herein designated VGAM RNA, and which when bound by VGAM2661 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2661 host target proteins.

[37220] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2661 gene, herein designated VGAM GENE, on one or more VGAM2661 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[37221] It is yet further appreciated that a function of VGAM2661 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2661 include diagnosis, prevention and treatment of viral infection by Potato virus A. Specific functions, and accordingly utilities, of VGAM2661 correlate with, and may be deduced from, the identity of the host target genes which VGAM2661 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[37222] Nucleotide sequences of the VGAM2661 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2661 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2661 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2661 are further described hereinbelow with reference to Table 1.

[37223] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the

complementarity of each of these host target binding sites to VGAM2661 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[37224] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2662 (VGAM2662) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[37225] VGAM2662 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2662 was detected is described hereinabove with reference to Figs. 2-8.

[37226] VGAM2662 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Potato virus A. VGAM2662 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[37227] VGAM2662 gene, herein designated VGAM GENE, encodes a VGAM2662 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2662 precursor RNA,

herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2662 precursor RNA is designated SEQ ID:2648, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2648 is located at position 4423 relative to the genome of Potato virus A.

[37228] VGAM2662 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2662 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[37229] An enzyme complex designated DICER COMPLEX, dices the VGAM2662 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2662 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 76%) nucleotide sequence of VGAM2662 RNA is designated SEQ ID:5373, and is provided hereinbelow with reference to the sequence listing part.

[37230] VGAM2662 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2662 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2662 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[37231] VGAM2662 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2662 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2662 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host

target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2662 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2662 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[37232] The complementary binding of VGAM2662 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2662 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2662 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2662 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[37233] It is appreciated that VGAM2662 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2662 host target genes. The mRNA of each one of this plurality of VGAM2662 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2662 RNA, herein designated VGAM RNA, and which when bound by VGAM2662 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2662 host target proteins.

[37234] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2662 gene, herein designated VGAM GENE, on one or more VGAM2662 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[37235] It is yet further appreciated that a function of VGAM2662 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2662 include diagnosis, prevention and treatment of viral infection by Potato virus A. Specific functions, and accordingly utilities, of VGAM2662 correlate with, and may be deduced from, the identity of the host target genes which VGAM2662 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[37236] Nucleotide sequences of the VGAM2662 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2662 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2662 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2662 are further described hereinbelow with reference to Table 1.

[37237] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2662 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[37238] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2663 (VGAM2663) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[37239] VGAM2663 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2663 was detected is described hereinabove with reference to Figs. 2-8.

[37240] VGAM2663 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Potato virus A. VGAM2663 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[37241] VGAM2663 gene, herein designated VGAM GENE, encodes a VGAM2663 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and un-

like most ordinary genes, VGAM2663 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2663 precursor RNA is designated SEQ ID:2649, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2649 is located at position 3193 relative to the genome of Potato virus A.

[37242] VGAM2663 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2663 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[37243] An enzyme complex designated DICER COMPLEX, dices the VGAM2663 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2663 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2663 RNA is designated SEQ ID:5374, and is provided hereinbelow with reference to the sequence listing part.

[37244] VGAM2663 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2663 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2663 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[37245] VGAM2663 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2663 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2663 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed

sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2663 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2663 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[37246] The complementary binding of VGAM2663 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2663 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2663 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2663 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target

protein is therefore outlined by a broken line.

[37247] It is appreciated that VGAM2663 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2663 host target genes. The mRNA of each one of this plurality of VGAM2663 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2663 RNA, herein designated VGAM RNA, and which when bound by VGAM2663 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2663 host target proteins.

[37248] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2663 gene, herein designated VGAM GENE, on one or more VGAM2663 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[37249] It is yet further appreciated that a function of VGAM2663 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2663 include diagnosis, prevention and treatment of viral infection by Potato virus A. Specific functions, and accordingly utilities, of VGAM2663 correlate with, and may be deduced from, the identity of the host target genes which VGAM2663 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[37250] Nucleotide sequences of the VGAM2663 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2663 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2663 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2663 are further described hereinbelow with reference to Table 1.

[37251] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2663 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[37252] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2664 (VGAM2664) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[37253] VGAM2664 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2664 was detected is described hereinabove with reference to Figs. 2-8.

[37254] VGAM2664 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cryphonectria parasitica mitovirus 1-NB631. VGAM2664 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[37255] VGAM2664 gene, herein designated VGAM GENE, encodes a VGAM2664 precursor RNA, herein designated VGAM

PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2664 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2664 precursor RNA is designated SEQ ID:2650, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2650 is located at position 1630 relative to the genome of Cryphonectria parasitica mitovirus 1-NB631.

[37256] VGAM2664 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2664 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[37257] An enzyme complex designated DICER COMPLEX, dices the VGAM2664 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2664 RNA,

herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 52%) nucleotide sequence of VGAM2664 RNA is designated SEQ ID:5375, and is provided hereinbelow with reference to the sequence listing part.

[37258] VGAM2664 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2664 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2664 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[37259] VGAM2664 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2664 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM2664 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2664 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2664 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[37260] The complementary binding of VGAM2664 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2664 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2664 host target RNA, herein designated VGAM HOST TARGET

RNA, into VGAM2664 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[37261] It is appreciated that VGAM2664 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2664 host target genes. The mRNA of each one of this plurality of VGAM2664 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2664 RNA, herein designated VGAM RNA, and which when bound by VGAM2664 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2664 host target proteins.

[37262] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2664 gene, herein designated VGAM GENE, on one or more VGAM2664 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[37263] It is yet further appreciated that a function of VGAM2664 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2664 include diagnosis, prevention and treatment of viral infection by Cryphonectria parasitica mitovirus 1-NB631. Specific functions, and accordingly utilities, of VGAM2664 correlate with, and may be deduced from, the identity of the host target genes which VGAM2664 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[37264] Nucleotide sequences of the VGAM2664 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2664 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2664 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2664 are further

described hereinbelow with reference to Table 1.

[37265] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2664 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[37266] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2665 (VGAM2665) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[37267] VGAM2665 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2665 was detected is described hereinabove with reference to Figs. 2-8.

[37268] VGAM2665 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cryphonectria parasitica mitovirus 1-NB631. VGAM2665 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[37269] VGAM2665 gene, herein designated VGAM GENE, encodes a VGAM2665 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2665 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2665 precursor RNA is designated SEQ ID:2651, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2651 is located at position 1362 relative to the genome of Cryphonectria parasitica mitovirus 1-NB631.

[37270] VGAM2665 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2665 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[37271] An enzyme complex designated DICER COMPLEX, dices

the VGAM2665 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2665 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2665 RNA is designated SEQ ID:5376, and is provided hereinbelow with reference to the sequence listing part.

[37272] VGAM2665 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2665 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2665 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[37273] VGAM2665 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2665 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2665 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2665 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2665 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[37274] The complementary binding of VGAM2665 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2665 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM2665 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2665 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[37275] It is appreciated that VGAM2665 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2665 host target genes. The mRNA of each one of this plurality of VGAM2665 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2665 RNA, herein designated VGAM RNA, and which when bound by VGAM2665 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2665 host target proteins.

[37276] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2665 gene, herein designated VGAM GENE, on one or more VGAM2665 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[37277] It is yet further appreciated that a function of VGAM2665 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2665 include diagnosis, prevention and treatment of viral infection by Cryphonectria parasitica mitovirus 1-NB631. Specific functions, and accordingly utilities, of VGAM2665 correlate with, and may be deduced from, the identity of the host target genes which VGAM2665 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[37278] Nucleotide sequences of the VGAM2665 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2665 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of

VGAM2665 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2665 are further described hereinbelow with reference to Table 1.

[37279] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2665 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[37280] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2666 (VGAM2666) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[37281] VGAM2666 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2666 was detected is described hereinabove with reference to Figs. 2-8.

[37282] VGAM2666 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cryphonectria parasitica mitovirus 1-NB631. VGAM2666 host target gene, herein

designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[37283] VGAM2666 gene, herein designated VGAM GENE, encodes a VGAM2666 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2666 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2666 precursor RNA is designated SEQ ID:2652, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2652 is located at position 680 relative to the genome of Cryphonectria parasitica mitovirus 1-NB631.

[37284] VGAM2666 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2666 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[37285] An enzyme complex designated DICER COMPLEX, dices the VGAM2666 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2666 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 73%) nucleotide sequence of VGAM2666 RNA is designated SEQ ID:5377, and is provided hereinbelow with reference to the sequence listing part.

[37286] VGAM2666 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2666 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2666 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[37287] VGAM2666 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM2666 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2666 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2666 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2666 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[37288] The complementary binding of VGAM2666 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM2666 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2666 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2666 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[37289] It is appreciated that VGAM2666 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2666 host target genes. The mRNA of each one of this plurality of VGAM2666 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2666 RNA, herein designated VGAM RNA, and which when bound by VGAM2666 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2666 host target proteins.

[37290] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2666 gene, herein designated VGAM GENE, on one or more VGAM2666 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[37291] It is yet further appreciated that a function of VGAM2666 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2666 include diagnosis, prevention and treatment of viral infection by Cryphonectria parasitica mitovirus 1-NB631. Specific functions, and accordingly utilities, of VGAM2666 correlate with, and may be deduced from, the identity of the host target genes which VGAM2666 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[37292] Nucleotide sequences of the VGAM2666 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

diced VGAM2666 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2666 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2666 are further described hereinbelow with reference to Table 1.

[37293] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2666 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[37294] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2667 (VGAM2667) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[37295] VGAM2667 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2667 was detected is described hereinabove with reference to Figs. 2-8.

[37296] VGAM2667 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of Bean common mosaic necrosis virus. VGAM2667 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[37297] VGAM2667 gene, herein designated VGAM GENE, encodes a VGAM2667 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2667 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2667 precursor RNA is designated SEQ ID:2653, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2653 is located at position 9077 relative to the genome of Bean common mosaic necrosis virus.

[37298] VGAM2667 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2667 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[37299] An enzyme complex designated DICER COMPLEX, dices the VGAM2667 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2667 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide sequence of VGAM2667 RNA is designated SEQ ID:5378, and is provided hereinbelow with reference to the sequence listing part.

[37300] VGAM2667 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2667 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2667 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN COD-

ING and 3UTR respectively.

[37301] VGAM2667 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2667 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2667 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2667 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2667 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[37302] The complementary binding of VGAM2667 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2667 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2667 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2667 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[37303] It is appreciated that VGAM2667 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2667 host target genes. The mRNA of each one of this plurality of VGAM2667 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2667 RNA, herein designated VGAM RNA, and which when bound by VGAM2667 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2667 host target proteins.

[37304] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2667 gene, herein designated VGAM GENE, on one

or more VGAM2667 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[37305] It is yet further appreciated that a function of VGAM2667 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2667 include diagnosis, prevention and treatment of viral infection by Bean common mosaic necrosis virus. Specific functions, and accordingly utilities, of VGAM2667 correlate with, and may be deduced from, the identity of the host target genes which VGAM2667 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[37306] Nucleotide sequences of the VGAM2667 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2667 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2667 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2667 are further described hereinbelow with reference to Table 1.

[37307] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2667 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[37308] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2668 (VGAM2668) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[37309] VGAM2668 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2668 was detected is de-

scribed hereinabove with reference to Figs. 2-8.

[37310] VGAM2668 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Bean common mosaic necrosis virus. VGAM2668 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[37311] VGAM2668 gene, herein designated VGAM GENE, encodes a VGAM2668 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2668 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2668 precursor RNA is designated SEQ ID:2654, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2654 is located at position 5617 relative to the genome of Bean common mosaic necrosis virus.

[37312] VGAM2668 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2668 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[37313] An enzyme complex designated DICER COMPLEX, dices the VGAM2668 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2668 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 84%) nucleotide sequence of VGAM2668 RNA is designated SEQ ID:5379, and is provided hereinbelow with reference to the sequence listing part.

[37314] VGAM2668 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2668 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2668 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding

gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[37315] VGAM2668 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2668 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2668 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2668 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2668 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be lo-

cated in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[37316] The complementary binding of VGAM2668 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2668 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2668 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2668 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[37317] It is appreciated that VGAM2668 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2668 host target genes. The mRNA of each one of this plurality of VGAM2668 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2668 RNA, herein designated VGAM RNA, and which when bound by VGAM2668 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2668 host target proteins.

[37318] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM2668 gene, herein designated VGAM GENE, on one or more VGAM2668 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[37319] It is yet further appreciated that a function of VGAM2668 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2668 include diagnosis, prevention and treatment of viral infection by Bean common mosaic necrosis virus. Specific functions, and accordingly utilities, of VGAM2668 correlate with, and may be deduced from, the identity of the host target genes which VGAM2668

binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[37320] Nucleotide sequences of the VGAM2668 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2668 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2668 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2668 are further described hereinbelow with reference to Table 1.

[37321] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2668 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[37322] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2669 (VGAM2669) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[37323] VGAM2669 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2669 was detected is described hereinabove with reference to Figs. 2-8.

[37324] VGAM2669 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Bean common mosaic necrosis virus. VGAM2669 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[37325] VGAM2669 gene, herein designated VGAM GENE, encodes a VGAM2669 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2669 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2669 precursor RNA is designated SEQ ID:2655, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2655 is located at position 1919 relative to the genome of Bean common mosaic necrosis virus.

[37326] VGAM2669 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2669 folded precursor RNA, herein designated VGAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[37327] An enzyme complex designated DICER COMPLEX, dices the VGAM2669 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2669 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2669 RNA is designated SEQ ID:5380, and is provided hereinbelow with reference to the sequence listing part.

[37328] VGAM2669 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2669 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2669 host target RNA,

herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[37329] VGAM2669 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2669 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2669 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2669 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2669 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host tar-

get binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[37330] The complementary binding of VGAM2669 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2669 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2669 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2669 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[37331] It is appreciated that VGAM2669 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2669 host target genes. The mRNA of each one of this plurality of VGAM2669 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2669 RNA, herein designated VGAM RNA, and which when bound by VGAM2669 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2669 host target proteins.

[37332] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2669 gene, herein designated VGAM GENE, on one or more VGAM2669 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[37333] It is yet further appreciated that a function of VGAM2669 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2669 include diagnosis, prevention and treatment of viral infection by Bean common mosaic necrosis virus. Specific functions, and accordingly utilities,

of VGAM2669 correlate with, and may be deduced from, the identity of the host target genes which VGAM2669 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[37334] Nucleotide sequences of the VGAM2669 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2669 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2669 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2669 are further described hereinbelow with reference to Table 1.

[37335] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2669 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[37336] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2670 (VGAM2670) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the

art.

[37337] VGAM2670 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2670 was detected is described hereinabove with reference to Figs. 2-8.

[37338] VGAM2670 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Bean common mosaic necrosis virus. VGAM2670 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[37339] VGAM2670 gene, herein designated VGAM GENE, encodes a VGAM2670 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2670 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2670 precursor RNA is designated SEQ ID:2656, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2656 is located at position 5302 relative to the genome of Bean common mosaic necrosis virus.

[37340] VGAM2670 precursor RNA, herein designated VGAM PRE-

CURSOR RNA, folds onto itself, forming VGAM2670 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[37341] An enzyme complex designated DICER COMPLEX, dices the VGAM2670 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2670 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2670 RNA is designated SEQ ID:5381, and is provided hereinbelow with reference to the sequence listing part.

[37342] VGAM2670 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM2670 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2670 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[37343] VGAM2670 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2670 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2670 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2670 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2670 host

target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[37344] The complementary binding of VGAM2670 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2670 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2670 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2670 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[37345] It is appreciated that VGAM2670 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2670 host target genes. The mRNA of each one of this plurality of VGAM2670 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2670 RNA, herein designated VGAM RNA, and which when bound by VGAM2670 RNA, herein

designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2670 host target proteins.

[37346] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2670 gene, herein designated VGAM GENE, on one or more VGAM2670 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[37347] It is yet further appreciated that a function of VGAM2670 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2670 include diagnosis, prevention and

treatment of viral infection by Bean common mosaic necrosis virus. Specific functions, and accordingly utilities, of VGAM2670 correlate with, and may be deduced from, the identity of the host target genes which VGAM2670 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[37348] Nucleotide sequences of the VGAM2670 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2670 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2670 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2670 are further described hereinbelow with reference to Table 1.

[37349] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2670 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[37350] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2671 (VGAM2671) viral gene, which modulates ex-

pression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[37351] VGAM2671 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2671 was detected is described hereinabove with reference to Figs. 2-8.

[37352] VGAM2671 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ophiostoma mitovirus 3a. VGAM2671 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[37353] VGAM2671 gene, herein designated VGAM GENE, encodes a VGAM2671 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2671 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2671 precursor RNA is designated SEQ ID:2657, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2657 is located at position 673 relative to the genome of Ophiostoma mitovirus 3a.

[37354] VGAM2671 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2671 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[37355] An enzyme complex designated DICER COMPLEX, dices the VGAM2671 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2671 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 58%) nucleotide sequence of VGAM2671 RNA is designated SEQ ID:5382, and is provided hereinbelow with reference to the sequence listing part.

[37356] VGAM2671 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2671 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2671 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[37357] VGAM2671 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2671 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2671 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2671 RNA, herein designated VGAM RNA, may have a different number of host target

binding sites in untranslated regions of a VGAM2671 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[37358] The complementary binding of VGAM2671 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2671 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2671 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2671 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[37359] It is appreciated that VGAM2671 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2671 host target genes. The mRNA of each one of this plurality of VGAM2671 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2671 RNA, herein designated VGAM

RNA, and which when bound by VGAM2671 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2671 host target proteins.

[37360] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2671 gene, herein designated VGAM GENE, on one or more VGAM2671 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[37361] It is yet further appreciated that a function of VGAM2671 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM2671 include diagnosis, prevention and treatment of viral infection by Ophiostoma mitovirus 3a. Specific functions, and accordingly utilities, of VGAM2671 correlate with, and may be deduced from, the identity of the host target genes which VGAM2671 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[37362] Nucleotide sequences of the VGAM2671 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2671 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2671 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2671 are further described hereinbelow with reference to Table 1.

[37363] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2671 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[37364] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Mes-

senger 2672 (VGAM2672) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[37365] VGAM2672 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2672 was detected is described hereinabove with reference to Figs. 2-8.

[37366] VGAM2672 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ophiostoma mitovirus 3a. VGAM2672 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[37367] VGAM2672 gene, herein designated VGAM GENE, encodes a VGAM2672 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2672 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2672 precursor RNA is designated SEQ ID:2658, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2658 is located at position 1136

relative to the genome of Ophiostoma mitovirus 3a.

[37368] VGAM2672 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2672 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[37369] An enzyme complex designated DICER COMPLEX, dices the VGAM2672 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2672 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2672 RNA is designated SEQ ID:5383, and is provided hereinbelow with reference to the sequence listing part.

[37370] VGAM2672 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2672 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2672 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[37371] VGAM2672 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2672 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2672 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2672 RNA, herein designated

VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2672 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[37372] The complementary binding of VGAM2672 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2672 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2672 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2672 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[37373] It is appreciated that VGAM2672 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2672 host target genes. The mRNA of each one of this plurality of VGAM2672 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM2672 RNA, herein designated VGAM RNA, and which when bound by VGAM2672 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2672 host target proteins.

[37374] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2672 gene, herein designated VGAM GENE, on one or more VGAM2672 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[37375] It is yet further appreciated that a function of VGAM2672 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2672 include diagnosis, prevention and treatment of viral infection by Ophiostoma mitovirus 3a. Specific functions, and accordingly utilities, of VGAM2672 correlate with, and may be deduced from, the identity of the host target genes which VGAM2672 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[37376] Nucleotide sequences of the VGAM2672 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2672 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2672 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2672 are further described hereinbelow with reference to Table 1.

[37377] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2672 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[37378] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present

invention, referred to here as Viral Genomic Address Messenger 2673 (VGAM2673) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[37379] VGAM2673 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2673 was detected is described hereinabove with reference to Figs. 2-8.

[37380] VGAM2673 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ophiostoma mitovirus 3a. VGAM2673 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[37381] VGAM2673 gene, herein designated VGAM GENE, encodes a VGAM2673 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2673 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2673 precursor RNA is designated SEQ ID:2659, and is provided hereinbelow with reference to the sequence listing part. Nu-

cleotide sequence SEQ ID:2659 is located at position 308 relative to the genome of Ophiostoma mitovirus 3a.

[37382] VGAM2673 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2673 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[37383] An enzyme complex designated DICER COMPLEX, dices the VGAM2673 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2673 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2673 RNA is designated SEQ ID:5384, and is provided hereinbelow with reference to the sequence

listing part.

[37384] VGAM2673 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2673 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2673 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[37385] VGAM2673 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2673 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2673 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not

meant to be limiting VGAM2673 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2673 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[37386] The complementary binding of VGAM2673 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2673 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2673 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2673 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[37387] It is appreciated that VGAM2673 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2673 host target genes. The mRNA of each one of this plurality of VGAM2673 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2673 RNA, herein designated VGAM RNA, and which when bound by VGAM2673 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2673 host target proteins.

[37388] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2673 gene, herein designated VGAM GENE, on one or more VGAM2673 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[37389] It is yet further appreciated that a function of VGAM2673

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2673 include diagnosis, prevention and treatment of viral infection by Ophiostoma mitovirus 3a. Specific functions, and accordingly utilities, of VGAM2673 correlate with, and may be deduced from, the identity of the host target genes which VGAM2673 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[37390] Nucleotide sequences of the VGAM2673 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2673 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2673 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2673 are further described hereinbelow with reference to Table 1.

[37391] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2673 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[37392] Fig. 1 further provides a conceptual description of another

novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2674 (VGAM2674) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[37393] VGAM2674 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2674 was detected is described hereinabove with reference to Figs. 2-8.

[37394] VGAM2674 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ophiostoma mitovirus 3a. VGAM2674 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[37395] VGAM2674 gene, herein designated VGAM GENE, encodes a VGAM2674 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2674 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2674 precursor RNA is designated SEQ ID:2660, and is provided here-

inbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2660 is located at position 2100 relative to the genome of Ophiostoma mitovirus 3a.

[37396] VGAM2674 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2674 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[37397] An enzyme complex designated DICER COMPLEX, dices the VGAM2674 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2674 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2674 RNA is designated SEQ ID:5385, and

is provided hereinbelow with reference to the sequence listing part.

[37398] VGAM2674 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2674 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2674 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[37399] VGAM2674 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2674 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2674 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites

shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2674 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2674 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[37400] The complementary binding of VGAM2674 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2674 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2674 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2674 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[37401] It is appreciated that VGAM2674 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2674 host target genes. The mRNA of each one of this plurality of VGAM2674 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2674 RNA, herein designated VGAM RNA, and which when bound by VGAM2674 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2674 host target proteins.

[37402] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2674 gene, herein designated VGAM GENE, on one or more VGAM2674 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[37403] It is yet further appreciated that a function of VGAM2674 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2674 include diagnosis, prevention and treatment of viral infection by Ophiostoma mitovirus 3a. Specific functions, and accordingly utilities, of VGAM2674 correlate with, and may be deduced from, the identity of the host target genes which VGAM2674 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[37404] Nucleotide sequences of the VGAM2674 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2674 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2674 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2674 are further described hereinbelow with reference to Table 1.

[37405] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2674 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[37406] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2675 (VGAM2675) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[37407] VGAM2675 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2675 was detected is described hereinabove with reference to Figs. 2-8.

[37408] VGAM2675 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ophiostoma mitovirus 3a. VGAM2675 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[37409] VGAM2675 gene, herein designated VGAM GENE, encodes a VGAM2675 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2675 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2675 precur-

sor RNA is designated SEQ ID:2661, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2661 is located at position 567 relative to the genome of Ophiostoma mitovirus 3a.

[37410] VGAM2675 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2675 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[37411] An enzyme complex designated DICER COMPLEX, dices the VGAM2675 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2675 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide se-

quence of VGAM2675 RNA is designated SEQ ID:5386, and is provided hereinbelow with reference to the sequence listing part.

[37412] VGAM2675 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2675 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2675 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[37413] VGAM2675 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2675 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2675 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is ap-

preciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2675 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2675 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[37414] The complementary binding of VGAM2675 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2675 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2675 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2675 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[37415] It is appreciated that VGAM2675 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2675 host target genes. The mRNA of

each one of this plurality of VGAM2675 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2675 RNA, herein designated VGAM RNA, and which when bound by VGAM2675 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2675 host target proteins.

[37416] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2675 gene, herein designated VGAM GENE, on one or more VGAM2675 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science

294,779 (2001)).

[37417] It is yet further appreciated that a function of VGAM2675 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2675 include diagnosis, prevention and treatment of viral infection by Ophiostoma mitovirus 3a. Specific functions, and accordingly utilities, of VGAM2675 correlate with, and may be deduced from, the identity of the host target genes which VGAM2675 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[37418] Nucleotide sequences of the VGAM2675 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2675 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2675 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2675 are further described hereinbelow with reference to Table 1.

[37419] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2675 RNA, herein designated VGAM RNA, are de-

scribed hereinbelow with reference to Table 2.

[37420] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2676 (VGAM2676) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[37421] VGAM2676 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2676 was detected is described hereinabove with reference to Figs. 2-8.

[37422] VGAM2676 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ophiostoma mitovirus 3a. VGAM2676 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[37423] VGAM2676 gene, herein designated VGAM GENE, encodes a VGAM2676 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2676 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly

similar to the nucleotide sequence of VGAM2676 precursor RNA is designated SEQ ID:2662, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2662 is located at position 905 relative to the genome of Ophiostoma mitovirus 3a.

[37424] VGAM2676 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2676 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[37425] An enzyme complex designated DICER COMPLEX, dices the VGAM2676 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2676 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 51%) nucleotide sequence of VGAM2676 RNA is designated SEQ ID:5387, and is provided hereinbelow with reference to the sequence listing part.

[37426] VGAM2676 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2676 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2676 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[37427] VGAM2676 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2676 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2676 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I,

BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2676 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2676 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[37428] The complementary binding of VGAM2676 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2676 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2676 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2676 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[37429] It is appreciated that VGAM2676 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM2676 host target genes. The mRNA of each one of this plurality of VGAM2676 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2676 RNA, herein designated VGAM RNA, and which when bound by VGAM2676 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2676 host target proteins.

[37430] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2676 gene, herein designated VGAM GENE, on one or more VGAM2676 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[37431] It is yet further appreciated that a function of VGAM2676 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2676 include diagnosis, prevention and treatment of viral infection by Ophiostoma mitovirus 3a. Specific functions, and accordingly utilities, of VGAM2676 correlate with, and may be deduced from, the identity of the host target genes which VGAM2676 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[37432] Nucleotide sequences of the VGAM2676 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2676 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2676 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2676 are further described hereinbelow with reference to Table 1.

[37433] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites

to VGAM2676 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[37434] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2677 (VGAM2677) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[37435] VGAM2677 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2677 was detected is described hereinabove with reference to Figs. 2-8.

[37436] VGAM2677 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ophiostoma mitovirus 3a. VGAM2677 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[37437] VGAM2677 gene, herein designated VGAM GENE, encodes a VGAM2677 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2677 precursor RNA, herein designated VGAM PRECURSOR RNA, does not en-

code a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2677 precursor RNA is designated SEQ ID:2663, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2663 is located at position 1465 relative to the genome of Ophiostoma mitovirus 3a.

[37438] VGAM2677 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2677 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[37439] An enzyme complex designated DICER COMPLEX, dices the VGAM2677 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2677 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 73%) nucleotide sequence of VGAM2677 RNA is designated SEQ ID:5388, and is provided hereinbelow with reference to the sequence listing part.

[37440] VGAM2677 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2677 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2677 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[37441] VGAM2677 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2677 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2677 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3

such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2677 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2677 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[37442] The complementary binding of VGAM2677 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2677 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2677 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2677 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[37443] It is appreciated that VGAM2677 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2677 host target genes. The mRNA of each one of this plurality of VGAM2677 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2677 RNA, herein designated VGAM RNA, and which when bound by VGAM2677 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2677 host target proteins.

[37444] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2677 gene, herein designated VGAM GENE, on one or more VGAM2677 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[37445] It is yet further appreciated that a function of VGAM2677 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2677 include diagnosis, prevention and treatment of viral infection by Ophiostoma mitovirus 3a. Specific functions, and accordingly utilities, of VGAM2677 correlate with, and may be deduced from, the identity of the host target genes which VGAM2677 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[37446] Nucleotide sequences of the VGAM2677 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2677 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2677 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2677 are further described hereinbelow with reference to Table 1.

[37447] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the

complementarity of each of these host target binding sites to VGAM2677 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[37448] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2678 (VGAM2678) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[37449] VGAM2678 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2678 was detected is described hereinabove with reference to Figs. 2-8.

[37450] VGAM2678 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ophiostoma novo-ulmi mitovirus 4-Ld. VGAM2678 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[37451] VGAM2678 gene, herein designated VGAM GENE, encodes a VGAM2678 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2678 precursor RNA,

herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2678 precursor RNA is designated SEQ ID:2664, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2664 is located at position 1520 relative to the genome of Ophiostoma novo-ulmi mitovirus 4-Ld.

[37452] VGAM2678 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2678 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[37453] An enzyme complex designated DICER COMPLEX, dices the VGAM2678 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2678 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2678 RNA is designated SEQ ID:5389, and is provided hereinbelow with reference to the sequence listing part.

[37454] VGAM2678 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2678 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2678 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[37455] VGAM2678 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2678 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2678 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed

sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2678 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2678 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[37456] The complementary binding of VGAM2678 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2678 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2678 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2678 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target

protein is therefore outlined by a broken line.

[37457] It is appreciated that VGAM2678 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2678 host target genes. The mRNA of each one of this plurality of VGAM2678 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2678 RNA, herein designated VGAM RNA, and which when bound by VGAM2678 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2678 host target proteins.

[37458] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2678 gene, herein designated VGAM GENE, on one or more VGAM2678 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[37459] It is yet further appreciated that a function of VGAM2678 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2678 include diagnosis, prevention and treatment of viral infection by Ophiostoma novo-ulmi mitovirus 4-Ld. Specific functions, and accordingly utilities, of VGAM2678 correlate with, and may be deduced from, the identity of the host target genes which VGAM2678 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[37460] Nucleotide sequences of the VGAM2678 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2678 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2678 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2678 are further described hereinbelow with reference to Table 1.

[37461] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2678 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[37462] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2679 (VGAM2679) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[37463] VGAM2679 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2679 was detected is described hereinabove with reference to Figs. 2-8.

[37464] VGAM2679 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ophiostoma novo-ulmi mitovirus 4-Ld. VGAM2679 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[37465] VGAM2679 gene, herein designated VGAM GENE, encodes a VGAM2679 precursor RNA, herein designated VGAM

PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2679 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2679 precursor RNA is designated SEQ ID:2665, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2665 is located at position 676 relative to the genome of Ophiostoma novo-ulmi mitovirus 4-Ld.

[37466] VGAM2679 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2679 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[37467] An enzyme complex designated DICER COMPLEX, dices the VGAM2679 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2679 RNA,

herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2679 RNA is designated SEQ ID:5390, and is provided hereinbelow with reference to the sequence listing part.

[37468] VGAM2679 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2679 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2679 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[37469] VGAM2679 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2679 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM2679 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2679 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2679 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[37470] The complementary binding of VGAM2679 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2679 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2679 host target RNA, herein designated VGAM HOST TARGET

RNA, into VGAM2679 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[37471] It is appreciated that VGAM2679 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2679 host target genes. The mRNA of each one of this plurality of VGAM2679 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2679 RNA, herein designated VGAM RNA, and which when bound by VGAM2679 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2679 host target proteins.

[37472] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2679 gene, herein designated VGAM GENE, on one or more VGAM2679 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[37473] It is yet further appreciated that a function of VGAM2679 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2679 include diagnosis, prevention and treatment of viral infection by Ophiostoma novo-ulmi mitovirus 4-Ld. Specific functions, and accordingly utilities, of VGAM2679 correlate with, and may be deduced from, the identity of the host target genes which VGAM2679 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[37474] Nucleotide sequences of the VGAM2679 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2679 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2679 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2679 are further

described hereinbelow with reference to Table 1.

[37475] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2679 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[37476] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2680 (VGAM2680) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[37477] VGAM2680 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2680 was detected is described hereinabove with reference to Figs. 2-8.

[37478] VGAM2680 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ophiostoma novo-ulmi mitovirus 4-Ld. VGAM2680 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[37479] VGAM2680 gene, herein designated VGAM GENE, encodes a VGAM2680 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2680 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2680 precursor RNA is designated SEQ ID:2666, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2666 is located at position 316 relative to the genome of Ophiostoma novo-ulmi mitovirus 4-Ld.

[37480] VGAM2680 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2680 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[37481] An enzyme complex designated DICER COMPLEX, dices

the VGAM2680 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2680 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 82%) nucleotide sequence of VGAM2680 RNA is designated SEQ ID:5391, and is provided hereinbelow with reference to the sequence listing part.

[37482] VGAM2680 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2680 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2680 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[37483] VGAM2680 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2680 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2680 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2680 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2680 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[37484] The complementary binding of VGAM2680 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2680 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM2680 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2680 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[37485] It is appreciated that VGAM2680 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2680 host target genes. The mRNA of each one of this plurality of VGAM2680 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2680 RNA, herein designated VGAM RNA, and which when bound by VGAM2680 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2680 host target proteins.

[37486] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2680 gene, herein designated VGAM GENE, on one or more VGAM2680 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[37487] It is yet further appreciated that a function of VGAM2680 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2680 include diagnosis, prevention and treatment of viral infection by Ophiostoma novo-ulmi mitovirus 4-Ld. Specific functions, and accordingly utilities, of VGAM2680 correlate with, and may be deduced from, the identity of the host target genes which VGAM2680 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[37488] Nucleotide sequences of the VGAM2680 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2680 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of

VGAM2680 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2680 are further described hereinbelow with reference to Table 1.

[37489] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2680 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[37490] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2681 (VGAM2681) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[37491] VGAM2681 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2681 was detected is described hereinabove with reference to Figs. 2-8.

[37492] VGAM2681 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ophiostoma novo-ulmi mitovirus 4-Ld. VGAM2681 host target gene, herein des-

ignated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[37493] VGAM2681 gene, herein designated VGAM GENE, encodes a VGAM2681 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2681 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2681 precursor RNA is designated SEQ ID:2667, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2667 is located at position 2192 relative to the genome of Ophiostoma novo-ulmi mitovirus 4-Ld.

[37494] VGAM2681 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2681 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[37495] An enzyme complex designated DICER COMPLEX, dices the VGAM2681 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2681 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2681 RNA is designated SEQ ID:5392, and is provided hereinbelow with reference to the sequence listing part.

[37496] VGAM2681 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2681 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2681 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[37497] VGAM2681 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM2681 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2681 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2681 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2681 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[37498] The complementary binding of VGAM2681 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM2681 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2681 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2681 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[37499] It is appreciated that VGAM2681 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2681 host target genes. The mRNA of each one of this plurality of VGAM2681 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2681 RNA, herein designated VGAM RNA, and which when bound by VGAM2681 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2681 host target proteins.

[37500] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2681 gene, herein designated VGAM GENE, on one or more VGAM2681 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[37501] It is yet further appreciated that a function of VGAM2681 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2681 include diagnosis, prevention and treatment of viral infection by Ophiostoma novo-ulmi mitovirus 4-Ld. Specific functions, and accordingly utilities, of VGAM2681 correlate with, and may be deduced from, the identity of the host target genes which VGAM2681 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[37502] Nucleotide sequences of the VGAM2681 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

diced VGAM2681 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2681 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2681 are further described hereinbelow with reference to Table 1.

[37503] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2681 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[37504] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2682 (VGAM2682) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[37505] VGAM2682 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2682 was detected is described hereinabove with reference to Figs. 2-8.

[37506] VGAM2682 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of Ophiostoma novo-ulmi mitovirus 4-Ld. VGAM2682 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[37507] VGAM2682 gene, herein designated VGAM GENE, encodes a VGAM2682 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2682 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2682 precursor RNA is designated SEQ ID:2668, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2668 is located at position 1099 relative to the genome of Ophiostoma novo-ulmi mitovirus 4-Ld.

[37508] VGAM2682 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2682 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[37509] An enzyme complex designated DICER COMPLEX, dices the VGAM2682 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2682 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of VGAM2682 RNA is designated SEQ ID:5393, and is provided hereinbelow with reference to the sequence listing part.

[37510] VGAM2682 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2682 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2682 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN COD-

ING and 3UTR respectively.

[37511] VGAM2682 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2682 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2682 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2682 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2682 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[37512] The complementary binding of VGAM2682 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2682 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2682 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2682 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[37513] It is appreciated that VGAM2682 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2682 host target genes. The mRNA of each one of this plurality of VGAM2682 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2682 RNA, herein designated VGAM RNA, and which when bound by VGAM2682 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2682 host target proteins.

[37514] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2682 gene, herein designated VGAM GENE, on one

or more VGAM2682 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[37515] It is yet further appreciated that a function of VGAM2682 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2682 include diagnosis, prevention and treatment of viral infection by Ophiostoma novo-ulmi mitovirus 4-Ld. Specific functions, and accordingly utilities, of VGAM2682 correlate with, and may be deduced from, the identity of the host target genes which VGAM2682 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[37516] Nucleotide sequences of the VGAM2682 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2682 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2682 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2682 are further described hereinbelow with reference to Table 1.

[37517] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2682 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[37518] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2683 (VGAM2683) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[37519] VGAM2683 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2683 was detected is de-

scribed hereinabove with reference to Figs. 2-8.

[37520] VGAM2683 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ophiostoma novo-ulmi mitovirus 4-Ld. VGAM2683 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[37521] VGAM2683 gene, herein designated VGAM GENE, encodes a VGAM2683 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2683 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2683 precursor RNA is designated SEQ ID:2669, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2669 is located at position 2286 relative to the genome of Ophiostoma novo-ulmi mitovirus 4-Ld.

[37522] VGAM2683 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2683 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[37523] An enzyme complex designated DICER COMPLEX, dices the VGAM2683 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2683 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2683 RNA is designated SEQ ID:5394, and is provided hereinbelow with reference to the sequence listing part.

[37524] VGAM2683 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2683 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2683 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding

gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[37525] VGAM2683 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2683 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2683 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2683 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2683 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be lo-

cated in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[37526] The complementary binding of VGAM2683 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2683 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2683 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2683 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[37527] It is appreciated that VGAM2683 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2683 host target genes. The mRNA of each one of this plurality of VGAM2683 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2683 RNA, herein designated VGAM RNA, and which when bound by VGAM2683 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2683 host target proteins.

[37528] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM2683 gene, herein designated VGAM GENE, on one or more VGAM2683 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[37529] It is yet further appreciated that a function of VGAM2683 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2683 include diagnosis, prevention and treatment of viral infection by Ophiostoma novo-ulmi mitovirus 4-Ld. Specific functions, and accordingly utilities, of VGAM2683 correlate with, and may be deduced from, the identity of the host target genes which VGAM2683

binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[37530] Nucleotide sequences of the VGAM2683 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2683 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2683 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2683 are further described hereinbelow with reference to Table 1.

[37531] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2683 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[37532] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2684 (VGAM2684) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[37533] VGAM2684 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2684 was detected is described hereinabove with reference to Figs. 2-8.

[37534] VGAM2684 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ophiostoma novo-ulmi mitovirus 5-Ld. VGAM2684 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[37535] VGAM2684 gene, herein designated VGAM GENE, encodes a VGAM2684 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2684 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2684 precursor RNA is designated SEQ ID:2670, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2670 is located at position 706 relative to the genome of Ophiostoma novo-ulmi mitovirus 5-Ld.

[37536] VGAM2684 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2684 folded precursor RNA, herein designated VGAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[37537] An enzyme complex designated DICER COMPLEX, dices the VGAM2684 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2684 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 49%) nucleotide sequence of VGAM2684 RNA is designated SEQ ID:5395, and is provided hereinbelow with reference to the sequence listing part.

[37538] VGAM2684 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2684 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2684 host target RNA,

herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[37539] VGAM2684 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2684 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2684 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2684 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2684 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host tar-

get binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[37540] The complementary binding of VGAM2684 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2684 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2684 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2684 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[37541] It is appreciated that VGAM2684 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2684 host target genes. The mRNA of each one of this plurality of VGAM2684 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2684 RNA, herein designated VGAM RNA, and which when bound by VGAM2684 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2684 host target proteins.

[37542] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2684 gene, herein designated VGAM GENE, on one or more VGAM2684 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[37543] It is yet further appreciated that a function of VGAM2684 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2684 include diagnosis, prevention and treatment of viral infection by Ophiostoma novo-ulmi mitovirus 5-Ld. Specific functions, and accordingly utilities,

of VGAM2684 correlate with, and may be deduced from, the identity of the host target genes which VGAM2684 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[37544] Nucleotide sequences of the VGAM2684 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2684 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2684 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2684 are further described hereinbelow with reference to Table 1.

[37545] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2684 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[37546] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2685 (VGAM2685) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the

art.

[37547] VGAM2685 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2685 was detected is described hereinabove with reference to Figs. 2-8.

[37548] VGAM2685 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ophiostoma novo-ulmi mitovirus 5-Ld. VGAM2685 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[37549] VGAM2685 gene, herein designated VGAM GENE, encodes a VGAM2685 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2685 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2685 precursor RNA is designated SEQ ID:2671, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2671 is located at position 1580 relative to the genome of Ophiostoma novo-ulmi mitovirus 5-Ld.

[37550] VGAM2685 precursor RNA, herein designated VGAM PRE-

CURSOR RNA, folds onto itself, forming VGAM2685 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[37551] An enzyme complex designated DICER COMPLEX, dices the VGAM2685 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2685 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of VGAM2685 RNA is designated SEQ ID:5396, and is provided hereinbelow with reference to the sequence listing part.

[37552] VGAM2685 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM2685 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2685 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[37553] VGAM2685 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2685 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2685 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2685 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2685 host

target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[37554] The complementary binding of VGAM2685 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2685 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2685 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2685 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[37555] It is appreciated that VGAM2685 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2685 host target genes. The mRNA of each one of this plurality of VGAM2685 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2685 RNA, herein designated VGAM RNA, and which when bound by VGAM2685 RNA, herein

designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2685 host target proteins.

[37556] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2685 gene, herein designated VGAM GENE, on one or more VGAM2685 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[37557] It is yet further appreciated that a function of VGAM2685 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2685 include diagnosis, prevention and

treatment of viral infection by Ophiostoma novo-ulmi mitovirus 5-Ld. Specific functions, and accordingly utilities, of VGAM2685 correlate with, and may be deduced from, the identity of the host target genes which VGAM2685 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[37558] Nucleotide sequences of the VGAM2685 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2685 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2685 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2685 are further described hereinbelow with reference to Table 1.

[37559] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2685 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[37560] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2686 (VGAM2686) viral gene, which modulates ex-

pression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[37561] VGAM2686 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2686 was detected is described hereinabove with reference to Figs. 2-8.

[37562] VGAM2686 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ophiostoma novo-ulmi mitovirus 5-Ld. VGAM2686 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[37563] VGAM2686 gene, herein designated VGAM GENE, encodes a VGAM2686 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2686 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2686 precursor RNA is designated SEQ ID:2672, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2672 is located at position 328 relative to the genome of Ophiostoma novo-ulmi mi-

tovirus 5-Ld.

[37564] VGAM2686 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2686 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[37565] An enzyme complex designated DICER COMPLEX, dices the VGAM2686 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2686 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2686 RNA is designated SEQ ID:5397, and is provided hereinbelow with reference to the sequence listing part.

[37566] VGAM2686 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2686 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2686 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[37567] VGAM2686 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2686 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2686 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2686 RNA, herein designated

VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2686 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[37568] The complementary binding of VGAM2686 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2686 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2686 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2686 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[37569] It is appreciated that VGAM2686 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2686 host target genes. The mRNA of each one of this plurality of VGAM2686 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM2686 RNA, herein designated VGAM RNA, and which when bound by VGAM2686 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2686 host target proteins.

[37570] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2686 gene, herein designated VGAM GENE, on one or more VGAM2686 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[37571] It is yet further appreciated that a function of VGAM2686 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2686 include diagnosis, prevention and treatment of viral infection by Ophiostoma novo-ulmi mitovirus 5-Ld. Specific functions, and accordingly utilities, of VGAM2686 correlate with, and may be deduced from, the identity of the host target genes which VGAM2686 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[37572] Nucleotide sequences of the VGAM2686 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2686 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2686 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2686 are further described hereinbelow with reference to Table 1.

[37573] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2686 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[37574] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present

invention, referred to here as Viral Genomic Address Messenger 2687 (VGAM2687) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[37575] VGAM2687 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2687 was detected is described hereinabove with reference to Figs. 2-8.

[37576] VGAM2687 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Southern bean mosaic virus. VGAM2687 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[37577] VGAM2687 gene, herein designated VGAM GENE, encodes a VGAM2687 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2687 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2687 precursor RNA is designated SEQ ID:2673, and is provided hereinbelow with reference to the sequence listing part. Nu-

cleotide sequence SEQ ID:2673 is located at position 820 relative to the genome of Southern bean mosaic virus.

[37578] VGAM2687 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2687 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[37579] An enzyme complex designated DICER COMPLEX, dices the VGAM2687 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2687 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2687 RNA is designated SEQ ID:5398, and is provided hereinbelow with reference to the sequence

listing part.

[37580] VGAM2687 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2687 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2687 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[37581] VGAM2687 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2687 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2687 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not

meant to be limiting VGAM2687 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2687 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[37582] The complementary binding of VGAM2687 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2687 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2687 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2687 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[37583] It is appreciated that VGAM2687 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2687 host target genes. The mRNA of each one of this plurality of VGAM2687 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2687 RNA, herein designated VGAM RNA, and which when bound by VGAM2687 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2687 host target proteins.

[37584] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2687 gene, herein designated VGAM GENE, on one or more VGAM2687 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[37585] It is yet further appreciated that a function of VGAM2687

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2687 include diagnosis, prevention and treatment of viral infection by Southern bean mosaic virus. Specific functions, and accordingly utilities, of VGAM2687 correlate with, and may be deduced from, the identity of the host target genes which VGAM2687 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[37586] Nucleotide sequences of the VGAM2687 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2687 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2687 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2687 are further described hereinbelow with reference to Table 1.

[37587] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2687 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[37588] Fig. 1 further provides a conceptual description of another

novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2688 (VGAM2688) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[37589] VGAM2688 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2688 was detected is described hereinabove with reference to Figs. 2-8.

[37590] VGAM2688 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Southern bean mosaic virus. VGAM2688 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[37591] VGAM2688 gene, herein designated VGAM GENE, encodes a VGAM2688 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2688 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2688 precursor RNA is designated SEQ ID:2674, and is provided here-

inbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2674 is located at position 2629 relative to the genome of Southern bean mosaic virus.

[37592] VGAM2688 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2688 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[37593] An enzyme complex designated DICER COMPLEX, dices the VGAM2688 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2688 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 82%) nucleotide sequence of VGAM2688 RNA is designated SEQ ID:5399, and

is provided hereinbelow with reference to the sequence listing part.

[37594] VGAM2688 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2688 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2688 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[37595] VGAM2688 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2688 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2688 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites

shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2688 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2688 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[37596] The complementary binding of VGAM2688 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2688 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2688 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2688 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[37597] It is appreciated that VGAM2688 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2688 host target genes. The mRNA of each one of this plurality of VGAM2688 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2688 RNA, herein designated VGAM RNA, and which when bound by VGAM2688 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2688 host target proteins.

[37598] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2688 gene, herein designated VGAM GENE, on one or more VGAM2688 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[37599] It is yet further appreciated that a function of VGAM2688 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2688 include diagnosis, prevention and treatment of viral infection by Southern bean mosaic virus. Specific functions, and accordingly utilities, of VGAM2688 correlate with, and may be deduced from, the identity of the host target genes which VGAM2688 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[37600] Nucleotide sequences of the VGAM2688 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2688 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2688 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2688 are further described hereinbelow with reference to Table 1.

[37601] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2688 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[37602] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2689 (VGAM2689) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[37603] VGAM2689 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2689 was detected is described hereinabove with reference to Figs. 2-8.

[37604] VGAM2689 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Southern bean mosaic virus. VGAM2689 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[37605] VGAM2689 gene, herein designated VGAM GENE, encodes a VGAM2689 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2689 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2689 precur-

sor RNA is designated SEQ ID:2675, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2675 is located at position 649 relative to the genome of Southern bean mosaic virus.

[37606] VGAM2689 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2689 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[37607] An enzyme complex designated DICER COMPLEX, dices the VGAM2689 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2689 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide se-

quence of VGAM2689 RNA is designated SEQ ID:5400, and is provided hereinbelow with reference to the sequence listing part.

[37608] VGAM2689 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2689 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2689 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[37609] VGAM2689 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2689 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2689 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is ap-

preciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2689 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2689 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[37610] The complementary binding of VGAM2689 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2689 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2689 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2689 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[37611] It is appreciated that VGAM2689 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2689 host target genes. The mRNA of

each one of this plurality of VGAM2689 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2689 RNA, herein designated VGAM RNA, and which when bound by VGAM2689 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2689 host target proteins.

[37612] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2689 gene, herein designated VGAM GENE, on one or more VGAM2689 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science

294,779 (2001)).

[37613] It is yet further appreciated that a function of VGAM2689 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2689 include diagnosis, prevention and treatment of viral infection by Southern bean mosaic virus. Specific functions, and accordingly utilities, of VGAM2689 correlate with, and may be deduced from, the identity of the host target genes which VGAM2689 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[37614] Nucleotide sequences of the VGAM2689 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2689 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2689 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2689 are further described hereinbelow with reference to Table 1.

[37615] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2689 RNA, herein designated VGAM RNA, are de-

scribed hereinbelow with reference to Table 2.

[37616] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2690 (VGAM2690) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[37617] VGAM2690 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2690 was detected is described hereinabove with reference to Figs. 2-8.

[37618] VGAM2690 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Phthorimaea operculella granulovirus. VGAM2690 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[37619] VGAM2690 gene, herein designated VGAM GENE, encodes a VGAM2690 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2690 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly

similar to the nucleotide sequence of VGAM2690 precursor RNA is designated SEQ ID:2676, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2676 is located at position 69388 relative to the genome of Phthorimaea operculella granulovirus.

[37620] VGAM2690 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2690 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[37621] An enzyme complex designated DICER COMPLEX, dices the VGAM2690 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2690 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2690 RNA is designated SEQ ID:5401, and is provided hereinbelow with reference to the sequence listing part.

[37622] VGAM2690 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2690 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2690 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[37623] VGAM2690 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2690 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2690 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3

such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2690 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2690 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[37624] The complementary binding of VGAM2690 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2690 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2690 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2690 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[37625] It is appreciated that VGAM2690 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2690 host target genes. The mRNA of each one of this plurality of VGAM2690 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2690 RNA, herein designated VGAM RNA, and which when bound by VGAM2690 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2690 host target proteins.

[37626] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2690 gene, herein designated VGAM GENE, on one or more VGAM2690 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[37627] It is yet further appreciated that a function of VGAM2690 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2690 include diagnosis, prevention and treatment of viral infection by Phthorimaea operculella granulovirus. Specific functions, and accordingly utilities, of VGAM2690 correlate with, and may be deduced from, the identity of the host target genes which VGAM2690 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[37628] Nucleotide sequences of the VGAM2690 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2690 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2690 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2690 are further described hereinbelow with reference to Table 1.

[37629] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the

complementarity of each of these host target binding sites to VGAM2690 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[37630] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2691 (VGAM2691) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[37631] VGAM2691 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2691 was detected is described hereinabove with reference to Figs. 2-8.

[37632] VGAM2691 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Phthorimaea operculella granulovirus. VGAM2691 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[37633] VGAM2691 gene, herein designated VGAM GENE, encodes a VGAM2691 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2691 precursor RNA,

herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2691 precursor RNA is designated SEQ ID:2677, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2677 is located at position 68718 relative to the genome of Phthorimaea operculella granulovirus.

[37634] VGAM2691 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2691 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[37635] An enzyme complex designated DICER COMPLEX, dices the VGAM2691 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2691 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 58%) nucleotide sequence of VGAM2691 RNA is designated SEQ ID:5402, and is provided hereinbelow with reference to the sequence listing part.

[37636] VGAM2691 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2691 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2691 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[37637] VGAM2691 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2691 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2691 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed

sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2691 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2691 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[37638] The complementary binding of VGAM2691 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2691 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2691 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2691 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target

protein is therefore outlined by a broken line.

[37639] It is appreciated that VGAM2691 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2691 host target genes. The mRNA of each one of this plurality of VGAM2691 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2691 RNA, herein designated VGAM RNA, and which when bound by VGAM2691 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2691 host target proteins.

[37640] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2691 gene, herein designated VGAM GENE, on one or more VGAM2691 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[37641] It is yet further appreciated that a function of VGAM2691 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2691 include diagnosis, prevention and treatment of viral infection by Phthorimaea operculella granulovirus. Specific functions, and accordingly utilities, of VGAM2691 correlate with, and may be deduced from, the identity of the host target genes which VGAM2691 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[37642] Nucleotide sequences of the VGAM2691 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2691 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2691 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2691 are further described hereinbelow with reference to Table 1.

[37643] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2691 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[37644] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2692 (VGAM2692) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[37645] VGAM2692 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2692 was detected is described hereinabove with reference to Figs. 2-8.

[37646] VGAM2692 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Phthorimaea operculella granulovirus. VGAM2692 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[37647] VGAM2692 gene, herein designated VGAM GENE, encodes a VGAM2692 precursor RNA, herein designated VGAM

PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2692 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2692 precursor RNA is designated SEQ ID:2678, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2678 is located at position 70677 relative to the genome of Phthorimaea operculella granulovirus.

[37648] VGAM2692 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2692 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[37649] An enzyme complex designated DICER COMPLEX, dices the VGAM2692 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2692 RNA,

herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide sequence of VGAM2692 RNA is designated SEQ ID:5403, and is provided hereinbelow with reference to the sequence listing part.

[37650] VGAM2692 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2692 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2692 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[37651] VGAM2692 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2692 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM2692 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2692 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2692 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[37652] The complementary binding of VGAM2692 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2692 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2692 host target RNA, herein designated VGAM HOST TARGET

RNA, into VGAM2692 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[37653] It is appreciated that VGAM2692 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2692 host target genes. The mRNA of each one of this plurality of VGAM2692 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2692 RNA, herein designated VGAM RNA, and which when bound by VGAM2692 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2692 host target proteins.

[37654] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2692 gene, herein designated VGAM GENE, on one or more VGAM2692 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[37655] It is yet further appreciated that a function of VGAM2692 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2692 include diagnosis, prevention and treatment of viral infection by Phthorimaea operculella granulovirus. Specific functions, and accordingly utilities, of VGAM2692 correlate with, and may be deduced from, the identity of the host target genes which VGAM2692 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[37656] Nucleotide sequences of the VGAM2692 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2692 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2692 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2692 are further

described hereinbelow with reference to Table 1.

[37657] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2692 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[37658] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2693 (VGAM2693) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[37659] VGAM2693 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2693 was detected is described hereinabove with reference to Figs. 2-8.

[37660] VGAM2693 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Phthorimaea operculella granulovirus. VGAM2693 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[37661] VGAM2693 gene, herein designated VGAM GENE, encodes a VGAM2693 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2693 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2693 precursor RNA is designated SEQ ID:2679, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2679 is located at position 70243 relative to the genome of Phthorimaea operculella granulovirus.

[37662] VGAM2693 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2693 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[37663] An enzyme complex designated DICER COMPLEX, dices

the VGAM2693 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2693 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 51%) nucleotide sequence of VGAM2693 RNA is designated SEQ ID:5404, and is provided hereinbelow with reference to the sequence listing part.

[37664] VGAM2693 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2693 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2693 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[37665] VGAM2693 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2693 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2693 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2693 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2693 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[37666] The complementary binding of VGAM2693 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2693 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM2693 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2693 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[37667] It is appreciated that VGAM2693 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2693 host target genes. The mRNA of each one of this plurality of VGAM2693 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2693 RNA, herein designated VGAM RNA, and which when bound by VGAM2693 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2693 host target proteins.

[37668] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2693 gene, herein designated VGAM GENE, on one or more VGAM2693 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[37669] It is yet further appreciated that a function of VGAM2693 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2693 include diagnosis, prevention and treatment of viral infection by Phthorimaea operculella granulovirus. Specific functions, and accordingly utilities, of VGAM2693 correlate with, and may be deduced from, the identity of the host target genes which VGAM2693 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[37670] Nucleotide sequences of the VGAM2693 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2693 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of

VGAM2693 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2693 are further described hereinbelow with reference to Table 1.

[37671] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2693 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[37672] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2694 (VGAM2694) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[37673] VGAM2694 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2694 was detected is described hereinabove with reference to Figs. 2-8.

[37674] VGAM2694 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Phthorimaea operculella granulovirus. VGAM2694 host target gene, herein desig-

nated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[37675] VGAM2694 gene, herein designated VGAM GENE, encodes a VGAM2694 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2694 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2694 precursor RNA is designated SEQ ID:2680, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2680 is located at position 71428 relative to the genome of Phthorimaea operculella granulovirus.

[37676] VGAM2694 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2694 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[37677] An enzyme complex designated DICER COMPLEX, dices the VGAM2694 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2694 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2694 RNA is designated SEQ ID:5405, and is provided hereinbelow with reference to the sequence listing part.

[37678] VGAM2694 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2694 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2694 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[37679] VGAM2694 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM2694 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2694 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2694 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2694 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[37680] The complementary binding of VGAM2694 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM2694 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2694 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2694 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[37681] It is appreciated that VGAM2694 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2694 host target genes. The mRNA of each one of this plurality of VGAM2694 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2694 RNA, herein designated VGAM RNA, and which when bound by VGAM2694 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2694 host target proteins.

[37682] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2694 gene, herein designated VGAM GENE, on one or more VGAM2694 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[37683] It is yet further appreciated that a function of VGAM2694 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2694 include diagnosis, prevention and treatment of viral infection by Phthorimaea operculella granulovirus. Specific functions, and accordingly utilities, of VGAM2694 correlate with, and may be deduced from, the identity of the host target genes which VGAM2694 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[37684] Nucleotide sequences of the VGAM2694 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

diced VGAM2694 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2694 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2694 are further described hereinbelow with reference to Table 1.

[37685] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2694 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[37686] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2695 (VGAM2695) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[37687] VGAM2695 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2695 was detected is described hereinabove with reference to Figs. 2-8.

[37688] VGAM2695 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of Fringilla coelebs papillomavirus (FPV). VGAM2695 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[37689] VGAM2695 gene, herein designated VGAM GENE, encodes a VGAM2695 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2695 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2695 precursor RNA is designated SEQ ID:2681, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2681 is located at position 1921 relative to the genome of Fringilla coelebs papillomavirus (FPV).

[37690] VGAM2695 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2695 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[37691] An enzyme complex designated DICER COMPLEX, dices the VGAM2695 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2695 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 84%) nucleotide sequence of VGAM2695 RNA is designated SEQ ID:5406, and is provided hereinbelow with reference to the sequence listing part.

[37692] VGAM2695 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2695 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2695 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN COD-

ING and 3UTR respectively.

[37693] VGAM2695 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2695 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2695 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2695 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2695 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[37694] The complementary binding of VGAM2695 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2695 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2695 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2695 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[37695] It is appreciated that VGAM2695 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2695 host target genes. The mRNA of each one of this plurality of VGAM2695 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2695 RNA, herein designated VGAM RNA, and which when bound by VGAM2695 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2695 host target proteins.

[37696] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2695 gene, herein designated VGAM GENE, on one

or more VGAM2695 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[37697] It is yet further appreciated that a function of VGAM2695 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2695 include diagnosis, prevention and treatment of viral infection by Fringilla coelebs papillomavirus (FPV). Specific functions, and accordingly utilities, of VGAM2695 correlate with, and may be deduced from, the identity of the host target genes which VGAM2695 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[37698] Nucleotide sequences of the VGAM2695 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2695 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2695 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2695 are further described hereinbelow with reference to Table 1.

[37699] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2695 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[37700] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2696 (VGAM2696) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[37701] VGAM2696 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2696 was detected is de-

scribed hereinabove with reference to Figs. 2-8.

[37702] VGAM2696 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Paprika mild mottle virus. VGAM2696 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[37703] VGAM2696 gene, herein designated VGAM GENE, encodes a VGAM2696 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2696 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2696 precursor RNA is designated SEQ ID:2682, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2682 is located at position 4675 relative to the genome of Paprika mild mottle virus.

[37704] VGAM2696 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2696 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[37705] An enzyme complex designated DICER COMPLEX, dices the VGAM2696 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2696 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 84%) nucleotide sequence of VGAM2696 RNA is designated SEQ ID:5407, and is provided hereinbelow with reference to the sequence listing part.

[37706] VGAM2696 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2696 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2696 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and

a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[37707] VGAM2696 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2696 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2696 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2696 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2696 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both

3UTR and 5UTR regions.

[37708] The complementary binding of VGAM2696 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2696 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2696 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2696 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[37709] It is appreciated that VGAM2696 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2696 host target genes. The mRNA of each one of this plurality of VGAM2696 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2696 RNA, herein designated VGAM RNA, and which when bound by VGAM2696 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2696 host target proteins.

[37710] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM2696 gene, herein designated VGAM GENE, on one or more VGAM2696 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[37711] It is yet further appreciated that a function of VGAM2696 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2696 include diagnosis, prevention and treatment of viral infection by Paprika mild mottle virus. Specific functions, and accordingly utilities, of VGAM2696 correlate with, and may be deduced from, the identity of the host target genes which VGAM2696 binds and inhibits, and the function of these host target genes, as

elaborated hereinbelow.

[37712] Nucleotide sequences of the VGAM2696 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2696 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2696 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2696 are further described hereinbelow with reference to Table 1.

[37713] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2696 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[37714] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2697 (VGAM2697) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[37715] VGAM2697 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene.

The method by which VGAM2697 was detected is described hereinabove with reference to Figs. 2-8.

[37716] VGAM2697 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Paprika mild mottle virus. VGAM2697 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[37717] VGAM2697 gene, herein designated VGAM GENE, encodes a VGAM2697 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2697 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2697 precursor RNA is designated SEQ ID:2683, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2683 is located at position 891 relative to the genome of Paprika mild mottle virus.

[37718] VGAM2697 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2697 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[37719] An enzyme complex designated DICER COMPLEX, dices the VGAM2697 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2697 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2697 RNA is designated SEQ ID:5408, and is provided hereinbelow with reference to the sequence listing part.

[37720] VGAM2697 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2697 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2697 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding

gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[37721] VGAM2697 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2697 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2697 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2697 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2697 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be lo-

cated in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[37722] The complementary binding of VGAM2697 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2697 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2697 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2697 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[37723] It is appreciated that VGAM2697 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2697 host target genes. The mRNA of each one of this plurality of VGAM2697 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2697 RNA, herein designated VGAM RNA, and which when bound by VGAM2697 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2697 host target proteins.

[37724] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2697 gene, herein designated VGAM GENE, on one

or more VGAM2697 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[37725] It is yet further appreciated that a function of VGAM2697 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2697 include diagnosis, prevention and treatment of viral infection by Paprika mild mottle virus. Specific functions, and accordingly utilities, of VGAM2697 correlate with, and may be deduced from, the identity of the host target genes which VGAM2697 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[37726] Nucleotide sequences of the VGAM2697 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2697 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2697 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2697 are further described hereinbelow with reference to Table 1.

[37727] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2697 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[37728] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2698 (VGAM2698) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[37729] VGAM2698 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2698 was detected is de-

scribed hereinabove with reference to Figs. 2-8.

[37730] VGAM2698 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Paprika mild mottle virus. VGAM2698 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[37731] VGAM2698 gene, herein designated VGAM GENE, encodes a VGAM2698 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2698 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2698 precursor RNA is designated SEQ ID:2684, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2684 is located at position 1275 relative to the genome of Paprika mild mottle virus.

[37732] VGAM2698 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2698 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[37733] An enzyme complex designated DICER COMPLEX, dices the VGAM2698 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2698 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2698 RNA is designated SEQ ID:5409, and is provided hereinbelow with reference to the sequence listing part.

[37734] VGAM2698 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2698 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2698 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and

a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[37735] VGAM2698 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2698 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2698 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2698 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2698 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both

3UTR and 5UTR regions.

[37736] The complementary binding of VGAM2698 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2698 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2698 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2698 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[37737] It is appreciated that VGAM2698 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2698 host target genes. The mRNA of each one of this plurality of VGAM2698 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2698 RNA, herein designated VGAM RNA, and which when bound by VGAM2698 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2698 host target proteins.

[37738] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM2698 gene, herein designated VGAM GENE, on one or more VGAM2698 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[37739] It is yet further appreciated that a function of VGAM2698 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2698 include diagnosis, prevention and treatment of viral infection by Paprika mild mottle virus. Specific functions, and accordingly utilities, of VGAM2698 correlate with, and may be deduced from, the identity of the host target genes which VGAM2698 binds and inhibits, and the function of these host target genes, as

elaborated hereinbelow.

[37740] Nucleotide sequences of the VGAM2698 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2698 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2698 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2698 are further described hereinbelow with reference to Table 1.

[37741] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2698 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[37742] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2699 (VGAM2699) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[37743] VGAM2699 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene.

The method by which VGAM2699 was detected is described hereinabove with reference to Figs. 2-8.

[37744] VGAM2699 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Paprika mild mottle virus. VGAM2699 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[37745] VGAM2699 gene, herein designated VGAM GENE, encodes a VGAM2699 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2699 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2699 precursor RNA is designated SEQ ID:2685, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2685 is located at position 2770 relative to the genome of Paprika mild mottle virus.

[37746] VGAM2699 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2699 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[37747] An enzyme complex designated DICER COMPLEX, dices the VGAM2699 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2699 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 54%) nucleotide sequence of VGAM2699 RNA is designated SEQ ID:5410, and is provided hereinbelow with reference to the sequence listing part.

[37748] VGAM2699 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2699 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2699 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding

gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[37749] VGAM2699 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2699 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2699 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2699 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2699 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be lo-

cated in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[37750] The complementary binding of VGAM2699 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2699 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2699 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2699 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[37751] It is appreciated that VGAM2699 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2699 host target genes. The mRNA of each one of this plurality of VGAM2699 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2699 RNA, herein designated VGAM RNA, and which when bound by VGAM2699 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2699 host target proteins.

[37752] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM2699 gene, herein designated VGAM GENE, on one or more VGAM2699 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[37753] It is yet further appreciated that a function of VGAM2699 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2699 include diagnosis, prevention and treatment of viral infection by Paprika mild mottle virus. Specific functions, and accordingly utilities, of VGAM2699 correlate with, and may be deduced from, the identity of the host target genes which VGAM2699 binds and in-

hibits, and the function of these host target genes, as elaborated hereinbelow.

[37754] Nucleotide sequences of the VGAM2699 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2699 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2699 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2699 are further described hereinbelow with reference to Table 1.

[37755] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2699 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[37756] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2700 (VGAM2700) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[37757] VGAM2700 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2700 was detected is described hereinabove with reference to Figs. 2-8.

[37758] VGAM2700 gene, herein designated VGAM GENE, is a viral gene contained in the genome of La Crosse virus. VGAM2700 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[37759] VGAM2700 gene, herein designated VGAM GENE, encodes a VGAM2700 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2700 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2700 precursor RNA is designated SEQ ID:2686, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2686 is located at position 1021 relative to the genome of La Crosse virus.

[37760] VGAM2700 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2700 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[37761] An enzyme complex designated DICER COMPLEX, dices the VGAM2700 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2700 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2700 RNA is designated SEQ ID:5411, and is provided hereinbelow with reference to the sequence listing part.

[37762] VGAM2700 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2700 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2700 host target RNA, herein designated VGAM HOST TARGET RNA, comprises

three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[37763] VGAM2700 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2700 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2700 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2700 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2700 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an

example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[37764] The complementary binding of VGAM2700 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2700 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2700 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2700 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[37765] It is appreciated that VGAM2700 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2700 host target genes. The mRNA of each one of this plurality of VGAM2700 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2700 RNA, herein designated VGAM RNA, and which when bound by VGAM2700 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2700 host target proteins.

[37766] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2700 gene, herein designated VGAM GENE, on one or more VGAM2700 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[37767] It is yet further appreciated that a function of VGAM2700 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2700 include diagnosis, prevention and treatment of viral infection by La Crosse virus. Specific functions, and accordingly utilities, of VGAM2700 correlate with, and may be deduced from, the identity of the

host target genes which VGAM2700 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[37768] Nucleotide sequences of the VGAM2700 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2700 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2700 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2700 are further described hereinbelow with reference to Table 1.

[37769] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2700 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[37770] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2701 (VGAM2701) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[37771] VGAM2701 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2701 was detected is described hereinabove with reference to Figs. 2-8.

[37772] VGAM2701 gene, herein designated VGAM GENE, is a viral gene contained in the genome of La Crosse virus. VGAM2701 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[37773] VGAM2701 gene, herein designated VGAM GENE, encodes a VGAM2701 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2701 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2701 precursor RNA is designated SEQ ID:2687, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2687 is located at position 4064 relative to the genome of La Crosse virus.

[37774] VGAM2701 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2701 folded precursor RNA, herein designated VGAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[37775] An enzyme complex designated DICER COMPLEX, dices the VGAM2701 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2701 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2701 RNA is designated SEQ ID:5412, and is provided hereinbelow with reference to the sequence listing part.

[37776] VGAM2701 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2701 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2701 host target RNA,

herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[37777] VGAM2701 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2701 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2701 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2701 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2701 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host tar-

get binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[37778] The complementary binding of VGAM2701 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2701 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2701 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2701 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[37779] It is appreciated that VGAM2701 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2701 host target genes. The mRNA of each one of this plurality of VGAM2701 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2701 RNA, herein designated VGAM RNA, and which when bound by VGAM2701 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2701 host target proteins.

[37780] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2701 gene, herein designated VGAM GENE, on one or more VGAM2701 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[37781] It is yet further appreciated that a function of VGAM2701 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2701 include diagnosis, prevention and treatment of viral infection by La Crosse virus. Specific functions, and accordingly utilities, of VGAM2701 corre-

late with, and may be deduced from, the identity of the host target genes which VGAM2701 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[37782] Nucleotide sequences of the VGAM2701 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2701 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2701 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2701 are further described hereinbelow with reference to Table 1.

[37783] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2701 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[37784] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2702 (VGAM2702) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the

art.

[37785] VGAM2702 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2702 was detected is described hereinabove with reference to Figs. 2-8.

[37786] VGAM2702 gene, herein designated VGAM GENE, is a viral gene contained in the genome of La Crosse virus. VGAM2702 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[37787] VGAM2702 gene, herein designated VGAM GENE, encodes a VGAM2702 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2702 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2702 precursor RNA is designated SEQ ID:2688, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2688 is located at position 4272 relative to the genome of La Crosse virus.

[37788] VGAM2702 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2702 folded

precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[37789] An enzyme complex designated DICER COMPLEX, dices the VGAM2702 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2702 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 47%) nucleotide sequence of VGAM2702 RNA is designated SEQ ID:5413, and is provided hereinbelow with reference to the sequence listing part.

[37790] VGAM2702 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2702 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM2702 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[37791] VGAM2702 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2702 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2702 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2702 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2702 host target RNA, herein designated VGAM HOST TARGET RNA.

It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[37792] The complementary binding of VGAM2702 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2702 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2702 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2702 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[37793] It is appreciated that VGAM2702 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2702 host target genes. The mRNA of each one of this plurality of VGAM2702 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2702 RNA, herein designated VGAM RNA, and which when bound by VGAM2702 RNA, herein designated VGAM RNA, causes inhibition of translation of

respective one or more VGAM2702 host target proteins.

[37794] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2702 gene, herein designated VGAM GENE, on one or more VGAM2702 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[37795] It is yet further appreciated that a function of VGAM2702 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2702 include diagnosis, prevention and treatment of viral infection by La Crosse virus. Specific

functions, and accordingly utilities, of VGAM2702 correlate with, and may be deduced from, the identity of the host target genes which VGAM2702 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[37796] Nucleotide sequences of the VGAM2702 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2702 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2702 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2702 are further described hereinbelow with reference to Table 1.

[37797] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2702 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[37798] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2703 (VGAM2703) viral gene, which modulates expression of respective host target genes thereof, the func-

tion and utility of which host target genes is known in the art.

[37799] VGAM2703 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2703 was detected is described hereinabove with reference to Figs. 2-8.

[37800] VGAM2703 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mamestra configurata nucleopolyhedrovirus B. VGAM2703 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[37801] VGAM2703 gene, herein designated VGAM GENE, encodes a VGAM2703 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2703 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2703 precursor RNA is designated SEQ ID:2689, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2689 is located at position 133043 relative to the genome of Mamestra configurata nucleopolyhedrovirus B.

[37802] VGAM2703 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2703 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[37803] An enzyme complex designated DICER COMPLEX, dices the VGAM2703 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2703 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 50%) nucleotide sequence of VGAM2703 RNA is designated SEQ ID:5414, and is provided hereinbelow with reference to the sequence listing part.

[37804] VGAM2703 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2703 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2703 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[37805] VGAM2703 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2703 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2703 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2703 RNA, herein designated VGAM RNA, may have a different number of host target

binding sites in untranslated regions of a VGAM2703 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[37806] The complementary binding of VGAM2703 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2703 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2703 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2703 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[37807] It is appreciated that VGAM2703 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2703 host target genes. The mRNA of each one of this plurality of VGAM2703 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2703 RNA, herein designated VGAM

RNA, and which when bound by VGAM2703 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2703 host target proteins.

[37808] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2703 gene, herein designated VGAM GENE, on one or more VGAM2703 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[37809] It is yet further appreciated that a function of VGAM2703 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM2703 include diagnosis, prevention and treatment of viral infection by Mamestra configurata nucleopolyhedrovirus B. Specific functions, and accordingly utilities, of VGAM2703 correlate with, and may be deduced from, the identity of the host target genes which VGAM2703 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[37810] Nucleotide sequences of the VGAM2703 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2703 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2703 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2703 are further described hereinbelow with reference to Table 1.

[37811] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2703 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[37812] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Mes-

senger 2704 (VGAM2704) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[37813] VGAM2704 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2704 was detected is described hereinabove with reference to Figs. 2-8.

[37814] VGAM2704 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mamestra configurata nucleopolyhedrovirus B. VGAM2704 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[37815] VGAM2704 gene, herein designated VGAM GENE, encodes a VGAM2704 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2704 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2704 precursor RNA is designated SEQ ID:2690, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2690 is located at position

133581 relative to the genome of Mamestra configurata nucleopolyhedrovirus B.

[37816] VGAM2704 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2704 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[37817] An enzyme complex designated DICER COMPLEX, dices the VGAM2704 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2704 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 86%) nucleotide sequence of VGAM2704 RNA is designated SEQ ID:5415, and is provided hereinbelow with reference to the sequence

listing part.

[37818] VGAM2704 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2704 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2704 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[37819] VGAM2704 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2704 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2704 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not

meant to be limiting VGAM2704 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2704 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[37820] The complementary binding of VGAM2704 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2704 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2704 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2704 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[37821] It is appreciated that VGAM2704 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2704 host target genes. The mRNA of each one of this plurality of VGAM2704 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2704 RNA, herein designated VGAM RNA, and which when bound by VGAM2704 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2704 host target proteins.

[37822] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2704 gene, herein designated VGAM GENE, on one or more VGAM2704 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[37823] It is yet further appreciated that a function of VGAM2704

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2704 include diagnosis, prevention and treatment of viral infection by Mamestra configurata nucleopolyhedrovirus B. Specific functions, and accordingly utilities, of VGAM2704 correlate with, and may be deduced from, the identity of the host target genes which VGAM2704 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[37824] Nucleotide sequences of the VGAM2704 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2704 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2704 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2704 are further described hereinbelow with reference to Table 1.

[37825] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2704 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[37826] Fig. 1 further provides a conceptual description of another

novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2705 (VGAM2705) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[37827] VGAM2705 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2705 was detected is described hereinabove with reference to Figs. 2-8.

[37828] VGAM2705 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Heliothis zea virus 1 (HZV-1). VGAM2705 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[37829] VGAM2705 gene, herein designated VGAM GENE, encodes a VGAM2705 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2705 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2705 precursor RNA is designated SEQ ID:2691, and is provided here-

inbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2691 is located at position 81066 relative to the genome of Heliothis zea virus 1 (HZV-1).

[37830] VGAM2705 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2705 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[37831] An enzyme complex designated DICER COMPLEX, dices the VGAM2705 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2705 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide se-

quence of VGAM2705 RNA is designated SEQ ID:5416, and is provided hereinbelow with reference to the sequence listing part.

[37832] VGAM2705 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2705 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2705 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[37833] VGAM2705 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2705 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2705 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is ap-

preciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2705 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2705 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[37834] The complementary binding of VGAM2705 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2705 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2705 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2705 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[37835] It is appreciated that VGAM2705 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2705 host target genes. The mRNA of

each one of this plurality of VGAM2705 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2705 RNA, herein designated VGAM RNA, and which when bound by VGAM2705 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2705 host target proteins.

[37836] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2705 gene, herein designated VGAM GENE, on one or more VGAM2705 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science

294,779 (2001)).

[37837] It is yet further appreciated that a function of VGAM2705 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2705 include diagnosis, prevention and treatment of viral infection by Heliothis zea virus 1 (HZV-1). Specific functions, and accordingly utilities, of VGAM2705 correlate with, and may be deduced from, the identity of the host target genes which VGAM2705 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[37838] Nucleotide sequences of the VGAM2705 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2705 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2705 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2705 are further described hereinbelow with reference to Table 1.

[37839] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2705 RNA, herein designated VGAM RNA, are de-

scribed hereinbelow with reference to Table 2.

[37840] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2706 (VGAM2706) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[37841] VGAM2706 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2706 was detected is described hereinabove with reference to Figs. 2-8.

[37842] VGAM2706 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Heliothis zea virus 1 (HZV-1). VGAM2706 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[37843] VGAM2706 gene, herein designated VGAM GENE, encodes a VGAM2706 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2706 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly

similar to the nucleotide sequence of VGAM2706 precursor RNA is designated SEQ ID:2692, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2692 is located at position 84781 relative to the genome of Heliothis zea virus 1 (HZV-1).

[37844] VGAM2706 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2706 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[37845] An enzyme complex designated DICER COMPLEX, dices the VGAM2706 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2706 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 49%) nucleotide sequence of VGAM2706 RNA is designated SEQ ID:5417, and is provided hereinbelow with reference to the sequence listing part.

[37846] VGAM2706 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2706 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2706 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[37847] VGAM2706 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2706 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2706 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3

such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2706 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2706 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[37848] The complementary binding of VGAM2706 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2706 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2706 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2706 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[37849] It is appreciated that VGAM2706 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2706 host target genes. The mRNA of each one of this plurality of VGAM2706 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2706 RNA, herein designated VGAM RNA, and which when bound by VGAM2706 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2706 host target proteins.

[37850] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2706 gene, herein designated VGAM GENE, on one or more VGAM2706 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[37851] It is yet further appreciated that a function of VGAM2706 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2706 include diagnosis, prevention and treatment of viral infection by Heliothis zea virus 1 (HZV-1). Specific functions, and accordingly utilities, of VGAM2706 correlate with, and may be deduced from, the identity of the host target genes which VGAM2706 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[37852] Nucleotide sequences of the VGAM2706 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2706 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2706 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2706 are further described hereinbelow with reference to Table 1.

[37853] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the

complementarity of each of these host target binding sites to VGAM2706 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[37854] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2707 (VGAM2707) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[37855] VGAM2707 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2707 was detected is described hereinabove with reference to Figs. 2-8.

[37856] VGAM2707 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Heliothis zea virus 1 (HZV-1). VGAM2707 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[37857] VGAM2707 gene, herein designated VGAM GENE, encodes a VGAM2707 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2707 precursor RNA,

herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2707 precursor RNA is designated SEQ ID:2693, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2693 is located at position 85718 relative to the genome of Heliothis zea virus 1 (HZV-1).

[37858] VGAM2707 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2707 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[37859] An enzyme complex designated DICER COMPLEX, dices the VGAM2707 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2707 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 70%) nucleotide sequence of VGAM2707 RNA is designated SEQ ID:5418, and is provided hereinbelow with reference to the sequence listing part.

[37860] VGAM2707 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2707 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2707 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[37861] VGAM2707 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2707 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2707 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed

sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2707 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2707 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[37862] The complementary binding of VGAM2707 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2707 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2707 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2707 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target

protein is therefore outlined by a broken line.

[37863] It is appreciated that VGAM2707 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2707 host target genes. The mRNA of each one of this plurality of VGAM2707 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2707 RNA, herein designated VGAM RNA, and which when bound by VGAM2707 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2707 host target proteins.

[37864] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2707 gene, herein designated VGAM GENE, on one or more VGAM2707 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[37865] It is yet further appreciated that a function of VGAM2707 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2707 include diagnosis, prevention and treatment of viral infection by Heliothis zea virus 1 (HZV-1). Specific functions, and accordingly utilities, of VGAM2707 correlate with, and may be deduced from, the identity of the host target genes which VGAM2707 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[37866] Nucleotide sequences of the VGAM2707 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2707 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2707 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2707 are further described hereinbelow with reference to Table 1.

[37867] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2707 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[37868] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2708 (VGAM2708) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[37869] VGAM2708 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2708 was detected is described hereinabove with reference to Figs. 2-8.

[37870] VGAM2708 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Heliothis zea virus 1 (HZV-1). VGAM2708 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[37871] VGAM2708 gene, herein designated VGAM GENE, encodes a VGAM2708 precursor RNA, herein designated VGAM

PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2708 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2708 precursor RNA is designated SEQ ID:2694, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2694 is located at position 91200 relative to the genome of Heliothis zea virus 1 (HZV-1).

[37872] VGAM2708 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2708 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[37873] An enzyme complex designated DICER COMPLEX, dices the VGAM2708 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2708 RNA,

herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2708 RNA is designated SEQ ID:5419, and is provided hereinbelow with reference to the sequence listing part.

[37874] VGAM2708 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2708 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2708 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[37875] VGAM2708 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2708 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM2708 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2708 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2708 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[37876] The complementary binding of VGAM2708 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2708 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2708 host target RNA, herein designated VGAM HOST TARGET

RNA, into VGAM2708 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[37877] It is appreciated that VGAM2708 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2708 host target genes. The mRNA of each one of this plurality of VGAM2708 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2708 RNA, herein designated VGAM RNA, and which when bound by VGAM2708 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2708 host target proteins.

[37878] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2708 gene, herein designated VGAM GENE, on one or more VGAM2708 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[37879] It is yet further appreciated that a function of VGAM2708 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2708 include diagnosis, prevention and treatment of viral infection by Heliothis zea virus 1 (HZV-1). Specific functions, and accordingly utilities, of VGAM2708 correlate with, and may be deduced from, the identity of the host target genes which VGAM2708 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[37880] Nucleotide sequences of the VGAM2708 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2708 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2708 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2708 are further

described hereinbelow with reference to Table 1.

[37881] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2708 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[37882] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2709 (VGAM2709) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[37883] VGAM2709 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2709 was detected is described hereinabove with reference to Figs. 2-8.

[37884] VGAM2709 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Heliothis zea virus 1 (HZV-1). VGAM2709 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[37885] VGAM2709 gene, herein designated VGAM GENE, encodes a VGAM2709 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2709 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2709 precursor RNA is designated SEQ ID:2695, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2695 is located at position 89310 relative to the genome of Heliothis zea virus 1 (HZV-1).

[37886] VGAM2709 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2709 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[37887] An enzyme complex designated DICER COMPLEX, dices

the VGAM2709 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2709 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide sequence of VGAM2709 RNA is designated SEQ ID:5420, and is provided hereinbelow with reference to the sequence listing part.

[37888] VGAM2709 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2709 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2709 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[37889] VGAM2709 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2709 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2709 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2709 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2709 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[37890] The complementary binding of VGAM2709 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2709 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM2709 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2709 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[37891] It is appreciated that VGAM2709 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2709 host target genes. The mRNA of each one of this plurality of VGAM2709 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2709 RNA, herein designated VGAM RNA, and which when bound by VGAM2709 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2709 host target proteins.

[37892] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2709 gene, herein designated VGAM GENE, on one or more VGAM2709 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[37893] It is yet further appreciated that a function of VGAM2709 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2709 include diagnosis, prevention and treatment of viral infection by Heliothis zea virus 1 (HZV-1). Specific functions, and accordingly utilities, of VGAM2709 correlate with, and may be deduced from, the identity of the host target genes which VGAM2709 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[37894] Nucleotide sequences of the VGAM2709 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2709 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of

VGAM2709 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2709 are further described hereinbelow with reference to Table 1.

[37895] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2709 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[37896] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2710 (VGAM2710) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[37897] VGAM2710 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2710 was detected is described hereinabove with reference to Figs. 2-8.

[37898] VGAM2710 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Heliothis zea virus 1 (HZV-1). VGAM2710 host target gene, herein designated

VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[37899] VGAM2710 gene, herein designated VGAM GENE, encodes a VGAM2710 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2710 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2710 precursor RNA is designated SEQ ID:2696, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2696 is located at position 224367 relative to the genome of Heliothis zea virus 1 (HZV-1).

[37900] VGAM2710 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2710 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[37901] An enzyme complex designated DICER COMPLEX, dices the VGAM2710 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2710 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 74%) nucleotide sequence of VGAM2710 RNA is designated SEQ ID:5421, and is provided hereinbelow with reference to the sequence listing part.

[37902] VGAM2710 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2710 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2710 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[37903] VGAM2710 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM2710 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2710 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2710 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2710 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[37904] The complementary binding of VGAM2710 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM2710 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2710 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2710 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[37905] It is appreciated that VGAM2710 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2710 host target genes. The mRNA of each one of this plurality of VGAM2710 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2710 RNA, herein designated VGAM RNA, and which when bound by VGAM2710 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2710 host target proteins.

[37906] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2710 gene, herein designated VGAM GENE, on one or more VGAM2710 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[37907] It is yet further appreciated that a function of VGAM2710 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2710 include diagnosis, prevention and treatment of viral infection by Heliothis zea virus 1 (HZV-1). Specific functions, and accordingly utilities, of VGAM2710 correlate with, and may be deduced from, the identity of the host target genes which VGAM2710 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[37908] Nucleotide sequences of the VGAM2710 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

diced VGAM2710 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2710 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2710 are further described hereinbelow with reference to Table 1.

[37909] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2710 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[37910] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2711 (VGAM2711) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[37911] VGAM2711 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2711 was detected is described hereinabove with reference to Figs. 2-8.

[37912] VGAM2711 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of Chikungunya virus. VGAM2711 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[37913] VGAM2711 gene, herein designated VGAM GENE, encodes a VGAM2711 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2711 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2711 precursor RNA is designated SEQ ID:2697, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2697 is located at position 7022 relative to the genome of Chikungunya virus.

[37914] VGAM2711 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2711 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[37915] An enzyme complex designated DICER COMPLEX, dices the VGAM2711 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2711 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2711 RNA is designated SEQ ID:5422, and is provided hereinbelow with reference to the sequence listing part.

[37916] VGAM2711 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2711 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2711 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[37917] VGAM2711 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2711 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2711 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2711 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2711 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[37918] The complementary binding of VGAM2711 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM2711 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2711 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2711 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[37919] It is appreciated that VGAM2711 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2711 host target genes. The mRNA of each one of this plurality of VGAM2711 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2711 RNA, herein designated VGAM RNA, and which when bound by VGAM2711 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2711 host target proteins.

[37920] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2711 gene, herein designated VGAM GENE, on one or more VGAM2711 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[37921] It is yet further appreciated that a function of VGAM2711 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2711 include diagnosis, prevention and treatment of viral infection by Chikungunya virus. Specific functions, and accordingly utilities, of VGAM2711 correlate with, and may be deduced from, the identity of the host target genes which VGAM2711 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[37922] Nucleotide sequences of the VGAM2711 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the diced VGAM2711 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2711 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2711 are further described hereinbelow with reference to Table 1.

[37923] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2711 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[37924] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2712 (VGAM2712) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[37925] VGAM2712 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2712 was detected is described hereinabove with reference to Figs. 2-8.

[37926] VGAM2712 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Chikungunya virus. VGAM2712 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[37927] VGAM2712 gene, herein designated VGAM GENE, encodes a VGAM2712 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2712 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2712 precursor RNA is designated SEQ ID:2698, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2698 is located at position 2249 relative to the genome of Chikungunya virus.

[37928] VGAM2712 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2712 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[37929] An enzyme complex designated DICER COMPLEX, dices the VGAM2712 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2712 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 73%) nucleotide sequence of VGAM2712 RNA is designated SEQ ID:5423, and is provided hereinbelow with reference to the sequence listing part.

[37930] VGAM2712 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2712 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2712 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN COD-

ING and 3UTR respectively.

[37931] VGAM2712 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2712 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2712 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2712 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2712 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[37932] The complementary binding of VGAM2712 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2712 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2712 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2712 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[37933] It is appreciated that VGAM2712 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2712 host target genes. The mRNA of each one of this plurality of VGAM2712 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2712 RNA, herein designated VGAM RNA, and which when bound by VGAM2712 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2712 host target proteins.

[37934] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2712 gene, herein designated VGAM GENE, on one

or more VGAM2712 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[37935] It is yet further appreciated that a function of VGAM2712 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2712 include diagnosis, prevention and treatment of viral infection by Chikungunya virus. Specific functions, and accordingly utilities, of VGAM2712 correlate with, and may be deduced from, the identity of the host target genes which VGAM2712 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[37936] Nucleotide sequences of the VGAM2712 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2712 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2712 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2712 are further described hereinbelow with reference to Table 1.

[37937] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2712 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[37938] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2713 (VGAM2713) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[37939] VGAM2713 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2713 was detected is de-

scribed hereinabove with reference to Figs. 2-8.

[37940] VGAM2713 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mammalian orthoreovirus 2. VGAM2713 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[37941] VGAM2713 gene, herein designated VGAM GENE, encodes a VGAM2713 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2713 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2713 precursor RNA is designated SEQ ID:2699, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2699 is located at position 1472 relative to the genome of Mammalian orthoreovirus 2.

[37942] VGAM2713 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2713 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[37943] An enzyme complex designated DICER COMPLEX, dices the VGAM2713 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2713 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2713 RNA is designated SEQ ID:5424, and is provided hereinbelow with reference to the sequence listing part.

[37944] VGAM2713 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2713 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2713 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and

a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[37945] VGAM2713 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2713 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2713 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2713 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2713 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both

3UTR and 5UTR regions.

[37946] The complementary binding of VGAM2713 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2713 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2713 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2713 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[37947] It is appreciated that VGAM2713 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2713 host target genes. The mRNA of each one of this plurality of VGAM2713 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2713 RNA, herein designated VGAM RNA, and which when bound by VGAM2713 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2713 host target proteins.

[37948] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM2713 gene, herein designated VGAM GENE, on one or more VGAM2713 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[37949] It is yet further appreciated that a function of VGAM2713 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2713 include diagnosis, prevention and treatment of viral infection by Mammalian orthoreovirus 2. Specific functions, and accordingly utilities, of VGAM2713 correlate with, and may be deduced from, the identity of the host target genes which VGAM2713 binds and inhibits, and the function of these host target genes, as

elaborated hereinbelow.

[37950] Nucleotide sequences of the VGAM2713 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2713 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2713 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2713 are further described hereinbelow with reference to Table 1.

[37951] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2713 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[37952] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2714 (VGAM2714) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[37953] VGAM2714 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene.

The method by which VGAM2714 was detected is described hereinabove with reference to Figs. 2-8.

[37954] VGAM2714 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mammalian orthoreovirus 2. VGAM2714 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[37955] VGAM2714 gene, herein designated VGAM GENE, encodes a VGAM2714 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2714 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2714 precursor RNA is designated SEQ ID:2700, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2700 is located at position 1237 relative to the genome of Mammalian orthoreovirus 2.

[37956] VGAM2714 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2714 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[37957] An enzyme complex designated DICER COMPLEX, dices the VGAM2714 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2714 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 82%) nucleotide sequence of VGAM2714 RNA is designated SEQ ID:5425, and is provided hereinbelow with reference to the sequence listing part.

[37958] VGAM2714 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2714 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2714 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding

gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[37959] VGAM2714 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2714 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2714 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2714 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2714 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be lo-

cated in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[37960] The complementary binding of VGAM2714 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2714 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2714 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2714 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[37961] It is appreciated that VGAM2714 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2714 host target genes. The mRNA of each one of this plurality of VGAM2714 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2714 RNA, herein designated VGAM RNA, and which when bound by VGAM2714 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2714 host target proteins.

[37962] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM2714 gene, herein designated VGAM GENE, on one or more VGAM2714 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[37963] It is yet further appreciated that a function of VGAM2714 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2714 include diagnosis, prevention and treatment of viral infection by Mammalian orthoreovirus 2. Specific functions, and accordingly utilities, of VGAM2714 correlate with, and may be deduced from, the identity of the host target genes which VGAM2714 binds and in-

hibits, and the function of these host target genes, as elaborated hereinbelow.

[37964] Nucleotide sequences of the VGAM2714 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2714 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2714 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2714 are further described hereinbelow with reference to Table 1.

[37965] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2714 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[37966] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2715 (VGAM2715) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[37967] VGAM2715 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2715 was detected is described hereinabove with reference to Figs. 2-8.

[37968] VGAM2715 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mammalian orthoreovirus 2. VGAM2715 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[37969] VGAM2715 gene, herein designated VGAM GENE, encodes a VGAM2715 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2715 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2715 precursor RNA is designated SEQ ID:2701, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2701 is located at position 1891 relative to the genome of Mammalian orthoreovirus 2.

[37970] VGAM2715 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2715 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[37971] An enzyme complex designated DICER COMPLEX, dices the VGAM2715 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2715 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2715 RNA is designated SEQ ID:5426, and is provided hereinbelow with reference to the sequence listing part.

[37972] VGAM2715 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2715 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2715 host target RNA, herein designated VGAM HOST TARGET RNA, comprises

three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[37973] VGAM2715 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2715 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2715 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2715 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2715 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an

example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[37974] The complementary binding of VGAM2715 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2715 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2715 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2715 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[37975] It is appreciated that VGAM2715 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2715 host target genes. The mRNA of each one of this plurality of VGAM2715 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2715 RNA, herein designated VGAM RNA, and which when bound by VGAM2715 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2715 host target proteins.

[37976] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2715 gene, herein designated VGAM GENE, on one or more VGAM2715 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[37977] It is yet further appreciated that a function of VGAM2715 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2715 include diagnosis, prevention and treatment of viral infection by Mammalian orthoreovirus 2. Specific functions, and accordingly utilities, of VGAM2715 correlate with, and may be deduced from, the identity of

the host target genes which VGAM2715 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[37978] Nucleotide sequences of the VGAM2715 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2715 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2715 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2715 are further described hereinbelow with reference to Table 1.

[37979] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2715 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[37980] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2716 (VGAM2716) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[37981] VGAM2716 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2716 was detected is described hereinabove with reference to Figs. 2-8.

[37982] VGAM2716 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Tacaribe virus. VGAM2716 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[37983] VGAM2716 gene, herein designated VGAM GENE, encodes a VGAM2716 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2716 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2716 precursor RNA is designated SEQ ID:2702, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2702 is located at position 2511 relative to the genome of Tacaribe virus.

[37984] VGAM2716 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2716 folded precursor RNA, herein designated VGAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[37985] An enzyme complex designated DICER COMPLEX, dices the VGAM2716 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2716 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of VGAM2716 RNA is designated SEQ ID:5427, and is provided hereinbelow with reference to the sequence listing part.

[37986] VGAM2716 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2716 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2716 host target RNA,

herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[37987] VGAM2716 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2716 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2716 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2716 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2716 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host tar-

get binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[37988] The complementary binding of VGAM2716 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2716 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2716 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2716 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[37989] It is appreciated that VGAM2716 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2716 host target genes. The mRNA of each one of this plurality of VGAM2716 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2716 RNA, herein designated VGAM RNA, and which when bound by VGAM2716 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2716 host target proteins.

[37990] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2716 gene, herein designated VGAM GENE, on one or more VGAM2716 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[37991] It is yet further appreciated that a function of VGAM2716 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2716 include diagnosis, prevention and treatment of viral infection by Tacaribe virus. Specific functions, and accordingly utilities, of VGAM2716 corre-

late with, and may be deduced from, the identity of the host target genes which VGAM2716 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[37992] Nucleotide sequences of the VGAM2716 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2716 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2716 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2716 are further described hereinbelow with reference to Table 1.

[37993] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2716 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[37994] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2717 (VGAM2717) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the

art.

[37995] VGAM2717 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2717 was detected is described hereinabove with reference to Figs. 2-8.

[37996] VGAM2717 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rachiplusia ou multiple nucleopolyhedrovirus. VGAM2717 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[37997] VGAM2717 gene, herein designated VGAM GENE, encodes a VGAM2717 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2717 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2717 precursor RNA is designated SEQ ID:2703, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2703 is located at position 55572 relative to the genome of Rachiplusia ou multiple nucleopolyhedrovirus.

[37998] VGAM2717 precursor RNA, herein designated VGAM PRE-

CURSOR RNA, folds onto itself, forming VGAM2717 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[37999] An enzyme complex designated DICER COMPLEX, dices the VGAM2717 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2717 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2717 RNA is designated SEQ ID:5428, and is provided hereinbelow with reference to the sequence listing part.

[38000] VGAM2717 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM2717 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2717 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[38001] VGAM2717 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2717 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2717 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2717 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2717 host

target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[38002] The complementary binding of VGAM2717 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2717 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2717 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2717 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[38003] It is appreciated that VGAM2717 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2717 host target genes. The mRNA of each one of this plurality of VGAM2717 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2717 RNA, herein designated VGAM RNA, and which when bound by VGAM2717 RNA, herein

designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2717 host target proteins.

[38004] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2717 gene, herein designated VGAM GENE, on one or more VGAM2717 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[38005] It is yet further appreciated that a function of VGAM2717 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2717 include diagnosis, prevention and

treatment of viral infection by Rachiplusia ou multiple nucleopolyhedrovirus. Specific functions, and accordingly utilities, of VGAM2717 correlate with, and may be deduced from, the identity of the host target genes which VGAM2717 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[38006] Nucleotide sequences of the VGAM2717 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2717 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2717 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2717 are further described hereinbelow with reference to Table 1.

[38007] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2717 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[38008] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2718 (VGAM2718) viral gene, which modulates ex-

pression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[38009] VGAM2718 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2718 was detected is described hereinabove with reference to Figs. 2-8.

[38010] VGAM2718 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rachiplusia ou multiple nucleopolyhedrovirus. VGAM2718 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[38011] VGAM2718 gene, herein designated VGAM GENE, encodes a VGAM2718 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2718 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2718 precursor RNA is designated SEQ ID:2704, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2704 is located at position 55389 relative to the genome of Rachiplusia ou multiple

nucleopolyhedrovirus.

[38012] VGAM2718 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2718 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[38013] An enzyme complex designated DICER COMPLEX, dices the VGAM2718 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2718 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 56%) nucleotide sequence of VGAM2718 RNA is designated SEQ ID:5429, and is provided hereinbelow with reference to the sequence listing part.

[38014] VGAM2718 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2718 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2718 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[38015] VGAM2718 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2718 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2718 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2718 RNA, herein designated

VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2718 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[38016] The complementary binding of VGAM2718 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2718 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2718 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2718 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[38017] It is appreciated that VGAM2718 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2718 host target genes. The mRNA of each one of this plurality of VGAM2718 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM2718 RNA, herein designated VGAM RNA, and which when bound by VGAM2718 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2718 host target proteins.

[38018] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2718 gene, herein designated VGAM GENE, on one or more VGAM2718 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[38019] It is yet further appreciated that a function of VGAM2718 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2718 include diagnosis, prevention and treatment of viral infection by Rachiplusia ou multiple nucleopolyhedrovirus. Specific functions, and accordingly utilities, of VGAM2718 correlate with, and may be deduced from, the identity of the host target genes which VGAM2718 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[38020] Nucleotide sequences of the VGAM2718 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2718 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2718 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2718 are further described hereinbelow with reference to Table 1.

[38021] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2718 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[38022] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present

invention, referred to here as Viral Genomic Address Messenger 2719 (VGAM2719) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[38023] VGAM2719 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2719 was detected is described hereinabove with reference to Figs. 2-8.

[38024] VGAM2719 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Aphid lethal paralysis virus. VGAM2719 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[38025] VGAM2719 gene, herein designated VGAM GENE, encodes a VGAM2719 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2719 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2719 precursor RNA is designated SEQ ID:2705, and is provided hereinbelow with reference to the sequence listing part. Nu-

cleotide sequence SEQ ID:2705 is located at position 5960 relative to the genome of Aphid lethal paralysis virus.

[38026] VGAM2719 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2719 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[38027] An enzyme complex designated DICER COMPLEX, dices the VGAM2719 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2719 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 57%) nucleotide sequence of VGAM2719 RNA is designated SEQ ID:5430, and is provided hereinbelow with reference to the sequence

listing part.

[38028] VGAM2719 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2719 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2719 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[38029] VGAM2719 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2719 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2719 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not

meant to be limiting VGAM2719 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2719 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[38030] The complementary binding of VGAM2719 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2719 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2719 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2719 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[38031] It is appreciated that VGAM2719 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2719 host target genes. The mRNA of each one of this plurality of VGAM2719 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2719 RNA, herein designated VGAM RNA, and which when bound by VGAM2719 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2719 host target proteins.

[38032] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2719 gene, herein designated VGAM GENE, on one or more VGAM2719 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[38033] It is yet further appreciated that a function of VGAM2719

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2719 include diagnosis, prevention and treatment of viral infection by Aphid lethal paralysis virus. Specific functions, and accordingly utilities, of VGAM2719 correlate with, and may be deduced from, the identity of the host target genes which VGAM2719 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[38034] Nucleotide sequences of the VGAM2719 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2719 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2719 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2719 are further described hereinbelow with reference to Table 1.

[38035] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2719 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[38036] Fig. 1 further provides a conceptual description of another

novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2720 (VGAM2720) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[38037] VGAM2720 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2720 was detected is described hereinabove with reference to Figs. 2-8.

[38038] VGAM2720 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Aphid lethal paralysis virus. VGAM2720 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[38039] VGAM2720 gene, herein designated VGAM GENE, encodes a VGAM2720 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2720 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2720 precursor RNA is designated SEQ ID:2706, and is provided here-

inbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2706 is located at position 4386 relative to the genome of Aphid lethal paralysis virus.

[38040] VGAM2720 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2720 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[38041] An enzyme complex designated DICER COMPLEX, dices the VGAM2720 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2720 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2720 RNA is designated SEQ ID:5431, and

is provided hereinbelow with reference to the sequence listing part.

[38042] VGAM2720 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2720 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2720 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[38043] VGAM2720 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2720 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2720 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites

shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2720 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2720 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[38044] The complementary binding of VGAM2720 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2720 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2720 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2720 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[38045] It is appreciated that VGAM2720 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2720 host target genes. The mRNA of each one of this plurality of VGAM2720 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2720 RNA, herein designated VGAM RNA, and which when bound by VGAM2720 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2720 host target proteins.

[38046] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2720 gene, herein designated VGAM GENE, on one or more VGAM2720 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[38047] It is yet further appreciated that a function of VGAM2720 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2720 include diagnosis, prevention and treatment of viral infection by Aphid lethal paralysis virus. Specific functions, and accordingly utilities, of VGAM2720 correlate with, and may be deduced from, the identity of the host target genes which VGAM2720 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[38048] Nucleotide sequences of the VGAM2720 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2720 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2720 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2720 are further described hereinbelow with reference to Table 1.

[38049] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2720 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[38050] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2721 (VGAM2721) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[38051] VGAM2721 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2721 was detected is described hereinabove with reference to Figs. 2-8.

[38052] VGAM2721 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Aphid lethal paralysis virus. VGAM2721 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[38053] VGAM2721 gene, herein designated VGAM GENE, encodes a VGAM2721 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2721 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2721 precur-

sor RNA is designated SEQ ID:2707, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2707 is located at position 3755 relative to the genome of Aphid lethal paralysis virus.

[38054] VGAM2721 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2721 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[38055] An enzyme complex designated DICER COMPLEX, dices the VGAM2721 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2721 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide se-

quence of VGAM2721 RNA is designated SEQ ID:5432, and is provided hereinbelow with reference to the sequence listing part.

[38056] VGAM2721 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2721 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2721 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[38057] VGAM2721 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2721 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2721 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is ap-

preciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2721 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2721 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[38058] The complementary binding of VGAM2721 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2721 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2721 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2721 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[38059] It is appreciated that VGAM2721 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2721 host target genes. The mRNA of

each one of this plurality of VGAM2721 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2721 RNA, herein designated VGAM RNA, and which when bound by VGAM2721 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2721 host target proteins.

[38060] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2721 gene, herein designated VGAM GENE, on one or more VGAM2721 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science

294,779 (2001)).

[38061] It is yet further appreciated that a function of VGAM2721 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2721 include diagnosis, prevention and treatment of viral infection by Aphid lethal paralysis virus. Specific functions, and accordingly utilities, of VGAM2721 correlate with, and may be deduced from, the identity of the host target genes which VGAM2721 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[38062] Nucleotide sequences of the VGAM2721 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2721 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2721 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2721 are further described hereinbelow with reference to Table 1.

[38063] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2721 RNA, herein designated VGAM RNA, are de-

scribed hereinbelow with reference to Table 2.

[38064] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2722 (VGAM2722) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[38065] VGAM2722 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2722 was detected is described hereinabove with reference to Figs. 2-8.

[38066] VGAM2722 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Aphid lethal paralysis virus. VGAM2722 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[38067] VGAM2722 gene, herein designated VGAM GENE, encodes a VGAM2722 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2722 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly

similar to the nucleotide sequence of VGAM2722 precursor RNA is designated SEQ ID:2708, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2708 is located at position 5202 relative to the genome of Aphid lethal paralysis virus.

[38068] VGAM2722 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2722 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[38069] An enzyme complex designated DICER COMPLEX, dices the VGAM2722 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2722 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 81%) nucleotide sequence of VGAM2722 RNA is designated SEQ ID:5433, and is provided hereinbelow with reference to the sequence listing part.

[38070] VGAM2722 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2722 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2722 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[38071] VGAM2722 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2722 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2722 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I,

BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2722 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2722 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[38072] The complementary binding of VGAM2722 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2722 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2722 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2722 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[38073] It is appreciated that VGAM2722 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM2722 host target genes. The mRNA of each one of this plurality of VGAM2722 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2722 RNA, herein designated VGAM RNA, and which when bound by VGAM2722 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2722 host target proteins.

[38074] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2722 gene, herein designated VGAM GENE, on one or more VGAM2722 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[38075] It is yet further appreciated that a function of VGAM2722 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2722 include diagnosis, prevention and treatment of viral infection by Aphid lethal paralysis virus. Specific functions, and accordingly utilities, of VGAM2722 correlate with, and may be deduced from, the identity of the host target genes which VGAM2722 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[38076] Nucleotide sequences of the VGAM2722 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2722 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2722 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2722 are further described hereinbelow with reference to Table 1.

[38077] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites

to VGAM2722 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[38078] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2723 (VGAM2723) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[38079] VGAM2723 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2723 was detected is described hereinabove with reference to Figs. 2-8.

[38080] VGAM2723 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Aphid lethal paralysis virus. VGAM2723 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[38081] VGAM2723 gene, herein designated VGAM GENE, encodes a VGAM2723 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2723 precursor RNA, herein designated VGAM PRECURSOR RNA, does not en-

code a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2723 precursor RNA is designated SEQ ID:2709, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2709 is located at position 3973 relative to the genome of Aphid lethal paralysis virus.

[38082] VGAM2723 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2723 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[38083] An enzyme complex designated DICER COMPLEX, dices the VGAM2723 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2723 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2723 RNA is designated SEQ ID:5434, and is provided hereinbelow with reference to the sequence listing part.

[38084] VGAM2723 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2723 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2723 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[38085] VGAM2723 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2723 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2723 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3

such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2723 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2723 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[38086] The complementary binding of VGAM2723 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2723 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2723 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2723 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[38087] It is appreciated that VGAM2723 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2723 host target genes. The mRNA of each one of this plurality of VGAM2723 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2723 RNA, herein designated VGAM RNA, and which when bound by VGAM2723 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2723 host target proteins.

[38088] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2723 gene, herein designated VGAM GENE, on one or more VGAM2723 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[38089] It is yet further appreciated that a function of VGAM2723 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2723 include diagnosis, prevention and treatment of viral infection by Aphid lethal paralysis virus. Specific functions, and accordingly utilities, of VGAM2723 correlate with, and may be deduced from, the identity of the host target genes which VGAM2723 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[38090] Nucleotide sequences of the VGAM2723 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2723 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2723 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2723 are further described hereinbelow with reference to Table 1.

[38091] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the

complementarity of each of these host target binding sites to VGAM2723 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[38092] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2724 (VGAM2724) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[38093] VGAM2724 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2724 was detected is described hereinabove with reference to Figs. 2-8.

[38094] VGAM2724 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Aphid lethal paralysis virus. VGAM2724 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[38095] VGAM2724 gene, herein designated VGAM GENE, encodes a VGAM2724 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2724 precursor RNA,

herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2724 precursor RNA is designated SEQ ID:2710, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2710 is located at position 1635 relative to the genome of Aphid lethal paralysis virus.

[38096] VGAM2724 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2724 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[38097] An enzyme complex designated DICER COMPLEX, dices the VGAM2724 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2724 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2724 RNA is designated SEQ ID:5435, and is provided hereinbelow with reference to the sequence listing part.

[38098] VGAM2724 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2724 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2724 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[38099] VGAM2724 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2724 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2724 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host

target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2724 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2724 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[38100] The complementary binding of VGAM2724 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2724 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2724 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2724 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[38101] It is appreciated that VGAM2724 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2724 host target genes. The mRNA of each one of this plurality of VGAM2724 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2724 RNA, herein designated VGAM RNA, and which when bound by VGAM2724 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2724 host target proteins.

[38102] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2724 gene, herein designated VGAM GENE, on one or more VGAM2724 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[38103] It is yet further appreciated that a function of VGAM2724 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2724 include diagnosis, prevention and treatment of viral infection by Aphid lethal paralysis virus. Specific functions, and accordingly utilities, of VGAM2724 correlate with, and may be deduced from, the identity of the host target genes which VGAM2724 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[38104] Nucleotide sequences of the VGAM2724 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2724 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2724 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2724 are further described hereinbelow with reference to Table 1.

[38105] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2724 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[38106] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2725 (VGAM2725) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[38107] VGAM2725 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2725 was detected is described hereinabove with reference to Figs. 2-8.

[38108] VGAM2725 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Aphid lethal paralysis virus. VGAM2725 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[38109] VGAM2725 gene, herein designated VGAM GENE, encodes a VGAM2725 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and un-

like most ordinary genes, VGAM2725 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2725 precursor RNA is designated SEQ ID:2711, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2711 is located at position 4120 relative to the genome of Aphid lethal paralysis virus.

[38110] VGAM2725 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2725 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[38111] An enzyme complex designated DICER COMPLEX, dices the VGAM2725 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2725 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 55%) nucleotide sequence of VGAM2725 RNA is designated SEQ ID:5436, and is provided hereinbelow with reference to the sequence listing part.

[38112] VGAM2725 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2725 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2725 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[38113] VGAM2725 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2725 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2725 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed

sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2725 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2725 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[38114] The complementary binding of VGAM2725 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2725 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2725 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2725 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target

protein is therefore outlined by a broken line.

[38115] It is appreciated that VGAM2725 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2725 host target genes. The mRNA of each one of this plurality of VGAM2725 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2725 RNA, herein designated VGAM RNA, and which when bound by VGAM2725 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2725 host target proteins.

[38116] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2725 gene, herein designated VGAM GENE, on one or more VGAM2725 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[38117] It is yet further appreciated that a function of VGAM2725 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2725 include diagnosis, prevention and treatment of viral infection by Aphid lethal paralysis virus. Specific functions, and accordingly utilities, of VGAM2725 correlate with, and may be deduced from, the identity of the host target genes which VGAM2725 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[38118] Nucleotide sequences of the VGAM2725 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2725 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2725 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2725 are further described hereinbelow with reference to Table 1.

[38119] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2725 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[38120] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2726 (VGAM2726) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[38121] VGAM2726 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2726 was detected is described hereinabove with reference to Figs. 2-8.

[38122] VGAM2726 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Aphid lethal paralysis virus. VGAM2726 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[38123] VGAM2726 gene, herein designated VGAM GENE, encodes a VGAM2726 precursor RNA, herein designated VGAM

PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2726 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2726 precursor RNA is designated SEQ ID:2712, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2712 is located at position 3591 relative to the genome of Aphid lethal paralysis virus.

[38124] VGAM2726 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2726 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[38125] An enzyme complex designated DICER COMPLEX, dices the VGAM2726 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2726 RNA, herein designated VGAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2726 RNA is designated SEQ ID:5437, and is provided hereinbelow with reference to the sequence listing part.

[38126] VGAM2726 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2726 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2726 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[38127] VGAM2726 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2726 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2726 RNA, herein designated

VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2726 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2726 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[38128] The complementary binding of VGAM2726 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2726 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2726 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2726 host target protein, herein desig-

nated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[38129] It is appreciated that VGAM2726 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2726 host target genes. The mRNA of each one of this plurality of VGAM2726 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2726 RNA, herein designated VGAM RNA, and which when bound by VGAM2726 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2726 host target proteins.

[38130] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2726 gene, herein designated VGAM GENE, on one or more VGAM2726 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[38131] It is yet further appreciated that a function of VGAM2726 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2726 include diagnosis, prevention and treatment of viral infection by Aphid lethal paralysis virus. Specific functions, and accordingly utilities, of VGAM2726 correlate with, and may be deduced from, the identity of the host target genes which VGAM2726 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[38132] Nucleotide sequences of the VGAM2726 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2726 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2726 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2726 are further described hereinbelow with reference to Table 1.

[38133] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2726 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[38134] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2727 (VGAM2727) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[38135] VGAM2727 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2727 was detected is described hereinabove with reference to Figs. 2-8.

[38136] VGAM2727 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Aphid lethal paralysis virus. VGAM2727 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[38137] VGAM2727 gene, herein designated VGAM GENE, encodes

a VGAM2727 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2727 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2727 precursor RNA is designated SEQ ID:2713, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2713 is located at position 4727 relative to the genome of Aphid lethal paralysis virus.

[38138] VGAM2727 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2727 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[38139] An enzyme complex designated DICER COMPLEX, dices the VGAM2727 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2727 RNA,

herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 54%) nucleotide sequence of VGAM2727 RNA is designated SEQ ID:5438, and is provided hereinbelow with reference to the sequence listing part.

[38140] VGAM2727 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2727 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2727 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[38141] VGAM2727 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2727 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM2727 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2727 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2727 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[38142] The complementary binding of VGAM2727 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2727 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2727 host target RNA, herein designated VGAM HOST TARGET

RNA, into VGAM2727 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[38143] It is appreciated that VGAM2727 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2727 host target genes. The mRNA of each one of this plurality of VGAM2727 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2727 RNA, herein designated VGAM RNA, and which when bound by VGAM2727 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2727 host target proteins.

[38144] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2727 gene, herein designated VGAM GENE, on one or more VGAM2727 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[38145] It is yet further appreciated that a function of VGAM2727 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2727 include diagnosis, prevention and treatment of viral infection by Aphid lethal paralysis virus. Specific functions, and accordingly utilities, of VGAM2727 correlate with, and may be deduced from, the identity of the host target genes which VGAM2727 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[38146] Nucleotide sequences of the VGAM2727 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2727 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2727 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2727 are further

described hereinbelow with reference to Table 1.

[38147] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2727 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[38148] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2728 (VGAM2728) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[38149] VGAM2728 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2728 was detected is described hereinabove with reference to Figs. 2-8.

[38150] VGAM2728 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Aphid lethal paralysis virus. VGAM2728 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[38151] VGAM2728 gene, herein designated VGAM GENE, encodes a VGAM2728 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2728 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2728 precursor RNA is designated SEQ ID:2714, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2714 is located at position 7888 relative to the genome of Aphid lethal paralysis virus.

[38152] VGAM2728 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2728 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[38153] An enzyme complex designated DICER COMPLEX, dices the VGAM2728 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, into VGAM2728 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide sequence of VGAM2728 RNA is designated SEQ ID:5439, and is provided hereinbelow with reference to the sequence listing part.

[38154] VGAM2728 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2728 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2728 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[38155] VGAM2728 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2728 host target RNA, herein designated VGAM HOST TARGET RNA. This

complementary binding is due to the fact that the nucleotide sequence of VGAM2728 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2728 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2728 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[38156] The complementary binding of VGAM2728 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2728 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2728

host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2728 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[38157] It is appreciated that VGAM2728 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2728 host target genes. The mRNA of each one of this plurality of VGAM2728 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2728 RNA, herein designated VGAM RNA, and which when bound by VGAM2728 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2728 host target proteins.

[38158] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2728 gene, herein designated VGAM GENE, on one or more VGAM2728 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[38159] It is yet further appreciated that a function of VGAM2728 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2728 include diagnosis, prevention and treatment of viral infection by Aphid lethal paralysis virus. Specific functions, and accordingly utilities, of VGAM2728 correlate with, and may be deduced from, the identity of the host target genes which VGAM2728 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[38160] Nucleotide sequences of the VGAM2728 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2728 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2728 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM2728 are further described hereinbelow with reference to Table 1.

[38161] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2728 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[38162] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2729 (VGAM2729) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[38163] VGAM2729 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2729 was detected is described hereinabove with reference to Figs. 2-8.

[38164] VGAM2729 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Aphid lethal paralysis virus. VGAM2729 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in

the human genome.

[38165] VGAM2729 gene, herein designated VGAM GENE, encodes a VGAM2729 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2729 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2729 precursor RNA is designated SEQ ID:2715, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2715 is located at position 7811 relative to the genome of Aphid lethal paralysis virus.

[38166] VGAM2729 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2729 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[38167] An enzyme complex designated DICER COMPLEX, dices

the VGAM2729 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2729 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2729 RNA is designated SEQ ID:5440, and is provided hereinbelow with reference to the sequence listing part.

[38168] VGAM2729 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2729 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2729 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[38169] VGAM2729 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2729 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2729 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2729 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2729 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[38170] The complementary binding of VGAM2729 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2729 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM2729 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2729 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[38171] It is appreciated that VGAM2729 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2729 host target genes. The mRNA of each one of this plurality of VGAM2729 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2729 RNA, herein designated VGAM RNA, and which when bound by VGAM2729 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2729 host target proteins.

[38172] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2729 gene, herein designated VGAM GENE, on one or more VGAM2729 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[38173] It is yet further appreciated that a function of VGAM2729 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2729 include diagnosis, prevention and treatment of viral infection by Aphid lethal paralysis virus. Specific functions, and accordingly utilities, of VGAM2729 correlate with, and may be deduced from, the identity of the host target genes which VGAM2729 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[38174] Nucleotide sequences of the VGAM2729 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2729 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of

VGAM2729 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2729 are further described hereinbelow with reference to Table 1.

[38175] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2729 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[38176] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2730 (VGAM2730) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[38177] VGAM2730 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2730 was detected is described hereinabove with reference to Figs. 2-8.

[38178] VGAM2730 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Callitrichine herpesvirus 3. VGAM2730 host target gene, herein designated VGAM

HOST TARGET GENE, is a human gene contained in the human genome.

[38179] VGAM2730 gene, herein designated VGAM GENE, encodes a VGAM2730 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2730 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2730 precursor RNA is designated SEQ ID:2716, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2716 is located at position 95914 relative to the genome of Callitrichine herpesvirus 3.

[38180] VGAM2730 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2730 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[38181] An enzyme complex designated DICER COMPLEX, dices the VGAM2730 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2730 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2730 RNA is designated SEQ ID:5441, and is provided hereinbelow with reference to the sequence listing part.

[38182] VGAM2730 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2730 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2730 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[38183] VGAM2730 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM2730 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2730 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2730 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2730 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[38184] The complementary binding of VGAM2730 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM2730 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2730 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2730 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[38185] It is appreciated that VGAM2730 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2730 host target genes. The mRNA of each one of this plurality of VGAM2730 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2730 RNA, herein designated VGAM RNA, and which when bound by VGAM2730 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2730 host target proteins.

[38186] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2730 gene, herein designated VGAM GENE, on one or more VGAM2730 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[38187] It is yet further appreciated that a function of VGAM2730 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2730 include diagnosis, prevention and treatment of viral infection by Callitrichine herpesvirus 3. Specific functions, and accordingly utilities, of VGAM2730 correlate with, and may be deduced from, the identity of the host target genes which VGAM2730 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[38188] Nucleotide sequences of the VGAM2730 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

diced VGAM2730 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2730 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2730 are further described hereinbelow with reference to Table 1.

[38189] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2730 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[38190] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2731 (VGAM2731) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[38191] VGAM2731 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2731 was detected is described hereinabove with reference to Figs. 2-8.

[38192] VGAM2731 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of Callitrichine herpesvirus 3. VGAM2731 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[38193] VGAM2731 gene, herein designated VGAM GENE, encodes a VGAM2731 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2731 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2731 precursor RNA is designated SEQ ID:2717, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2717 is located at position 96552 relative to the genome of Callitrichine herpesvirus 3.

[38194] VGAM2731 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2731 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[38195] An enzyme complex designated DICER COMPLEX, dices the VGAM2731 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2731 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 76%) nucleotide sequence of VGAM2731 RNA is designated SEQ ID:5442, and is provided hereinbelow with reference to the sequence listing part.

[38196] VGAM2731 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2731 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2731 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN COD-

ING and 3UTR respectively.

[38197] VGAM2731 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2731 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2731 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2731 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2731 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[38198] The complementary binding of VGAM2731 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2731 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2731 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2731 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[38199] It is appreciated that VGAM2731 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2731 host target genes. The mRNA of each one of this plurality of VGAM2731 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2731 RNA, herein designated VGAM RNA, and which when bound by VGAM2731 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2731 host target proteins.

[38200] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2731 gene, herein designated VGAM GENE, on one

or more VGAM2731 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[38201] It is yet further appreciated that a function of VGAM2731 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2731 include diagnosis, prevention and treatment of viral infection by Callitrichine herpesvirus 3. Specific functions, and accordingly utilities, of VGAM2731 correlate with, and may be deduced from, the identity of the host target genes which VGAM2731 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[38202] Nucleotide sequences of the VGAM2731 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2731 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2731 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2731 are further described hereinbelow with reference to Table 1.

[38203] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2731 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[38204] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2732 (VGAM2732) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[38205] VGAM2732 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2732 was detected is de-

scribed hereinabove with reference to Figs. 2-8.

[38206] VGAM2732 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Callitrichine herpesvirus 3. VGAM2732 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[38207] VGAM2732 gene, herein designated VGAM GENE, encodes a VGAM2732 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2732 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2732 precursor RNA is designated SEQ ID:2718, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2718 is located at position 136708 relative to the genome of Callitrichine herpesvirus 3.

[38208] VGAM2732 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2732 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[38209] An enzyme complex designated DICER COMPLEX, dices the VGAM2732 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2732 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2732 RNA is designated SEQ ID:5443, and is provided hereinbelow with reference to the sequence listing part.

[38210] VGAM2732 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2732 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2732 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding

gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[38211] VGAM2732 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2732 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2732 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2732 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2732 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be lo-

cated in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[38212] The complementary binding of VGAM2732 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2732 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2732 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2732 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[38213] It is appreciated that VGAM2732 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2732 host target genes. The mRNA of each one of this plurality of VGAM2732 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2732 RNA, herein designated VGAM RNA, and which when bound by VGAM2732 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2732 host target proteins.

[38214] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM2732 gene, herein designated VGAM GENE, on one or more VGAM2732 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[38215] It is yet further appreciated that a function of VGAM2732 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2732 include diagnosis, prevention and treatment of viral infection by Callitrichine herpesvirus 3. Specific functions, and accordingly utilities, of VGAM2732 correlate with, and may be deduced from, the identity of the host target genes which VGAM2732 binds and in-

hibits, and the function of these host target genes, as elaborated hereinbelow.

[38216] Nucleotide sequences of the VGAM2732 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2732 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2732 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2732 are further described hereinbelow with reference to Table 1.

[38217] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2732 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[38218] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2733 (VGAM2733) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[38219] VGAM2733 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2733 was detected is described hereinabove with reference to Figs. 2-8.

[38220] VGAM2733 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Broad bean necrosis virus. VGAM2733 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[38221] VGAM2733 gene, herein designated VGAM GENE, encodes a VGAM2733 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2733 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2733 precursor RNA is designated SEQ ID:2719, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2719 is located at position 1316 relative to the genome of Broad bean necrosis virus.

[38222] VGAM2733 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2733 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[38223] An enzyme complex designated DICER COMPLEX, dices the VGAM2733 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2733 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide sequence of VGAM2733 RNA is designated SEQ ID:5444, and is provided hereinbelow with reference to the sequence listing part.

[38224] VGAM2733 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2733 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2733 host target RNA, herein designated VGAM HOST TARGET RNA, comprises

three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[38225] VGAM2733 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2733 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2733 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2733 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2733 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an

example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[38226] The complementary binding of VGAM2733 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2733 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2733 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2733 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[38227] It is appreciated that VGAM2733 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2733 host target genes. The mRNA of each one of this plurality of VGAM2733 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2733 RNA, herein designated VGAM RNA, and which when bound by VGAM2733 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2733 host target proteins.

[38228] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2733 gene, herein designated VGAM GENE, on one or more VGAM2733 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[38229] It is yet further appreciated that a function of VGAM2733 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2733 include diagnosis, prevention and treatment of viral infection by Broad bean necrosis virus. Specific functions, and accordingly utilities, of VGAM2733 correlate with, and may be deduced from, the identity of

the host target genes which VGAM2733 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[38230] Nucleotide sequences of the VGAM2733 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2733 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2733 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2733 are further described hereinbelow with reference to Table 1.

[38231] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2733 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[38232] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2734 (VGAM2734) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[38233] VGAM2734 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2734 was detected is described hereinabove with reference to Figs. 2-8.

[38234] VGAM2734 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Broad bean necrosis virus. VGAM2734 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[38235] VGAM2734 gene, herein designated VGAM GENE, encodes a VGAM2734 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2734 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2734 precursor RNA is designated SEQ ID:2720, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2720 is located at position 3664 relative to the genome of Broad bean necrosis virus.

[38236] VGAM2734 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2734 folded precursor RNA, herein designated VGAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[38237] An enzyme complex designated DICER COMPLEX, dices the VGAM2734 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2734 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 88%) nucleotide sequence of VGAM2734 RNA is designated SEQ ID:5445, and is provided hereinbelow with reference to the sequence listing part.

[38238] VGAM2734 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2734 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2734 host target RNA,

herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[38239] VGAM2734 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2734 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2734 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2734 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2734 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host tar-

get binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[38240] The complementary binding of VGAM2734 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2734 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2734 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2734 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[38241] It is appreciated that VGAM2734 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2734 host target genes. The mRNA of each one of this plurality of VGAM2734 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2734 RNA, herein designated VGAM RNA, and which when bound by VGAM2734 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2734 host target proteins.

[38242] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2734 gene, herein designated VGAM GENE, on one or more VGAM2734 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[38243] It is yet further appreciated that a function of VGAM2734 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2734 include diagnosis, prevention and treatment of viral infection by Broad bean necrosis virus. Specific functions, and accordingly utilities, of VGAM2734

correlate with, and may be deduced from, the identity of the host target genes which VGAM2734 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[38244] Nucleotide sequences of the VGAM2734 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2734 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2734 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2734 are further described hereinbelow with reference to Table 1.

[38245] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2734 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[38246] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2735 (VGAM2735) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the

art.

[38247] VGAM2735 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2735 was detected is described hereinabove with reference to Figs. 2-8.

[38248] VGAM2735 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Broad bean necrosis virus. VGAM2735 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[38249] VGAM2735 gene, herein designated VGAM GENE, encodes a VGAM2735 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2735 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2735 precursor RNA is designated SEQ ID:2721, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2721 is located at position 2997 relative to the genome of Broad bean necrosis virus.

[38250] VGAM2735 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2735 folded

precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[38251] An enzyme complex designated DICER COMPLEX, dices the VGAM2735 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2735 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2735 RNA is designated SEQ ID:5446, and is provided hereinbelow with reference to the sequence listing part.

[38252] VGAM2735 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2735 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM2735 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[38253] VGAM2735 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2735 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2735 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2735 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2735 host target RNA, herein designated VGAM HOST TARGET RNA.

It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[38254] The complementary binding of VGAM2735 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2735 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2735 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2735 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[38255] It is appreciated that VGAM2735 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2735 host target genes. The mRNA of each one of this plurality of VGAM2735 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2735 RNA, herein designated VGAM RNA, and which when bound by VGAM2735 RNA, herein designated VGAM RNA, causes inhibition of translation of

respective one or more VGAM2735 host target proteins.

[38256] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2735 gene, herein designated VGAM GENE, on one or more VGAM2735 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[38257] It is yet further appreciated that a function of VGAM2735 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2735 include diagnosis, prevention and treatment of viral infection by Broad bean necrosis virus.

Specific functions, and accordingly utilities, of VGAM2735 correlate with, and may be deduced from, the identity of the host target genes which VGAM2735 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[38258] Nucleotide sequences of the VGAM2735 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2735 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2735 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2735 are further described hereinbelow with reference to Table 1.

[38259] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2735 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[38260] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2736 (VGAM2736) viral gene, which modulates expression of respective host target genes thereof, the func-

tion and utility of which host target genes is known in the art.

[38261] VGAM2736 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2736 was detected is described hereinabove with reference to Figs. 2-8.

[38262] VGAM2736 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Broad bean necrosis virus. VGAM2736 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[38263] VGAM2736 gene, herein designated VGAM GENE, encodes a VGAM2736 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2736 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2736 precursor RNA is designated SEQ ID:2722, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2722 is located at position 2155 relative to the genome of Broad bean necrosis virus.

[38264] VGAM2736 precursor RNA, herein designated VGAM PRE-

CURSOR RNA, folds onto itself, forming VGAM2736 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[38265] An enzyme complex designated DICER COMPLEX, dices the VGAM2736 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2736 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2736 RNA is designated SEQ ID:5447, and is provided hereinbelow with reference to the sequence listing part.

[38266] VGAM2736 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM2736 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2736 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[38267] VGAM2736 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2736 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2736 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2736 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2736 host

target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[38268] The complementary binding of VGAM2736 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2736 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2736 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2736 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[38269] It is appreciated that VGAM2736 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2736 host target genes. The mRNA of each one of this plurality of VGAM2736 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2736 RNA, herein designated VGAM RNA, and which when bound by VGAM2736 RNA, herein

designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2736 host target proteins.

[38270] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2736 gene, herein designated VGAM GENE, on one or more VGAM2736 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[38271] It is yet further appreciated that a function of VGAM2736 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2736 include diagnosis, prevention and

treatment of viral infection by Broad bean necrosis virus. Specific functions, and accordingly utilities, of VGAM2736 correlate with, and may be deduced from, the identity of the host target genes which VGAM2736 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[38272] Nucleotide sequences of the VGAM2736 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2736 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2736 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2736 are further described hereinbelow with reference to Table 1.

[38273] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2736 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[38274] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2737 (VGAM2737) viral gene, which modulates ex-

pression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[38275] VGAM2737 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2737 was detected is described hereinabove with reference to Figs. 2-8.

[38276] VGAM2737 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Broad bean necrosis virus. VGAM2737 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[38277] VGAM2737 gene, herein designated VGAM GENE, encodes a VGAM2737 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2737 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2737 precursor RNA is designated SEQ ID:2723, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2723 is located at position 4765 relative to the genome of Broad bean necrosis virus.

[38278] VGAM2737 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2737 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[38279] An enzyme complex designated DICER COMPLEX, dices the VGAM2737 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2737 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2737 RNA is designated SEQ ID:5448, and is provided hereinbelow with reference to the sequence listing part.

[38280] VGAM2737 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2737 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2737 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[38281] VGAM2737 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2737 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2737 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2737 RNA, herein designated VGAM RNA, may have a different number of host target

binding sites in untranslated regions of a VGAM2737 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[38282] The complementary binding of VGAM2737 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2737 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2737 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2737 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[38283] It is appreciated that VGAM2737 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2737 host target genes. The mRNA of each one of this plurality of VGAM2737 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2737 RNA, herein designated VGAM

RNA, and which when bound by VGAM2737 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2737 host target proteins.

[38284] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2737 gene, herein designated VGAM GENE, on one or more VGAM2737 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[38285] It is yet further appreciated that a function of VGAM2737 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM2737 include diagnosis, prevention and treatment of viral infection by Broad bean necrosis virus. Specific functions, and accordingly utilities, of VGAM2737 correlate with, and may be deduced from, the identity of the host target genes which VGAM2737 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[38286] Nucleotide sequences of the VGAM2737 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2737 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2737 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2737 are further described hereinbelow with reference to Table 1.

[38287] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2737 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[38288] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Mes-

senger 2738 (VGAM2738) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[38289] VGAM2738 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2738 was detected is described hereinabove with reference to Figs. 2-8.

[38290] VGAM2738 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Broad bean necrosis virus. VGAM2738 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[38291] VGAM2738 gene, herein designated VGAM GENE, encodes a VGAM2738 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2738 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2738 precursor RNA is designated SEQ ID:2724, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2724 is located at position 4423

relative to the genome of Broad bean necrosis virus.

[38292] VGAM2738 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2738 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[38293] An enzyme complex designated DICER COMPLEX, dices the VGAM2738 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2738 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2738 RNA is designated SEQ ID:5449, and is provided hereinbelow with reference to the sequence listing part.

[38294] VGAM2738 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2738 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2738 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[38295] VGAM2738 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2738 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2738 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting VGAM2738 RNA, herein designated

VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2738 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[38296] The complementary binding of VGAM2738 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2738 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2738 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2738 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[38297] It is appreciated that VGAM2738 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2738 host target genes. The mRNA of each one of this plurality of VGAM2738 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM2738 RNA, herein designated VGAM RNA, and which when bound by VGAM2738 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2738 host target proteins.

[38298] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2738 gene, herein designated VGAM GENE, on one or more VGAM2738 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[38299] It is yet further appreciated that a function of VGAM2738 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2738 include diagnosis, prevention and treatment of viral infection by Broad bean necrosis virus. Specific functions, and accordingly utilities, of VGAM2738 correlate with, and may be deduced from, the identity of the host target genes which VGAM2738 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[38300] Nucleotide sequences of the VGAM2738 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2738 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2738 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2738 are further described hereinbelow with reference to Table 1.

[38301] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2738 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[38302] Fig. 1 further provides a conceptual description of another novel bioinformatically detected viral gene of the present

invention, referred to here as Viral Genomic Address Messenger 2739 (VGAM2739) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[38303] VGAM2739 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2739 was detected is described hereinabove with reference to Figs. 2-8.

[38304] VGAM2739 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Broad bean necrosis virus. VGAM2739 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[38305] VGAM2739 gene, herein designated VGAM GENE, encodes a VGAM2739 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2739 precursor RNA, herein designated VGAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2739 precursor RNA is designated SEQ ID:2725, and is provided hereinbelow with reference to the sequence listing part. Nu-

cleotide sequence SEQ ID:2725 is located at position 2143 relative to the genome of Broad bean necrosis virus.

[38306] VGAM2739 precursor RNA, herein designated VGAM PRECURSOR RNA, folds onto itself, forming VGAM2739 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[38307] An enzyme complex designated DICER COMPLEX, dices the VGAM2739 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, into VGAM2739 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2739 RNA is designated SEQ ID:5450, and is provided hereinbelow with reference to the sequence

listing part.

[38308] VGAM2739 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2739 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2739 host target RNA, herein designated VGAM HOST TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[38309] VGAM2739 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2739 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2739 RNA, herein designated VGAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows 3 such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not

meant to be limiting VGAM2739 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2739 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3UTR region, this is meant as an example only these host target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[38310] The complementary binding of VGAM2739 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2739 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2739 host target RNA, herein designated VGAM HOST TARGET RNA, into VGAM2739 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[38311] It is appreciated that VGAM2739 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2739 host target genes. The mRNA of each one of this plurality of VGAM2739 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2739 RNA, herein designated VGAM RNA, and which when bound by VGAM2739 RNA, herein designated VGAM RNA, causes inhibition of translation of respective one or more VGAM2739 host target proteins.

[38312] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2739 gene, herein designated VGAM GENE, on one or more VGAM2739 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[38313] It is yet further appreciated that a function of VGAM2739

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2739 include diagnosis, prevention and treatment of viral infection by Broad bean necrosis virus. Specific functions, and accordingly utilities, of VGAM2739 correlate with, and may be deduced from, the identity of the host target genes which VGAM2739 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[38314] Nucleotide sequences of the VGAM2739 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the diced VGAM2739 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2739 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2739 are further described hereinbelow with reference to Table 1.

[38315] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on, and schematic representation of the complementarity of each of these host target binding sites to VGAM2739 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[38316] Fig. 9 further provides a conceptual description of novel

bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2740(VGR2740) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[38317] VGR2740 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2740 gene was detected is described hereinabove with reference to Figs. 6-15.

[38318] VGR2740 gene encodes VGR2740 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38319] VGR2740 precursor RNA folds spatially, forming VGR2740 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2740 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2740 precursor RNA comprises a plurality of segments, the first half

of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38320] VGR2740 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM15 precursor RNA and VGAM16 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[38321] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM15 RNA and VGAM16 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[38322] VGAM15 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM15 host target RNA, herein schematically represented by VGAM1

HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM15 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM15 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[38323] VGAM16 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM16 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM16 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM16 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[38324] It is appreciated that a function of VGR2740 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attack-

ing a host. Accordingly, utilities of VGR2740 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2740 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2740 gene: VGAM15 host target protein and VGAM16 host target protein, herein schematically represented by VGAM1 HOST TARGET PRO-TEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated herein-above with reference to VGAM15 and VGAM16

[38325] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2741(VGR2741) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[38326] VGR2741 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2741 gene was

detected is described hereinabove with reference to Figs. 6-15.

[38327] VGR2741 gene encodes VGR2741 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38328] VGR2741 precursor RNA folds spatially, forming VGR2741 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2741 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2741 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38329] VGR2741 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM18 precursor RNA, VGAM19 precursor RNA, VGAM20 precursor RNA, VGAM21 precursor RNA, VGAM22 precursor RNA, VGAM23 precursor RNA, VGAM24 precursor RNA and VGAM25 precursor RNA,

herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR, VGAM5 PRECURSOR, VGAM6 PRECURSOR, VGAM7 PRECURSOR and VGAM8 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[38330] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM18 RNA, VGAM19 RNA, VGAM20 RNA, VGAM21 RNA, VGAM22 RNA, VGAM23 RNA, VGAM24 RNA and VGAM25 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA, VGAM5 RNA, VGAM6 RNA, VGAM7 RNA and VGAM8 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[38331] VGAM18 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM18 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM18 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM18 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[38332] VGAM19 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM19 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM19 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM19 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[38333] VGAM20 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM20 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corre-

sponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM20 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM20 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[38334] VGAM21 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM21 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM21 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM21 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[38335] VGAM22 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM22 host target RNA, herein schematically represented by VGAM5

HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM22 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM22 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[38336] VGAM23 RNA, herein schematically represented by VGAM6 binds complimentarily to a host target binding site located in an untranslated region of VGAM23 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM23 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA into VGAM23 host target protein, herein schematically represented by VGAM6 HOST TARGET PROTEIN, both of Fig. 1.

[38337] VGAM24 RNA, herein schematically represented by VGAM7 binds complimentarily to a host target binding site located in an untranslated region of VGAM24 host

target RNA, herein schematically represented by VGAM7 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM24 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA into VGAM24 host target protein, herein schematically represented by VGAM7 HOST TARGET PROTEIN, both of Fig. 1.

[38338] VGAM25 RNA, herein schematically represented by VGAM8 binds complimentarily to a host target binding site located in an untranslated region of VGAM25 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM25 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA into VGAM25 host target protein, herein schematically represented by VGAM8 HOST TARGET PROTEIN, both of Fig. 1.

[38339] It is appreciated that a function of VGR2741 gene, herein designated VGR GENE, is inhibition of expression of host

target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2741 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2741 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2741 gene: VGAM18 host target protein, VGAM19 host target protein, VGAM20 host target protein, VGAM21 host target protein, VGAM22 host target protein, VGAM23 host target protein, VGAM24 host target protein and VGAM25 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM18, VGAM19, VGAM20, VGAM21, VGAM22, VGAM23, VGAM24 and VGAM25

[38340] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2742(VGR2742) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates

expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[38341] VGR2742 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2742 gene was detected is described hereinabove with reference to Figs. 6-15.

[38342] VGR2742 gene encodes VGR2742 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38343] VGR2742 precursor RNA folds spatially, forming VGR2742 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2742 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2742 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38344] VGR2742 folded precursor RNA, herein designated VGR

FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM26 precursor RNA, VGAM27 precursor RNA, VGAM28 precursor RNA, VGAM29 precursor RNA, VGAM30 precursor RNA, VGAM31 precursor RNA, VGAM32 precursor RNA and VGAM33 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR, VGAM5 PRECURSOR, VGAM6 PRECURSOR, VGAM7 PRECURSOR and VGAM8 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[38345] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM26 RNA, VGAM27 RNA, VGAM28 RNA, VGAM29 RNA, VGAM30 RNA, VGAM31 RNA, VGAM32 RNA and VGAM33 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA, VGAM5 RNA, VGAM6 RNA, VGAM7 RNA and VGAM8 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[38346] VGAM26 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM26 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM26 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM26 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[38347] VGAM27 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM27 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM27 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM27 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of

Fig. 1.

[38348] VGAM28 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM28 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM28 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM28 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[38349] VGAM29 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM29 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM29 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM29 host target protein, herein schematically

represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[38350] VGAM30 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM30 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM30 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM30 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[38351] VGAM31 RNA, herein schematically represented by VGAM6 binds complimentarily to a host target binding site located in an untranslated region of VGAM31 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM31 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA

into VGAM31 host target protein, herein schematically represented by VGAM6 HOST TARGET PROTEIN, both of Fig. 1.

[38352] VGAM32 RNA, herein schematically represented by VGAM7 binds complimentarily to a host target binding site located in an untranslated region of VGAM32 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM32 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA into VGAM32 host target protein, herein schematically represented by VGAM7 HOST TARGET PROTEIN, both of Fig. 1.

[38353] VGAM33 RNA, herein schematically represented by VGAM8 binds complimentarily to a host target binding site located in an untranslated region of VGAM33 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM33 host target RNA, herein

schematically represented by VGAM8 HOST TARGET RNA into VGAM33 host target protein, herein schematically represented by VGAM8 HOST TARGET PROTEIN, both of Fig. 1.

[38354] It is appreciated that a function of VGR2742 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2742 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2742 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2742 gene: VGAM26 host target protein, VGAM27 host target protein, VGAM28 host target protein, VGAM29 host target protein, VGAM30 host target protein, VGAM31 host target protein, VGAM32 host target protein and VGAM33 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM26, VGAM27, VGAM28, VGAM29, VGAM30, VGAM31, VGAM32 and

VGAM33

[38355] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2743(VGR2743) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[38356] VGR2743 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2743 gene was detected is described hereinabove with reference to Figs. 6-15.

[38357] VGR2743 gene encodes VGR2743 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38358] VGR2743 precursor RNA folds spatially, forming VGR2743 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2743 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to

the fact that the nucleotide sequence of VGR2743 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38359] VGR2743 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM34 precursor RNA, VGAM35 precursor RNA, VGAM36 precursor RNA, VGAM37 precursor RNA, VGAM38 precursor RNA, VGAM39 precursor RNA, VGAM40 precursor RNA and VGAM41 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR, VGAM5 PRECURSOR, VGAM6 PRECURSOR, VGAM7 PRECURSOR and VGAM8 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[38360] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM34 RNA, VGAM35 RNA, VGAM36 RNA, VGAM37 RNA, VGAM38

RNA, VGAM39 RNA, VGAM40 RNA and VGAM41 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA, VGAM5 RNA, VGAM6 RNA, VGAM7 RNA and VGAM8 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[38361] VGAM34 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM34 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM34 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM34 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[38362] VGAM35 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM35 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corre-

sponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM35 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM35 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[38363] VGAM36 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM36 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM36 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM36 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[38364] VGAM37 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM37 host target RNA, herein schematically represented by VGAM4

HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM37 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM37 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[38365] VGAM38 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM38 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM38 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM38 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[38366] VGAM39 RNA, herein schematically represented by VGAM6 binds complimentarily to a host target binding site located in an untranslated region of VGAM39 host

target RNA, herein schematically represented by VGAM6 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM39 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA into VGAM39 host target protein, herein schematically represented by VGAM6 HOST TARGET PROTEIN, both of Fig. 1.

[38367] VGAM40 RNA, herein schematically represented by VGAM7 binds complimentarily to a host target binding site located in an untranslated region of VGAM40 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM40 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA into VGAM40 host target protein, herein schematically represented by VGAM7 HOST TARGET PROTEIN, both of Fig. 1.

[38368] VGAM41 RNA, herein schematically represented by VGAM8 binds complimentarily to a host target binding

site located in an untranslated region of VGAM41 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM41 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA into VGAM41 host target protein, herein schematically represented by VGAM8 HOST TARGET PROTEIN, both of Fig. 1.

[38369] It is appreciated that a function of VGR2743 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2743 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2743 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2743 gene: VGAM34 host target protein, VGAM35 host target protein, VGAM36 host target protein, VGAM37 host target protein, VGAM38 host target protein, VGAM39 host target protein, VGAM40 host

target protein and VGAM41 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM34, VGAM35, VGAM36, VGAM37, VGAM38, VGAM39, VGAM40 and VGAM41

[38370] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2744(VGR2744) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[38371] VGR2744 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2744 gene was detected is described hereinabove with reference to Figs. 6-15.

[38372] VGR2744 gene encodes VGR2744 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38373] VGR2744 precursor RNA folds spatially, forming VGR2744 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2744 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2744 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38374] VGR2744 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM42 precursor RNA, VGAM43 precursor RNA, VGAM44 precursor RNA, VGAM45 precursor RNA, VGAM46 precursor RNA, VGAM47 precursor RNA, VGAM48 precursor RNA and VGAM49 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR, VGAM5 PRECURSOR, VGAM6 PRECURSOR, VGAM7 PRECURSOR and VGAM8 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin

shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[38375] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM42 RNA, VGAM43 RNA, VGAM44 RNA, VGAM45 RNA, VGAM46 RNA, VGAM47 RNA, VGAM48 RNA and VGAM49 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA, VGAM5 RNA, VGAM6 RNA, VGAM7 RNA and VGAM8 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[38376] VGAM42 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM42 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM42 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM42 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of

Fig. 1.

[38377] VGAM43 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM43 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM43 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM43 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[38378] VGAM44 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM44 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM44 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM44 host target protein, herein schematically

represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[38379] VGAM45 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM45 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM45 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM45 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[38380] VGAM46 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM46 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM46 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA

into VGAM46 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[38381] VGAM47 RNA, herein schematically represented by VGAM6 binds complimentarily to a host target binding site located in an untranslated region of VGAM47 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM47 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA into VGAM47 host target protein, herein schematically represented by VGAM6 HOST TARGET PROTEIN, both of Fig. 1.

[38382] VGAM48 RNA, herein schematically represented by VGAM7 binds complimentarily to a host target binding site located in an untranslated region of VGAM48 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM48 host target RNA, herein

schematically represented by VGAM7 HOST TARGET RNA into VGAM48 host target protein, herein schematically represented by VGAM7 HOST TARGET PROTEIN, both of Fig. 1.

[38383] VGAM49 RNA, herein schematically represented by VGAM8 binds complimentarily to a host target binding site located in an untranslated region of VGAM49 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM49 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA into VGAM49 host target protein, herein schematically represented by VGAM8 HOST TARGET PROTEIN, both of Fig. 1.

[38384] It is appreciated that a function of VGR2744 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2744 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2744 gene, herein designated VGR GENE, correlate with, and

may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2744 gene: VGAM42 host target protein, VGAM43 host target protein, VGAM44 host target protein, VGAM45 host target protein, VGAM46 host target protein, VGAM47 host target protein, VGAM48 host target protein and VGAM49 host target protein, herein schematically represented by VGAM1 HOST TARGET PRO-TEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM42, VGAM43, VGAM44, VGAM45, VGAM46, VGAM47, VGAM48 and VGAM49

[38385] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2745(VGR2745) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[38386] VGR2745 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding,

RNA viral gene. The method by which VGR2745 gene was detected is described hereinabove with reference to Figs. 6-15.

[38387] VGR2745 gene encodes VGR2745 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38388] VGR2745 precursor RNA folds spatially, forming VGR2745 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2745 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2745 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38389] VGR2745 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM50 precursor RNA, VGAM51 precursor RNA, VGAM52 precursor RNA, VGAM53 precursor RNA, VGAM54 precursor RNA, VGAM55 precursor RNA,

VGAM56 precursor RNA and VGAM57 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR, VGAM5 PRECURSOR, VGAM6 PRECURSOR, VGAM7 PRECURSOR and VGAM8 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[38390] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM50 RNA, VGAM51 RNA, VGAM52 RNA, VGAM53 RNA, VGAM54 RNA, VGAM55 RNA, VGAM56 RNA and VGAM57 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA, VGAM5 RNA, VGAM6 RNA, VGAM7 RNA and VGAM8 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[38391] VGAM50 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM50 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corre-

sponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM50 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM50 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[38392] VGAM51 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM51 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM51 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM51 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[38393] VGAM52 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM52 host target RNA, herein schematically represented by VGAM3

HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM52 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM52 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[38394] VGAM53 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM53 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM53 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM53 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[38395] VGAM54 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM54 host

target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM54 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM54 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[38396] VGAM55 RNA, herein schematically represented by VGAM6 binds complimentarily to a host target binding site located in an untranslated region of VGAM55 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM55 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA into VGAM55 host target protein, herein schematically represented by VGAM6 HOST TARGET PROTEIN, both of Fig. 1.

[38397] VGAM56 RNA, herein schematically represented by VGAM7 binds complimentarily to a host target binding

site located in an untranslated region of VGAM56 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM56 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA into VGAM56 host target protein, herein schematically represented by VGAM7 HOST TARGET PROTEIN, both of Fig. 1.

[38398] VGAM57 RNA, herein schematically represented by VGAM8 binds complimentarily to a host target binding site located in an untranslated region of VGAM57 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM57 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA into VGAM57 host target protein, herein schematically represented by VGAM8 HOST TARGET PROTEIN, both of Fig. 1.

[38399] It is appreciated that a function of VGR2745 gene, herein

designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2745 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2745 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2745 gene: VGAM50 host target protein, VGAM51 host target protein, VGAM52 host target protein, VGAM53 host target protein, VGAM54 host target protein, VGAM55 host target protein, VGAM56 host target protein and VGAM57 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM50, VGAM51, VGAM52, VGAM53, VGAM54, VGAM55, VGAM56 and VGAM57

[38400] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2746(VGR2746) viral gene, which encodes an operon-like cluster of novel viral

micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[38401] VGR2746 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2746 gene was detected is described hereinabove with reference to Figs. 6-15.

[38402] VGR2746 gene encodes VGR2746 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38403] VGR2746 precursor RNA folds spatially, forming VGR2746 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2746 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2746 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38404] VGR2746 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM58 precursor RNA, VGAM59 precursor RNA, VGAM60 precursor RNA, VGAM61 precursor RNA, VGAM62 precursor RNA, VGAM63 precursor RNA, VGAM64 precursor RNA and VGAM65 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR, VGAM5 PRECURSOR, VGAM6 PRECURSOR, VGAM7 PRECURSOR and VGAM8 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[38405] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM58 RNA, VGAM59 RNA, VGAM60 RNA, VGAM61 RNA, VGAM62 RNA, VGAM63 RNA, VGAM64 RNA and VGAM65 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA, VGAM5 RNA, VGAM6 RNA, VGAM7 RNA and VGAM8 RNA respectively, each of which VGAM RNAs corresponding to VGAM

RNA of Fig. 8.

[38406] VGAM58 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM58 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM58 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM58 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[38407] VGAM59 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM59 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM59 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM59 host target protein, herein schematically

represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[38408] VGAM60 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM60 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM60 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM60 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[38409] VGAM61 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM61 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM61 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA

into VGAM61 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[38410] VGAM62 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM62 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM62 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM62 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[38411] VGAM63 RNA, herein schematically represented by VGAM6 binds complimentarily to a host target binding site located in an untranslated region of VGAM63 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM63 host target RNA, herein

schematically represented by VGAM6 HOST TARGET RNA into VGAM63 host target protein, herein schematically represented by VGAM6 HOST TARGET PROTEIN, both of Fig. 1.

[38412] VGAM64 RNA, herein schematically represented by VGAM7 binds complimentarily to a host target binding site located in an untranslated region of VGAM64 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM64 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA into VGAM64 host target protein, herein schematically represented by VGAM7 HOST TARGET PROTEIN, both of Fig. 1.

[38413] VGAM65 RNA, herein schematically represented by VGAM8 binds complimentarily to a host target binding site located in an untranslated region of VGAM65 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby in-

hibiting translation of VGAM65 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA into VGAM65 host target protein, herein schematically represented by VGAM8 HOST TARGET PROTEIN, both of Fig. 1.

[38414] It is appreciated that a function of VGR2746 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2746 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2746 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2746 gene: VGAM58 host target protein, VGAM59 host target protein, VGAM60 host target protein, VGAM61 host target protein, VGAM62 host target protein, VGAM63 host target protein, VGAM64 host target protein and VGAM65 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM58, VGAM59,

VGAM60, VGAM61, VGAM62, VGAM63, VGAM64 and VGAM65

[38415] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2747(VGR2747) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[38416] VGR2747 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2747 gene was detected is described hereinabove with reference to Figs. 6-15.

[38417] VGR2747 gene encodes VGR2747 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38418] VGR2747 precursor RNA folds spatially, forming VGR2747 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2747 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art

as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2747 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38419] VGR2747 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM66 precursor RNA, VGAM67 precursor RNA, VGAM68 precursor RNA, VGAM69 precursor RNA, VGAM70 precursor RNA, VGAM71 precursor RNA, VGAM72 precursor RNA and VGAM73 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR, VGAM5 PRECURSOR, VGAM6 PRECURSOR, VGAM7 PRECURSOR and VGAM8 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[38420] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM66

RNA, VGAM67 RNA, VGAM68 RNA, VGAM69 RNA, VGAM70 RNA, VGAM71 RNA, VGAM72 RNA and VGAM73 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA, VGAM5 RNA, VGAM6 RNA, VGAM7 RNA and VGAM8 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[38421] VGAM66 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM66 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM66 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM66 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[38422] VGAM67 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM67 host target RNA, herein schematically represented by VGAM2

HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM67 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM67 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[38423] VGAM68 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM68 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM68 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM68 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[38424] VGAM69 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM69 host

target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM69 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM69 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[38425] VGAM70 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM70 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM70 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM70 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[38426] VGAM71 RNA, herein schematically represented by VGAM6 binds complimentarily to a host target binding

site located in an untranslated region of VGAM71 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM71 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA into VGAM71 host target protein, herein schematically represented by VGAM6 HOST TARGET PROTEIN, both of Fig. 1.

[38427] VGAM72 RNA, herein schematically represented by VGAM7 binds complimentarily to a host target binding site located in an untranslated region of VGAM72 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM72 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA into VGAM72 host target protein, herein schematically represented by VGAM7 HOST TARGET PROTEIN, both of Fig. 1.

[38428] VGAM73 RNA, herein schematically represented by

VGAM8 binds complimentarily to a host target binding site located in an untranslated region of VGAM73 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM73 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA into VGAM73 host target protein, herein schematically represented by VGAM8 HOST TARGET PROTEIN, both of Fig. 1.

[38429] It is appreciated that a function of VGR2747 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2747 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2747 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2747 gene: VGAM66 host target protein, VGAM67 host target protein, VGAM68 host target protein, VGAM69 host target protein, VGAM70 host

target protein, VGAM71 host target protein, VGAM72 host target protein and VGAM73 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM66, VGAM67, VGAM68, VGAM69, VGAM70, VGAM71, VGAM72 and VGAM73

[38430] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2748(VGR2748) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[38431] VGR2748 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2748 gene was detected is described hereinabove with reference to Figs. 6-15.

[38432] VGR2748 gene encodes VGR2748 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typi-

cally several hundred nucleotides long.

[38433] VGR2748 precursor RNA folds spatially, forming VGR2748 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2748 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2748 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38434] VGR2748 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM76 precursor RNA and VGAM77 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[38435] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA

segments of about 22 nucleotides in length, VGAM76 RNA and VGAM77 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[38436] VGAM76 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM76 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM76 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM76 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[38437] VGAM77 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM77 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM77 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM77 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[38438] It is appreciated that a function of VGR2748 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2748 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2748 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2748 gene: VGAM76 host target protein and VGAM77 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM76 and VGAM77

[38439] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred

to here as Viral Genomic Record 2749(VGR2749) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[38440] VGR2749 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2749 gene was detected is described hereinabove with reference to Figs. 6-15.

[38441] VGR2749 gene encodes VGR2749 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38442] VGR2749 precursor RNA folds spatially, forming VGR2749 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2749 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2749 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which

is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38443] VGR2749 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM78 precursor RNA, VGAM79 precursor RNA, VGAM80 precursor RNA, VGAM81 precursor RNA, VGAM82 precursor RNA, VGAM83 precursor RNA, VGAM84 precursor RNA and VGAM85 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR, VGAM5 PRECURSOR, VGAM6 PRECURSOR, VGAM7 PRECURSOR and VGAM8 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[38444] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM78 RNA, VGAM79 RNA, VGAM80 RNA, VGAM81 RNA, VGAM82 RNA, VGAM83 RNA, VGAM84 RNA and VGAM85 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA, VGAM5

RNA, VGAM6 RNA, VGAM7 RNA and VGAM8 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[38445] VGAM78 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM78 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM78 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM78 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[38446] VGAM79 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM79 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM79 host target RNA, herein

schematically represented by VGAM2 HOST TARGET RNA into VGAM79 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[38447] VGAM80 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM80 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM80 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM80 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[38448] VGAM81 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM81 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby in-

hibiting translation of VGAM81 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM81 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[38449] VGAM82 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM82 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM82 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM82 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[38450] VGAM83 RNA, herein schematically represented by VGAM6 binds complimentarily to a host target binding site located in an untranslated region of VGAM83 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM83 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA into VGAM83 host target protein, herein schematically represented by VGAM6 HOST TARGET PROTEIN, both of Fig. 1.

[38451] VGAM84 RNA, herein schematically represented by VGAM7 binds complimentarily to a host target binding site located in an untranslated region of VGAM84 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM84 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA into VGAM84 host target protein, herein schematically represented by VGAM7 HOST TARGET PROTEIN, both of Fig. 1.

[38452] VGAM85 RNA, herein schematically represented by VGAM8 binds complimentarily to a host target binding site located in an untranslated region of VGAM85 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA, which host target binding site corre-

sponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM85 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA into VGAM85 host target protein, herein schematically represented by VGAM8 HOST TARGET PROTEIN, both of Fig. 1.

[38453] It is appreciated that a function of VGR2749 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2749 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2749 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2749 gene: VGAM78 host target protein, VGAM79 host target protein, VGAM80 host target protein, VGAM81 host target protein, VGAM82 host target protein, VGAM83 host target protein, VGAM84 host target protein and VGAM85 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively.

The function of these host target genes is elaborated hereinabove with reference to VGAM78, VGAM79, VGAM80, VGAM81, VGAM82, VGAM83, VGAM84 and VGAM85

[38454] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2750(VGR2750) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[38455] VGR2750 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2750 gene was detected is described hereinabove with reference to Figs. 6-15.

[38456] VGR2750 gene encodes VGR2750 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38457] VGR2750 precursor RNA folds spatially, forming VGR2750 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2750 folded

precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2750 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38458] VGR2750 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM86 precursor RNA, VGAM87 precursor RNA, VGAM88 precursor RNA, VGAM89 precursor RNA, VGAM90 precursor RNA, VGAM91 precursor RNA, VGAM92 precursor RNA and VGAM93 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR, VGAM5 PRECURSOR, VGAM6 PRECURSOR, VGAM7 PRECURSOR and VGAM8 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[38459] The above mentioned VGAM precursor RNAs are diced by

DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM86 RNA, VGAM87 RNA, VGAM88 RNA, VGAM89 RNA, VGAM90 RNA, VGAM91 RNA, VGAM92 RNA and VGAM93 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA, VGAM5 RNA, VGAM6 RNA, VGAM7 RNA and VGAM8 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[38460] VGAM86 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM86 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM86 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM86 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[38461] VGAM87 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding

site located in an untranslated region of VGAM87 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM87 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM87 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[38462] VGAM88 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM88 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM88 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM88 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[38463] VGAM89 RNA, herein schematically represented by

VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM89 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM89 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM89 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[38464] VGAM90 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM90 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM90 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM90 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[38465] VGAM91 RNA, herein schematically represented by VGAM6 binds complimentarily to a host target binding site located in an untranslated region of VGAM91 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM91 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA into VGAM91 host target protein, herein schematically represented by VGAM6 HOST TARGET PROTEIN, both of Fig. 1.

[38466] VGAM92 RNA, herein schematically represented by VGAM7 binds complimentarily to a host target binding site located in an untranslated region of VGAM92 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM92 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA into VGAM92 host target protein, herein schematically represented by VGAM7 HOST TARGET PROTEIN, both of

Fig. 1.

[38467] VGAM93 RNA, herein schematically represented by VGAM8 binds complimentarily to a host target binding site located in an untranslated region of VGAM93 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM93 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA into VGAM93 host target protein, herein schematically represented by VGAM8 HOST TARGET PROTEIN, both of Fig. 1.

[38468] It is appreciated that a function of VGR2750 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2750 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2750 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2750 gene: VGAM86 host

target protein, VGAM87 host target protein, VGAM88 host target protein, VGAM89 host target protein, VGAM90 host target protein, VGAM91 host target protein, VGAM92 host target protein and VGAM93 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM86, VGAM87, VGAM88, VGAM89, VGAM90, VGAM91, VGAM92 and VGAM93

[38469] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2751(VGR2751) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[38470] VGR2751 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2751 gene was detected is described hereinabove with reference to Figs. 6-15.

[38471] VGR2751 gene encodes VGR2751 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38472] VGR2751 precursor RNA folds spatially, forming VGR2751 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2751 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2751 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38473] VGR2751 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM94 precursor RNA, VGAM95 precursor RNA, VGAM96 precursor RNA, VGAM97 precursor RNA, VGAM98 precursor RNA, VGAM99 precursor RNA, VGAM100 precursor RNA and VGAM101 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRE-

CURSOR, VGAM5 PRECURSOR, VGAM6 PRECURSOR, VGAM7 PRECURSOR and VGAM8 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[38474] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM94 RNA, VGAM95 RNA, VGAM96 RNA, VGAM97 RNA, VGAM98 RNA, VGAM99 RNA, VGAM100 RNA and VGAM101 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA, VGAM5 RNA, VGAM6 RNA, VGAM7 RNA and VGAM8 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[38475] VGAM94 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM94 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM94 host target RNA, herein

schematically represented by VGAM1 HOST TARGET RNA into VGAM94 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[38476] VGAM95 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM95 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM95 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM95 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[38477] VGAM96 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM96 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby in-

hibiting translation of VGAM96 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM96 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[38478] VGAM97 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM97 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM97 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM97 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[38479] VGAM98 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM98 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM98 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM98 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[38480] VGAM99 RNA, herein schematically represented by VGAM6 binds complimentarily to a host target binding site located in an untranslated region of VGAM99 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM99 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA into VGAM99 host target protein, herein schematically represented by VGAM6 HOST TARGET PROTEIN, both of Fig. 1.

[38481] VGAM100 RNA, herein schematically represented by VGAM7 binds complimentarily to a host target binding site located in an untranslated region of VGAM100 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA, which host target binding site corre-

sponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM100 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA into VGAM100 host target protein, herein schematically represented by VGAM7 HOST TARGET PROTEIN, both of Fig. 1.

[38482] VGAM101 RNA, herein schematically represented by VGAM8 binds complimentarily to a host target binding site located in an untranslated region of VGAM101 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM101 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA into VGAM101 host target protein, herein schematically represented by VGAM8 HOST TARGET PROTEIN, both of Fig. 1.

[38483] It is appreciated that a function of VGR2751 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2751 gene include

diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2751 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2751 gene: VGAM94 host target protein, VGAM95 host target protein, VGAM96 host target protein, VGAM97 host target protein, VGAM98 host target protein, VGAM99 host target protein, VGAM100 host target protein and VGAM101 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM94, VGAM95, VGAM96, VGAM97, VGAM98, VGAM99, VGAM100 and VGAM101

[38484] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2752(VGR2752) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known

in the art.

[38485] VGR2752 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2752 gene was detected is described hereinabove with reference to Figs. 6-15.

[38486] VGR2752 gene encodes VGR2752 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38487] VGR2752 precursor RNA folds spatially, forming VGR2752 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2752 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2752 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38488] VGR2752 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate VGAM pre-

cursor RNAs, VGAM102 precursor RNA, VGAM103 precursor RNA, VGAM104 precursor RNA and VGAM105 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR and VGAM4 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[38489] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM102 RNA, VGAM103 RNA, VGAM104 RNA and VGAM105 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA and VGAM4 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[38490] VGAM102 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM102 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM102 host target RNA, herein

schematically represented by VGAM1 HOST TARGET RNA into VGAM102 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[38491] VGAM103 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM103 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM103 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM103 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[38492] VGAM104 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM104 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby in-

hibiting translation of VGAM104 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM104 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[38493] VGAM105 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM105 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM105 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM105 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[38494] It is appreciated that a function of VGR2752 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2752 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2752

gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2752 gene: VGAM102 host target protein, VGAM103 host target protein, VGAM104 host target protein and VGAM105 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM102, VGAM103, VGAM104 and VGAM105

[38495] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2753(VGR2753) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[38496] VGR2753 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2753 gene was detected is described hereinabove with reference to Figs.

6-15.

[38497] VGR2753 gene encodes VGR2753 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38498] VGR2753 precursor RNA folds spatially, forming VGR2753 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2753 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2753 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38499] VGR2753 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM106 precursor RNA, VGAM107 precursor RNA, VGAM108 precursor RNA and VGAM109 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR and VGAM4 PRECURSOR respectively, each of which VGAM

precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[38500] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM106 RNA, VGAM107 RNA, VGAM108 RNA and VGAM109 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA and VGAM4 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[38501] VGAM106 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM106 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM106 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM106 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[38502] VGAM107 RNA, herein schematically represented by

VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM107 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM107 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM107 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[38503] VGAM108 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM108 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM108 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM108 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[38504] VGAM109 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM109 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM109 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM109 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[38505] It is appreciated that a function of VGR2753 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2753 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2753 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2753 gene: VGAM106 host target protein, VGAM107 host target protein, VGAM108

host target protein and VGAM109 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM106, VGAM107, VGAM108 and VGAM109

[38506] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2754(VGR2754) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[38507] VGR2754 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2754 gene was detected is described hereinabove with reference to Figs. 6-15.

[38508] VGR2754 gene encodes VGR2754 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38509] VGR2754 precursor RNA folds spatially, forming VGR2754

folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2754 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2754 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38510] VGR2754 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM110 precursor RNA, VGAM111 precursor RNA, VGAM112 precursor RNA, VGAM113 precursor RNA, VGAM114 precursor RNA, VGAM115 precursor RNA, VGAM116 precursor RNA and VGAM117 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR, VGAM5 PRECURSOR, VGAM6 PRECURSOR, VGAM7 PRECURSOR and VGAM8 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECUR-

SOR RNA of Fig. 8.

[38511] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM110 RNA, VGAM111 RNA, VGAM112 RNA, VGAM113 RNA, VGAM114 RNA, VGAM115 RNA, VGAM116 RNA and VGAM117 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA, VGAM5 RNA, VGAM6 RNA, VGAM7 RNA and VGAM8 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[38512] VGAM110 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM110 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM110 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM110 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[38513] VGAM111 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM111 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM111 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM111 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[38514] VGAM112 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM112 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM112 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM112 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of

Fig. 1.

[38515] VGAM113 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM113 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM113 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM113 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[38516] VGAM114 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM114 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM114 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM114 host target protein, herein schematically

represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[38517] VGAM115 RNA, herein schematically represented by VGAM6 binds complimentarily to a host target binding site located in an untranslated region of VGAM115 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM115 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA into VGAM115 host target protein, herein schematically represented by VGAM6 HOST TARGET PROTEIN, both of Fig. 1.

[38518] VGAM116 RNA, herein schematically represented by VGAM7 binds complimentarily to a host target binding site located in an untranslated region of VGAM116 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM116 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA

into VGAM116 host target protein, herein schematically represented by VGAM7 HOST TARGET PROTEIN, both of Fig. 1.

[38519] VGAM117 RNA, herein schematically represented by VGAM8 binds complimentarily to a host target binding site located in an untranslated region of VGAM117 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM117 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA into VGAM117 host target protein, herein schematically represented by VGAM8 HOST TARGET PROTEIN, both of Fig. 1.

[38520] It is appreciated that a function of VGR2754 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2754 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2754 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target

genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2754 gene: VGAM110 host target protein, VGAM111 host target protein, VGAM112 host target protein, VGAM113 host target protein, VGAM114 host target protein, VGAM115 host target protein, VGAM116 host target protein and VGAM117 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM110, VGAM111, VGAM112, VGAM113, VGAM114, VGAM115, VGAM116 and VGAM117

[38521] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2755(VGR2755) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[38522] VGR2755 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2755 gene was

detected is described hereinabove with reference to Figs. 6-15.

[38523] VGR2755 gene encodes VGR2755 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38524] VGR2755 precursor RNA folds spatially, forming VGR2755 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2755 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2755 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38525] VGR2755 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM118 precursor RNA, VGAM119 precursor RNA, VGAM120 precursor RNA, VGAM121 precursor RNA, VGAM122 precursor RNA, VGAM123 precursor RNA, VGAM124 precursor RNA and VGAM125 precursor RNA,

herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR, VGAM5 PRECURSOR, VGAM6 PRECURSOR, VGAM7 PRECURSOR and VGAM8 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[38526] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM118 RNA, VGAM119 RNA, VGAM120 RNA, VGAM121 RNA, VGAM122 RNA, VGAM123 RNA, VGAM124 RNA and VGAM125 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA, VGAM5 RNA, VGAM6 RNA, VGAM7 RNA and VGAM8 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[38527] VGAM118 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM118 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM118 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM118 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[38528] VGAM119 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM119 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM119 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM119 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[38529] VGAM120 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM120 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corre-

sponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM120 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM120 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[38530] VGAM121 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM121 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM121 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM121 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[38531] VGAM122 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM122 host target RNA, herein schematically represented by VGAM5

HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM122 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM122 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[38532] VGAM123 RNA, herein schematically represented by VGAM6 binds complimentarily to a host target binding site located in an untranslated region of VGAM123 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM123 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA into VGAM123 host target protein, herein schematically represented by VGAM6 HOST TARGET PROTEIN, both of Fig. 1.

[38533] VGAM124 RNA, herein schematically represented by VGAM7 binds complimentarily to a host target binding site located in an untranslated region of VGAM124 host

target RNA, herein schematically represented by VGAM7 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM124 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA into VGAM124 host target protein, herein schematically represented by VGAM7 HOST TARGET PROTEIN, both of Fig. 1.

[38534] VGAM125 RNA, herein schematically represented by VGAM8 binds complimentarily to a host target binding site located in an untranslated region of VGAM125 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM125 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA into VGAM125 host target protein, herein schematically represented by VGAM8 HOST TARGET PROTEIN, both of Fig. 1.

[38535] It is appreciated that a function of VGR2755 gene, herein designated VGR GENE, is inhibition of expression of host

target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2755 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2755 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2755 gene: VGAM118 host target protein, VGAM119 host target protein, VGAM120 host target protein, VGAM121 host target protein, VGAM122 host target protein, VGAM123 host target protein, VGAM124 host target protein and VGAM125 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM118, VGAM119, VGAM120, VGAM121, VGAM122, VGAM123, VGAM124 and VGAM125

[38536] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2756(VGR2756) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates

expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[38537] VGR2756 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2756 gene was detected is described hereinabove with reference to Figs. 6-15.

[38538] VGR2756 gene encodes VGR2756 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38539] VGR2756 precursor RNA folds spatially, forming VGR2756 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2756 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2756 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38540] VGR2756 folded precursor RNA, herein designated VGR

FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM126 precursor RNA, VGAM127 precursor RNA, VGAM128 precursor RNA, VGAM129 precursor RNA, VGAM130 precursor RNA, VGAM131 precursor RNA, VGAM132 precursor RNA and VGAM133 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR, VGAM5 PRECURSOR, VGAM6 PRECURSOR, VGAM7 PRECURSOR and VGAM8 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[38541] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM126 RNA, VGAM127 RNA, VGAM128 RNA, VGAM129 RNA, VGAM130 RNA, VGAM131 RNA, VGAM132 RNA and VGAM133 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA, VGAM5 RNA, VGAM6 RNA, VGAM7 RNA and VGAM8 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[38542] VGAM126 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM126 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM126 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM126 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[38543] VGAM127 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM127 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM127 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM127 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of

Fig. 1.

[38544] VGAM128 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM128 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM128 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM128 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[38545] VGAM129 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM129 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM129 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM129 host target protein, herein schematically

represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[38546] VGAM130 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM130 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM130 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM130 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[38547] VGAM131 RNA, herein schematically represented by VGAM6 binds complimentarily to a host target binding site located in an untranslated region of VGAM131 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM131 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA

into VGAM131 host target protein, herein schematically represented by VGAM6 HOST TARGET PROTEIN, both of Fig. 1.

[38548] VGAM132 RNA, herein schematically represented by VGAM7 binds complimentarily to a host target binding site located in an untranslated region of VGAM132 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM132 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA into VGAM132 host target protein, herein schematically represented by VGAM7 HOST TARGET PROTEIN, both of Fig. 1.

[38549] VGAM133 RNA, herein schematically represented by VGAM8 binds complimentarily to a host target binding site located in an untranslated region of VGAM133 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM133 host target RNA, herein

schematically represented by VGAM8 HOST TARGET RNA into VGAM133 host target protein, herein schematically represented by VGAM8 HOST TARGET PROTEIN, both of Fig. 1.

[38550] It is appreciated that a function of VGR2756 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2756 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2756 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2756 gene: VGAM126 host target protein, VGAM127 host target protein, VGAM128 host target protein, VGAM129 host target protein, VGAM130 host target protein, VGAM131 host target protein, VGAM132 host target protein and VGAM133 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM126, VGAM127, VGAM128, VGAM129, VGAM130,

VGAM131, VGAM132 and VGAM133

[38551] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2757(VGR2757) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[38552] VGR2757 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2757 gene was detected is described hereinabove with reference to Figs. 6-15.

[38553] VGR2757 gene encodes VGR2757 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38554] VGR2757 precursor RNA folds spatially, forming VGR2757 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2757 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to

the fact that the nucleotide sequence of VGR2757 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38555] VGR2757 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM134 precursor RNA, VGAM135 precursor RNA, VGAM136 precursor RNA, VGAM137 precursor RNA, VGAM138 precursor RNA, VGAM139 precursor RNA, VGAM140 precursor RNA and VGAM141 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR, VGAM5 PRECURSOR, VGAM6 PRECURSOR, VGAM7 PRECURSOR and VGAM8 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[38556] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM134 RNA, VGAM135 RNA, VGAM136 RNA, VGAM137 RNA,

VGAM138 RNA, VGAM139 RNA, VGAM140 RNA and VGAM141 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA, VGAM5 RNA, VGAM6 RNA, VGAM7 RNA and VGAM8 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[38557] VGAM134 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM134 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM134 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM134 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[38558] VGAM135 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM135 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corre-

sponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM135 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM135 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[38559] VGAM136 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM136 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM136 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM136 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[38560] VGAM137 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM137 host target RNA, herein schematically represented by VGAM4

HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM137 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM137 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[38561] VGAM138 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM138 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM138 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM138 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[38562] VGAM139 RNA, herein schematically represented by VGAM6 binds complimentarily to a host target binding site located in an untranslated region of VGAM139 host

target RNA, herein schematically represented by VGAM6 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM139 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA into VGAM139 host target protein, herein schematically represented by VGAM6 HOST TARGET PROTEIN, both of Fig. 1.

[38563] VGAM140 RNA, herein schematically represented by VGAM7 binds complimentarily to a host target binding site located in an untranslated region of VGAM140 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM140 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA into VGAM140 host target protein, herein schematically represented by VGAM7 HOST TARGET PROTEIN, both of Fig. 1.

[38564] VGAM141 RNA, herein schematically represented by VGAM8 binds complimentarily to a host target binding

site located in an untranslated region of VGAM141 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM141 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA into VGAM141 host target protein, herein schematically represented by VGAM8 HOST TARGET PROTEIN, both of Fig. 1.

[38565] It is appreciated that a function of VGR2757 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2757 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2757 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2757 gene: VGAM134 host target protein, VGAM135 host target protein, VGAM136 host target protein, VGAM137 host target protein, VGAM138 host target protein, VGAM139 host target pro-

tein, VGAM140 host target protein and VGAM141 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM134, VGAM135, VGAM136, VGAM137, VGAM138, VGAM139, VGAM140 and VGAM141

[38566] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2758(VGR2758) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[38567] VGR2758 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2758 gene was detected is described hereinabove with reference to Figs. 6-15.

[38568] VGR2758 gene encodes VGR2758 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38569] VGR2758 precursor RNA folds spatially, forming VGR2758 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2758 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2758 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38570] VGR2758 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM142 precursor RNA, VGAM143 precursor RNA, VGAM144 precursor RNA, VGAM145 precursor RNA, VGAM146 precursor RNA, VGAM147 precursor RNA, VGAM148 precursor RNA and VGAM149 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR, VGAM5 PRECURSOR, VGAM6 PRECURSOR, VGAM7 PRECURSOR and VGAM8 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin

shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[38571] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM142 RNA, VGAM143 RNA, VGAM144 RNA, VGAM145 RNA, VGAM146 RNA, VGAM147 RNA, VGAM148 RNA and VGAM149 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA, VGAM5 RNA, VGAM6 RNA, VGAM7 RNA and VGAM8 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[38572] VGAM142 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM142 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM142 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM142 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of

Fig. 1.

[38573] VGAM143 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM143 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM143 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM143 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[38574] VGAM144 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM144 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM144 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM144 host target protein, herein schematically

represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[38575] VGAM145 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM145 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM145 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM145 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[38576] VGAM146 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM146 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM146 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA

into VGAM146 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[38577] VGAM147 RNA, herein schematically represented by VGAM6 binds complimentarily to a host target binding site located in an untranslated region of VGAM147 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM147 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA into VGAM147 host target protein, herein schematically represented by VGAM6 HOST TARGET PROTEIN, both of Fig. 1.

[38578] VGAM148 RNA, herein schematically represented by VGAM7 binds complimentarily to a host target binding site located in an untranslated region of VGAM148 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM148 host target RNA, herein

schematically represented by VGAM7 HOST TARGET RNA into VGAM148 host target protein, herein schematically represented by VGAM7 HOST TARGET PROTEIN, both of Fig. 1.

[38579] VGAM149 RNA, herein schematically represented by VGAM8 binds complimentarily to a host target binding site located in an untranslated region of VGAM149 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM149 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA into VGAM149 host target protein, herein schematically represented by VGAM8 HOST TARGET PROTEIN, both of Fig. 1.

[38580] It is appreciated that a function of VGR2758 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2758 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2758 gene, herein designated VGR GENE, correlate with, and

may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2758 gene: VGAM142 host target protein, VGAM143 host target protein, VGAM144 host target protein, VGAM145 host target protein, VGAM146 host target protein, VGAM147 host target protein, VGAM148 host target protein and VGAM149 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM142, VGAM143, VGAM144, VGAM145, VGAM146, VGAM147, VGAM148 and VGAM149

[38581] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2759(VGR2759) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[38582] VGR2759 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding,

RNA viral gene. The method by which VGR2759 gene was detected is described hereinabove with reference to Figs. 6-15.

[38583] VGR2759 gene encodes VGR2759 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38584] VGR2759 precursor RNA folds spatially, forming VGR2759 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2759 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2759 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38585] VGR2759 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM150 precursor RNA, VGAM151 precursor RNA, VGAM152 precursor RNA, VGAM153 precursor RNA, VGAM154 precursor RNA, VGAM155 precursor RNA,

VGAM156 precursor RNA and VGAM157 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR, VGAM5 PRECURSOR, VGAM6 PRECURSOR, VGAM7 PRECURSOR and VGAM8 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[38586] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM150 RNA, VGAM151 RNA, VGAM152 RNA, VGAM153 RNA, VGAM154 RNA, VGAM155 RNA, VGAM156 RNA and VGAM157 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA, VGAM5 RNA, VGAM6 RNA, VGAM7 RNA and VGAM8 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[38587] VGAM150 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM150 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corre-

sponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM150 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM150 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[38588] VGAM151 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM151 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM151 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM151 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[38589] VGAM152 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM152 host target RNA, herein schematically represented by VGAM3

HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM152 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM152 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[38590] VGAM153 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM153 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM153 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM153 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[38591] VGAM154 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM154 host

target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM154 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM154 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[38592] VGAM155 RNA, herein schematically represented by VGAM6 binds complimentarily to a host target binding site located in an untranslated region of VGAM155 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM155 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA into VGAM155 host target protein, herein schematically represented by VGAM6 HOST TARGET PROTEIN, both of Fig. 1.

[38593] VGAM156 RNA, herein schematically represented by VGAM7 binds complimentarily to a host target binding

site located in an untranslated region of VGAM156 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM156 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA into VGAM156 host target protein, herein schematically represented by VGAM7 HOST TARGET PROTEIN, both of Fig. 1.

[38594] VGAM157 RNA, herein schematically represented by VGAM8 binds complimentarily to a host target binding site located in an untranslated region of VGAM157 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM157 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA into VGAM157 host target protein, herein schematically represented by VGAM8 HOST TARGET PROTEIN, both of Fig. 1.

[38595] It is appreciated that a function of VGR2759 gene, herein

designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2759 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2759 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2759 gene: VGAM150 host target protein, VGAM151 host target protein, VGAM152 host target protein, VGAM153 host target protein, VGAM154 host target protein, VGAM155 host target protein, VGAM156 host target protein and VGAM157 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM150, VGAM151, VGAM152, VGAM153, VGAM154, VGAM155, VGAM156 and VGAM157

[38596] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2760(VGR2760) viral gene, which encodes an operon-like cluster of novel viral

micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[38597] VGR2760 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2760 gene was detected is described hereinabove with reference to Figs. 6-15.

[38598] VGR2760 gene encodes VGR2760 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38599] VGR2760 precursor RNA folds spatially, forming VGR2760 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2760 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2760 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38600] VGR2760 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM158 precursor RNA, VGAM159 precursor RNA, VGAM160 precursor RNA, VGAM161 precursor RNA, VGAM162 precursor RNA, VGAM163 precursor RNA, VGAM164 precursor RNA and VGAM165 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR, VGAM5 PRECURSOR, VGAM6 PRECURSOR, VGAM7 PRECURSOR and VGAM8 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[38601] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM158 RNA, VGAM159 RNA, VGAM160 RNA, VGAM161 RNA, VGAM162 RNA, VGAM163 RNA, VGAM164 RNA and VGAM165 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA, VGAM5 RNA, VGAM6 RNA, VGAM7 RNA and VGAM8 RNA respectively, each of which VGAM RNAs correspond-

ing to VGAM RNA of Fig. 8.

[38602] VGAM158 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM158 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM158 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM158 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[38603] VGAM159 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM159 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM159 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM159 host target protein, herein schematically

represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[38604] VGAM160 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM160 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM160 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM160 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[38605] VGAM161 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM161 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM161 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA

into VGAM161 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[38606] VGAM162 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM162 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM162 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM162 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[38607] VGAM163 RNA, herein schematically represented by VGAM6 binds complimentarily to a host target binding site located in an untranslated region of VGAM163 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM163 host target RNA, herein

schematically represented by VGAM6 HOST TARGET RNA into VGAM163 host target protein, herein schematically represented by VGAM6 HOST TARGET PROTEIN, both of Fig. 1.

[38608] VGAM164 RNA, herein schematically represented by VGAM7 binds complimentarily to a host target binding site located in an untranslated region of VGAM164 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM164 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA into VGAM164 host target protein, herein schematically represented by VGAM7 HOST TARGET PROTEIN, both of Fig. 1.

[38609] VGAM165 RNA, herein schematically represented by VGAM8 binds complimentarily to a host target binding site located in an untranslated region of VGAM165 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby in-

hibiting translation of VGAM165 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA into VGAM165 host target protein, herein schematically represented by VGAM8 HOST TARGET PROTEIN, both of Fig. 1.

[38610] It is appreciated that a function of VGR2760 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2760 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2760 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2760 gene: VGAM158 host target protein, VGAM159 host target protein, VGAM160 host target protein, VGAM161 host target protein, VGAM162 host target protein, VGAM163 host target protein, VGAM164 host target protein and VGAM165 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to

VGAM158, VGAM159, VGAM160, VGAM161, VGAM162, VGAM163, VGAM164 and VGAM165

[38611] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2761(VGR2761) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[38612] VGR2761 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2761 gene was detected is described hereinabove with reference to Figs. 6-15.

[38613] VGR2761 gene encodes VGR2761 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38614] VGR2761 precursor RNA folds spatially, forming VGR2761 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2761 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art

as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2761 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38615] VGR2761 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM166 precursor RNA, VGAM167 precursor RNA, VGAM168 precursor RNA, VGAM169 precursor RNA, VGAM170 precursor RNA, VGAM171 precursor RNA, VGAM172 precursor RNA and VGAM173 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR, VGAM5 PRECURSOR, VGAM6 PRECURSOR, VGAM7 PRECURSOR and VGAM8 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[38616] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM166

RNA, VGAM167 RNA, VGAM168 RNA, VGAM169 RNA, VGAM170 RNA, VGAM171 RNA, VGAM172 RNA and VGAM173 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA, VGAM5 RNA, VGAM6 RNA, VGAM7 RNA and VGAM8 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[38617] VGAM166 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM166 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM166 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM166 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[38618] VGAM167 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM167 host target RNA, herein schematically represented by VGAM2

HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM167 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM167 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[38619] VGAM168 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM168 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM168 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM168 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[38620] VGAM169 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM169 host

target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM169 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM169 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[38621] VGAM170 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM170 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM170 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM170 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[38622] VGAM171 RNA, herein schematically represented by VGAM6 binds complimentarily to a host target binding

site located in an untranslated region of VGAM171 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM171 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA into VGAM171 host target protein, herein schematically represented by VGAM6 HOST TARGET PROTEIN, both of Fig. 1.

[38623] VGAM172 RNA, herein schematically represented by VGAM7 binds complimentarily to a host target binding site located in an untranslated region of VGAM172 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM172 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA into VGAM172 host target protein, herein schematically represented by VGAM7 HOST TARGET PROTEIN, both of Fig. 1.

[38624] VGAM173 RNA, herein schematically represented by

VGAM8 binds complimentarily to a host target binding site located in an untranslated region of VGAM173 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM173 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA into VGAM173 host target protein, herein schematically represented by VGAM8 HOST TARGET PROTEIN, both of Fig. 1.

[38625] It is appreciated that a function of VGR2761 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2761 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2761 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2761 gene: VGAM166 host target protein, VGAM167 host target protein, VGAM168 host target protein, VGAM169 host target protein,

VGAM170 host target protein, VGAM171 host target protein, VGAM172 host target protein and VGAM173 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM166, VGAM167, VGAM168, VGAM169, VGAM170, VGAM171, VGAM172 and VGAM173

[38626] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2762(VGR2762) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[38627] VGR2762 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2762 gene was detected is described hereinabove with reference to Figs. 6-15.

[38628] VGR2762 gene encodes VGR2762 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typi-

cally several hundred nucleotides long.

[38629] VGR2762 precursor RNA folds spatially, forming VGR2762 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2762 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2762 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38630] VGR2762 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM174 precursor RNA, VGAM175 precursor RNA, VGAM176 precursor RNA, VGAM177 precursor RNA, VGAM178 precursor RNA, VGAM179 precursor RNA, VGAM180 precursor RNA and VGAM181 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR, VGAM5 PRECURSOR, VGAM6 PRECURSOR, VGAM7 PRECURSOR and VGAM8 PRECURSOR respectively,

each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[38631] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM174 RNA, VGAM175 RNA, VGAM176 RNA, VGAM177 RNA, VGAM178 RNA, VGAM179 RNA, VGAM180 RNA and VGAM181 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA, VGAM5 RNA, VGAM6 RNA, VGAM7 RNA and VGAM8 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[38632] VGAM174 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM174 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM174 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM174 host target protein, herein schematically

represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[38633] VGAM175 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM175 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM175 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM175 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[38634] VGAM176 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM176 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM176 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA

into VGAM176 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[38635] VGAM177 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM177 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM177 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM177 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[38636] VGAM178 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM178 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM178 host target RNA, herein

schematically represented by VGAM5 HOST TARGET RNA into VGAM178 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[38637] VGAM179 RNA, herein schematically represented by VGAM6 binds complimentarily to a host target binding site located in an untranslated region of VGAM179 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM179 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA into VGAM179 host target protein, herein schematically represented by VGAM6 HOST TARGET PROTEIN, both of Fig. 1.

[38638] VGAM180 RNA, herein schematically represented by VGAM7 binds complimentarily to a host target binding site located in an untranslated region of VGAM180 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby in-

hibiting translation of VGAM180 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA into VGAM180 host target protein, herein schematically represented by VGAM7 HOST TARGET PROTEIN, both of Fig. 1.

[38639] VGAM181 RNA, herein schematically represented by VGAM8 binds complimentarily to a host target binding site located in an untranslated region of VGAM181 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM181 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA into VGAM181 host target protein, herein schematically represented by VGAM8 HOST TARGET PROTEIN, both of Fig. 1.

[38640] It is appreciated that a function of VGR2762 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2762 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2762

gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2762 gene: VGAM174 host target protein, VGAM175 host target protein, VGAM176 host target protein, VGAM177 host target protein, VGAM178 host target protein, VGAM179 host target protein, VGAM180 host target protein and VGAM181 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM174, VGAM175, VGAM176, VGAM177, VGAM178, VGAM179, VGAM180 and VGAM181

[38641] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2763(VGR2763) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[38642] VGR2763 gene, herein designated VGR GENE, is a novel

bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2763 gene was detected is described hereinabove with reference to Figs. 6-15.

[38643] VGR2763 gene encodes VGR2763 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38644] VGR2763 precursor RNA folds spatially, forming VGR2763 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2763 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2763 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38645] VGR2763 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM182 precursor RNA, VGAM183 precursor RNA, VGAM184 precursor RNA, VGAM185 precursor

RNA, VGAM186 precursor RNA, VGAM187 precursor RNA, VGAM188 precursor RNA and VGAM189 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR, VGAM5 PRECURSOR, VGAM6 PRECURSOR, VGAM7 PRECURSOR and VGAM8 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[38646] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM182 RNA, VGAM183 RNA, VGAM184 RNA, VGAM185 RNA, VGAM186 RNA, VGAM187 RNA, VGAM188 RNA and VGAM189 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA, VGAM5 RNA, VGAM6 RNA, VGAM7 RNA and VGAM8 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[38647] VGAM182 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM182 host target RNA, herein schematically represented by VGAM1

HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM182 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM182 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[38648] VGAM183 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM183 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM183 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM183 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[38649] VGAM184 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM184 host

target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM184 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM184 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[38650] VGAM185 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM185 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM185 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM185 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[38651] VGAM186 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding

site located in an untranslated region of VGAM186 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM186 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM186 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[38652] VGAM187 RNA, herein schematically represented by VGAM6 binds complimentarily to a host target binding site located in an untranslated region of VGAM187 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM187 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA into VGAM187 host target protein, herein schematically represented by VGAM6 HOST TARGET PROTEIN, both of Fig. 1.

[38653] VGAM188 RNA, herein schematically represented by

VGAM7 binds complimentarily to a host target binding site located in an untranslated region of VGAM188 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM188 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA into VGAM188 host target protein, herein schematically represented by VGAM7 HOST TARGET PROTEIN, both of Fig. 1.

[38654] VGAM189 RNA, herein schematically represented by VGAM8 binds complimentarily to a host target binding site located in an untranslated region of VGAM189 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM189 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA into VGAM189 host target protein, herein schematically represented by VGAM8 HOST TARGET PROTEIN, both of Fig. 1.

[38655] It is appreciated that a function of VGR2763 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2763 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2763 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2763 gene: VGAM182 host target protein, VGAM183 host target protein, VGAM184 host target protein, VGAM185 host target protein, VGAM186 host target protein, VGAM187 host target protein, VGAM188 host target protein and VGAM189 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM182, VGAM183, VGAM184, VGAM185, VGAM186, VGAM187, VGAM188 and VGAM189

[38656] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2764(VGR2764) viral

gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[38657] VGR2764 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2764 gene was detected is described hereinabove with reference to Figs. 6-15.

[38658] VGR2764 gene encodes VGR2764 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38659] VGR2764 precursor RNA folds spatially, forming VGR2764 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2764 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2764 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the

second half thereof, as is well known in the art.

[38660] VGR2764 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM190 precursor RNA, VGAM191 precursor RNA, VGAM192 precursor RNA, VGAM193 precursor RNA, VGAM194 precursor RNA, VGAM195 precursor RNA, VGAM196 precursor RNA and VGAM197 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR, VGAM5 PRECURSOR, VGAM6 PRECURSOR, VGAM7 PRECURSOR and VGAM8 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[38661] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM190 RNA, VGAM191 RNA, VGAM192 RNA, VGAM193 RNA, VGAM194 RNA, VGAM195 RNA, VGAM196 RNA and VGAM197 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA, VGAM5 RNA, VGAM6 RNA, VGAM7 RNA and VGAM8

RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[38662] VGAM190 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM190 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM190 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM190 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[38663] VGAM191 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM191 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM191 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA

into VGAM191 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[38664] VGAM192 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM192 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM192 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM192 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[38665] VGAM193 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM193 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM193 host target RNA, herein

schematically represented by VGAM4 HOST TARGET RNA into VGAM193 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[38666] VGAM194 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM194 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM194 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM194 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[38667] VGAM195 RNA, herein schematically represented by VGAM6 binds complimentarily to a host target binding site located in an untranslated region of VGAM195 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby in-

hibiting translation of VGAM195 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA into VGAM195 host target protein, herein schematically represented by VGAM6 HOST TARGET PROTEIN, both of Fig. 1.

[38668] VGAM196 RNA, herein schematically represented by VGAM7 binds complimentarily to a host target binding site located in an untranslated region of VGAM196 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM196 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA into VGAM196 host target protein, herein schematically represented by VGAM7 HOST TARGET PROTEIN, both of Fig. 1.

[38669] VGAM197 RNA, herein schematically represented by VGAM8 binds complimentarily to a host target binding site located in an untranslated region of VGAM197 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM197 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA into VGAM197 host target protein, herein schematically represented by VGAM8 HOST TARGET PROTEIN, both of Fig. 1.

[38670] It is appreciated that a function of VGR2764 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2764 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2764 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2764 gene: VGAM190 host target protein, VGAM191 host target protein, VGAM192 host target protein, VGAM193 host target protein, VGAM194 host target protein, VGAM195 host target protein, VGAM196 host target protein and VGAM197 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host tar-

get genes is elaborated hereinabove with reference to VGAM190, VGAM191, VGAM192, VGAM193, VGAM194, VGAM195, VGAM196 and VGAM197

[38671] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2765(VGR2765) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[38672] VGR2765 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2765 gene was detected is described hereinabove with reference to Figs. 6-15.

[38673] VGR2765 gene encodes VGR2765 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38674] VGR2765 precursor RNA folds spatially, forming VGR2765 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2765 folded precursor RNA, herein designated VGR FOLDED PRECUR-

SOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2765 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38675] VGR2765 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM198 precursor RNA, VGAM199 precursor RNA, VGAM200 precursor RNA, VGAM201 precursor RNA, VGAM202 precursor RNA, VGAM203 precursor RNA, VGAM204 precursor RNA and VGAM205 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR, VGAM5 PRECURSOR, VGAM6 PRECURSOR, VGAM7 PRECURSOR and VGAM8 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[38676] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA

segments of about 22 nucleotides in length, VGAM198 RNA, VGAM199 RNA, VGAM200 RNA, VGAM201 RNA, VGAM202 RNA, VGAM203 RNA, VGAM204 RNA and VGAM205 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA, VGAM5 RNA, VGAM6 RNA, VGAM7 RNA and VGAM8 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[38677] VGAM198 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM198 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM198 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM198 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[38678] VGAM199 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM199 host

target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM199 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM199 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[38679] VGAM200 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM200 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM200 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM200 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[38680] VGAM201 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding

site located in an untranslated region of VGAM201 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM201 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM201 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[38681] VGAM202 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM202 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM202 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM202 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[38682] VGAM203 RNA, herein schematically represented by

VGAM6 binds complimentarily to a host target binding site located in an untranslated region of VGAM203 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM203 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA into VGAM203 host target protein, herein schematically represented by VGAM6 HOST TARGET PROTEIN, both of Fig. 1.

[38683] VGAM204 RNA, herein schematically represented by VGAM7 binds complimentarily to a host target binding site located in an untranslated region of VGAM204 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM204 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA into VGAM204 host target protein, herein schematically represented by VGAM7 HOST TARGET PROTEIN, both of Fig. 1.

[38684] VGAM205 RNA, herein schematically represented by VGAM8 binds complimentarily to a host target binding site located in an untranslated region of VGAM205 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM205 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA into VGAM205 host target protein, herein schematically represented by VGAM8 HOST TARGET PROTEIN, both of Fig. 1.

[38685] It is appreciated that a function of VGR2765 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2765 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2765 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2765 gene: VGAM198 host target protein, VGAM199 host target protein, VGAM200

host target protein, VGAM201 host target protein, VGAM202 host target protein, VGAM203 host target protein, VGAM204 host target protein and VGAM205 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM198, VGAM199, VGAM200, VGAM201, VGAM202, VGAM203, VGAM204 and VGAM205

[38686] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2766(VGR2766) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[38687] VGR2766 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2766 gene was detected is described hereinabove with reference to Figs. 6-15.

[38688] VGR2766 gene encodes VGR2766 precursor RNA, herein

designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38689] VGR2766 precursor RNA folds spatially, forming VGR2766 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2766 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2766 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38690] VGR2766 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM206 precursor RNA, VGAM207 precursor RNA, VGAM208 precursor RNA, VGAM209 precursor RNA and VGAM210 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR and VGAM5 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to

VGAM PRECURSOR RNA of Fig. 8.

[38691] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM206 RNA, VGAM207 RNA, VGAM208 RNA, VGAM209 RNA and VGAM210 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA and VGAM5 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[38692] VGAM206 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM206 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM206 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM206 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[38693] VGAM207 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding

site located in an untranslated region of VGAM207 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM207 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM207 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[38694] VGAM208 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM208 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM208 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM208 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[38695] VGAM209 RNA, herein schematically represented by

VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM209 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM209 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM209 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[38696] VGAM210 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM210 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM210 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM210 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[38697] It is appreciated that a function of VGR2766 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2766 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2766 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2766 gene: VGAM206 host target protein, VGAM207 host target protein, VGAM208 host target protein, VGAM209 host target protein and VGAM210 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM206, VGAM207, VGAM208, VGAM209 and VGAM210

[38698] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2767(VGR2767) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates

expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[38699] VGR2767 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2767 gene was detected is described hereinabove with reference to Figs. 6-15.

[38700] VGR2767 gene encodes VGR2767 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38701] VGR2767 precursor RNA folds spatially, forming VGR2767 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2767 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2767 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38702] VGR2767 folded precursor RNA, herein designated VGR

FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM211 precursor RNA, VGAM212 precursor RNA and VGAM213 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR and VGAM3 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[38703] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM211 RNA, VGAM212 RNA and VGAM213 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA and VGAM3 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[38704] VGAM211 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM211 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM211 host target RNA, herein

schematically represented by VGAM1 HOST TARGET RNA into VGAM211 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[38705] VGAM212 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM212 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM212 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM212 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[38706] VGAM213 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM213 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby in-

hibiting translation of VGAM213 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM213 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[38707] It is appreciated that a function of VGR2767 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2767 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2767 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2767 gene: VGAM211 host target protein, VGAM212 host target protein and VGAM213 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM211, VGAM212 and VGAM213

[38708] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred

to here as Viral Genomic Record 2768(VGR2768) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[38709] VGR2768 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2768 gene was detected is described hereinabove with reference to Figs. 6-15.

[38710] VGR2768 gene encodes VGR2768 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38711] VGR2768 precursor RNA folds spatially, forming VGR2768 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2768 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2768 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which

is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38712] VGR2768 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM214 precursor RNA and VGAM215 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[38713] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM214 RNA and VGAM215 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[38714] VGAM214 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM214 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corre-

sponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM214 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM214 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[38715] VGAM215 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM215 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM215 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM215 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[38716] It is appreciated that a function of VGR2768 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2768 gene include

diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2768 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2768 gene: VGAM214 host target protein and VGAM215 host target protein, herein schematically represented by VGAM1 HOST TARGET PRO-TEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated herein-above with reference to VGAM214 and VGAM215

[38717] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2769(VGR2769) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[38718] VGR2769 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2769 gene was detected is described hereinabove with reference to Figs.

6-15.

[38719] VGR2769 gene encodes VGR2769 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38720] VGR2769 precursor RNA folds spatially, forming VGR2769 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2769 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2769 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38721] VGR2769 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM216 precursor RNA and VGAM217 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig.

8.

[38722] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM216 RNA and VGAM217 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[38723] VGAM216 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM216 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM216 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM216 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[38724] VGAM217 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM217 host

target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM217 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM217 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[38725] It is appreciated that a function of VGR2769 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2769 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2769 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2769 gene: VGAM216 host target protein and VGAM217 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated herein-

above with reference to VGAM216 and VGAM217

[38726] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2770(VGR2770) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[38727] VGR2770 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2770 gene was detected is described hereinabove with reference to Figs. 6-15.

[38728] VGR2770 gene encodes VGR2770 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38729] VGR2770 precursor RNA folds spatially, forming VGR2770 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2770 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to

the fact that the nucleotide sequence of VGR2770 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38730] VGR2770 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM218 precursor RNA and VGAM219 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[38731] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM218 RNA and VGAM219 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[38732] VGAM218 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding

site located in an untranslated region of VGAM218 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM218 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM218 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[38733] VGAM219 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM219 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM219 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM219 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[38734] It is appreciated that a function of VGR2770 gene, herein

designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2770 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2770 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2770 gene: VGAM218 host target protein and VGAM219 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM218 and VGAM219

[38735] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2771(VGR2771) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[38736] VGR2771 gene, herein designated VGR GENE, is a novel

bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2771 gene was detected is described hereinabove with reference to Figs. 6-15.

[38737] VGR2771 gene encodes VGR2771 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38738] VGR2771 precursor RNA folds spatially, forming VGR2771 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2771 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2771 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38739] VGR2771 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM220 precursor RNA, VGAM221 precursor RNA, VGAM222 precursor RNA, VGAM223 precursor

RNA, VGAM224 precursor RNA, VGAM225 precursor RNA, VGAM226 precursor RNA and VGAM227 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR, VGAM5 PRECURSOR, VGAM6 PRECURSOR, VGAM7 PRECURSOR and VGAM8 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[38740] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM220 RNA, VGAM221 RNA, VGAM222 RNA, VGAM223 RNA, VGAM224 RNA, VGAM225 RNA, VGAM226 RNA and VGAM227 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA, VGAM5 RNA, VGAM6 RNA, VGAM7 RNA and VGAM8 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[38741] VGAM220 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM220 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM220 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM220 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[38742] VGAM221 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM221 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM221 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM221 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of

Fig. 1.

[38743] VGAM222 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM222 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM222 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM222 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[38744] VGAM223 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM223 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM223 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM223 host target protein, herein schematically

represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[38745] VGAM224 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM224 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM224 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM224 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[38746] VGAM225 RNA, herein schematically represented by VGAM6 binds complimentarily to a host target binding site located in an untranslated region of VGAM225 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM225 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA

into VGAM225 host target protein, herein schematically represented by VGAM6 HOST TARGET PROTEIN, both of Fig. 1.

[38747] VGAM226 RNA, herein schematically represented by VGAM7 binds complimentarily to a host target binding site located in an untranslated region of VGAM226 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM226 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA into VGAM226 host target protein, herein schematically represented by VGAM7 HOST TARGET PROTEIN, both of Fig. 1.

[38748] VGAM227 RNA, herein schematically represented by VGAM8 binds complimentarily to a host target binding site located in an untranslated region of VGAM227 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM227 host target RNA, herein

schematically represented by VGAM8 HOST TARGET RNA into VGAM227 host target protein, herein schematically represented by VGAM8 HOST TARGET PROTEIN, both of Fig. 1.

[38749] It is appreciated that a function of VGR2771 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2771 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2771 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2771 gene: VGAM220 host target protein, VGAM221 host target protein, VGAM222 host target protein, VGAM223 host target protein, VGAM224 host target protein, VGAM225 host target protein, VGAM226 host target protein and VGAM227 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM220, VGAM221, VGAM222, VGAM223, VGAM224,

VGAM225, VGAM226 and VGAM227

[38750] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2772(VGR2772) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[38751] VGR2772 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2772 gene was detected is described hereinabove with reference to Figs. 6-15.

[38752] VGR2772 gene encodes VGR2772 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38753] VGR2772 precursor RNA folds spatially, forming VGR2772 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2772 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to

the fact that the nucleotide sequence of VGR2772 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38754] VGR2772 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM228 precursor RNA, VGAM229 precursor RNA, VGAM230 precursor RNA, VGAM231 precursor RNA, VGAM232 precursor RNA, VGAM233 precursor RNA, VGAM234 precursor RNA and VGAM235 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR, VGAM5 PRECURSOR, VGAM6 PRECURSOR, VGAM7 PRECURSOR and VGAM8 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[38755] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM228 RNA, VGAM229 RNA, VGAM230 RNA, VGAM231 RNA,

VGAM232 RNA, VGAM233 RNA, VGAM234 RNA and VGAM235 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA, VGAM5 RNA, VGAM6 RNA, VGAM7 RNA and VGAM8 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[38756] VGAM228 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM228 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM228 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM228 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[38757] VGAM229 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM229 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corre-

sponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM229 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM229 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[38758] VGAM230 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM230 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM230 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM230 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[38759] VGAM231 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM231 host target RNA, herein schematically represented by VGAM4

HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM231 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM231 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[38760] VGAM232 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM232 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM232 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM232 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[38761] VGAM233 RNA, herein schematically represented by VGAM6 binds complimentarily to a host target binding site located in an untranslated region of VGAM233 host

target RNA, herein schematically represented by VGAM6 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM233 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA into VGAM233 host target protein, herein schematically represented by VGAM6 HOST TARGET PROTEIN, both of Fig. 1.

[38762] VGAM234 RNA, herein schematically represented by VGAM7 binds complimentarily to a host target binding site located in an untranslated region of VGAM234 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM234 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA into VGAM234 host target protein, herein schematically represented by VGAM7 HOST TARGET PROTEIN, both of Fig. 1.

[38763] VGAM235 RNA, herein schematically represented by VGAM8 binds complimentarily to a host target binding

site located in an untranslated region of VGAM235 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM235 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA into VGAM235 host target protein, herein schematically represented by VGAM8 HOST TARGET PROTEIN, both of Fig. 1.

[38764] It is appreciated that a function of VGR2772 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2772 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2772 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2772 gene: VGAM228 host target protein, VGAM229 host target protein, VGAM230 host target protein, VGAM231 host target protein, VGAM232 host target protein, VGAM233 host target pro-

tein, VGAM234 host target protein and VGAM235 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM228, VGAM229, VGAM230, VGAM231, VGAM232, VGAM233, VGAM234 and VGAM235

[38765] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2773(VGR2773) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[38766] VGR2773 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2773 gene was detected is described hereinabove with reference to Figs. 6-15.

[38767] VGR2773 gene encodes VGR2773 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38768] VGR2773 precursor RNA folds spatially, forming VGR2773 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2773 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2773 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38769] VGR2773 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM236 precursor RNA, VGAM237 precursor RNA, VGAM238 precursor RNA, VGAM239 precursor RNA, VGAM240 precursor RNA, VGAM241 precursor RNA, VGAM242 precursor RNA and VGAM243 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR, VGAM5 PRECURSOR, VGAM6 PRECURSOR, VGAM7 PRECURSOR and VGAM8 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin

shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[38770] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM236 RNA, VGAM237 RNA, VGAM238 RNA, VGAM239 RNA, VGAM240 RNA, VGAM241 RNA, VGAM242 RNA and VGAM243 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA, VGAM5 RNA, VGAM6 RNA, VGAM7 RNA and VGAM8 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[38771] VGAM236 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM236 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM236 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM236 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of

Fig. 1.

[38772] VGAM237 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM237 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM237 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM237 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[38773] VGAM238 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM238 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM238 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM238 host target protein, herein schematically

represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[38774] VGAM239 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM239 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM239 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM239 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[38775] VGAM240 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM240 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM240 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA

into VGAM240 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[38776] VGAM241 RNA, herein schematically represented by VGAM6 binds complimentarily to a host target binding site located in an untranslated region of VGAM241 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM241 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA into VGAM241 host target protein, herein schematically represented by VGAM6 HOST TARGET PROTEIN, both of Fig. 1.

[38777] VGAM242 RNA, herein schematically represented by VGAM7 binds complimentarily to a host target binding site located in an untranslated region of VGAM242 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM242 host target RNA, herein

schematically represented by VGAM7 HOST TARGET RNA into VGAM242 host target protein, herein schematically represented by VGAM7 HOST TARGET PROTEIN, both of Fig. 1.

[38778] VGAM243 RNA, herein schematically represented by VGAM8 binds complimentarily to a host target binding site located in an untranslated region of VGAM243 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM243 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA into VGAM243 host target protein, herein schematically represented by VGAM8 HOST TARGET PROTEIN, both of Fig. 1.

[38779] It is appreciated that a function of VGR2773 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2773 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2773 gene, herein designated VGR GENE, correlate with, and

may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2773 gene: VGAM236 host target protein, VGAM237 host target protein, VGAM238 host target protein, VGAM239 host target protein, VGAM240 host target protein, VGAM241 host target protein, VGAM242 host target protein and VGAM243 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM236, VGAM237, VGAM238, VGAM239, VGAM240, VGAM241, VGAM242 and VGAM243

[38780] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2774(VGR2774) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[38781] VGR2774 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding,

RNA viral gene. The method by which VGR2774 gene was detected is described hereinabove with reference to Figs. 6-15.

[38782] VGR2774 gene encodes VGR2774 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38783] VGR2774 precursor RNA folds spatially, forming VGR2774 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2774 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2774 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38784] VGR2774 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM244 precursor RNA, VGAM245 precursor RNA, VGAM246 precursor RNA, VGAM247 precursor RNA, VGAM248 precursor RNA, VGAM249 precursor RNA,

VGAM250 precursor RNA and VGAM251 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR, VGAM5 PRECURSOR, VGAM6 PRECURSOR, VGAM7 PRECURSOR and VGAM8 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[38785] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM244 RNA, VGAM245 RNA, VGAM246 RNA, VGAM247 RNA, VGAM248 RNA, VGAM249 RNA, VGAM250 RNA and VGAM251 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA, VGAM5 RNA, VGAM6 RNA, VGAM7 RNA and VGAM8 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[38786] VGAM244 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM244 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corre-

sponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM244 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM244 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[38787] VGAM245 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM245 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM245 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM245 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[38788] VGAM246 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM246 host target RNA, herein schematically represented by VGAM3

HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM246 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM246 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[38789] VGAM247 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM247 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM247 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM247 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[38790] VGAM248 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM248 host

target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM248 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM248 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[38791] VGAM249 RNA, herein schematically represented by VGAM6 binds complimentarily to a host target binding site located in an untranslated region of VGAM249 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM249 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA into VGAM249 host target protein, herein schematically represented by VGAM6 HOST TARGET PROTEIN, both of Fig. 1.

[38792] VGAM250 RNA, herein schematically represented by VGAM7 binds complimentarily to a host target binding

site located in an untranslated region of VGAM250 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM250 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA into VGAM250 host target protein, herein schematically represented by VGAM7 HOST TARGET PROTEIN, both of Fig. 1.

[38793] VGAM251 RNA, herein schematically represented by VGAM8 binds complimentarily to a host target binding site located in an untranslated region of VGAM251 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM251 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA into VGAM251 host target protein, herein schematically represented by VGAM8 HOST TARGET PROTEIN, both of Fig. 1.

[38794] It is appreciated that a function of VGR2774 gene, herein

designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2774 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2774 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2774 gene: VGAM244 host target protein, VGAM245 host target protein, VGAM246 host target protein, VGAM247 host target protein, VGAM248 host target protein, VGAM249 host target protein, VGAM250 host target protein and VGAM251 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM244, VGAM245, VGAM246, VGAM247, VGAM248, VGAM249, VGAM250 and VGAM251

[38795] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2775(VGR2775) viral gene, which encodes an operon-like cluster of novel viral

micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[38796] VGR2775 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2775 gene was detected is described hereinabove with reference to Figs. 6-15.

[38797] VGR2775 gene encodes VGR2775 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38798] VGR2775 precursor RNA folds spatially, forming VGR2775 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2775 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2775 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38799] VGR2775 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM252 precursor RNA, VGAM253 precursor RNA, VGAM254 precursor RNA, VGAM255 precursor RNA, VGAM256 precursor RNA, VGAM257 precursor RNA, VGAM258 precursor RNA and VGAM259 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR, VGAM5 PRECURSOR, VGAM6 PRECURSOR, VGAM7 PRECURSOR and VGAM8 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[38800] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM252 RNA, VGAM253 RNA, VGAM254 RNA, VGAM255 RNA, VGAM256 RNA, VGAM257 RNA, VGAM258 RNA and VGAM259 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA, VGAM5 RNA, VGAM6 RNA, VGAM7 RNA and VGAM8 RNA respectively, each of which VGAM RNAs correspond-

ing to VGAM RNA of Fig. 8.

[38801] VGAM252 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM252 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM252 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM252 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[38802] VGAM253 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM253 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM253 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM253 host target protein, herein schematically

represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[38803] VGAM254 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM254 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM254 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM254 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[38804] VGAM255 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM255 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM255 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA

into VGAM255 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[38805] VGAM256 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM256 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM256 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM256 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[38806] VGAM257 RNA, herein schematically represented by VGAM6 binds complimentarily to a host target binding site located in an untranslated region of VGAM257 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM257 host target RNA, herein

schematically represented by VGAM6 HOST TARGET RNA into VGAM257 host target protein, herein schematically represented by VGAM6 HOST TARGET PROTEIN, both of Fig. 1.

[38807] VGAM258 RNA, herein schematically represented by VGAM7 binds complimentarily to a host target binding site located in an untranslated region of VGAM258 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM258 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA into VGAM258 host target protein, herein schematically represented by VGAM7 HOST TARGET PROTEIN, both of Fig. 1.

[38808] VGAM259 RNA, herein schematically represented by VGAM8 binds complimentarily to a host target binding site located in an untranslated region of VGAM259 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby in-

hibiting translation of VGAM259 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA into VGAM259 host target protein, herein schematically represented by VGAM8 HOST TARGET PROTEIN, both of Fig. 1.

[38809] It is appreciated that a function of VGR2775 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2775 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2775 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2775 gene: VGAM252 host target protein, VGAM253 host target protein, VGAM254 host target protein, VGAM255 host target protein, VGAM256 host target protein, VGAM257 host target protein, VGAM258 host target protein and VGAM259 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to

VGAM252, VGAM253, VGAM254, VGAM255, VGAM256, VGAM257, VGAM258 and VGAM259

[38810] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2776(VGR2776) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[38811] VGR2776 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2776 gene was detected is described hereinabove with reference to Figs. 6-15.

[38812] VGR2776 gene encodes VGR2776 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38813] VGR2776 precursor RNA folds spatially, forming VGR2776 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2776 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art

as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2776 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38814] VGR2776 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 6 separate VGAM precursor RNAs, VGAM260 precursor RNA, VGAM261 precursor RNA, VGAM262 precursor RNA, VGAM263 precursor RNA, VGAM264 precursor RNA and VGAM265 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR, VGAM5 PRECURSOR and VGAM6 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[38815] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM260 RNA, VGAM261 RNA, VGAM262 RNA, VGAM263 RNA, VGAM264 RNA and VGAM265 RNA respectively, herein

schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA, VGAM5 RNA and VGAM6 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[38816] VGAM260 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM260 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM260 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM260 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[38817] VGAM261 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM261 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby in-

hibiting translation of VGAM261 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM261 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[38818] VGAM262 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM262 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM262 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM262 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[38819] VGAM263 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM263 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM263 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM263 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[38820] VGAM264 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM264 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM264 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM264 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[38821] VGAM265 RNA, herein schematically represented by VGAM6 binds complimentarily to a host target binding site located in an untranslated region of VGAM265 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA, which host target binding site corre-

sponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM265 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA into VGAM265 host target protein, herein schematically represented by VGAM6 HOST TARGET PROTEIN, both of Fig. 1.

[38822] It is appreciated that a function of VGR2776 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2776 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2776 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2776 gene: VGAM260 host target protein, VGAM261 host target protein, VGAM262 host target protein, VGAM263 host target protein, VGAM264 host target protein and VGAM265 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is

elaborated hereinabove with reference to VGAM260, VGAM261, VGAM262, VGAM263, VGAM264 and VGAM265

[38823] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2777(VGR2777) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[38824] VGR2777 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2777 gene was detected is described hereinabove with reference to Figs. 6-15.

[38825] VGR2777 gene encodes VGR2777 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38826] VGR2777 precursor RNA folds spatially, forming VGR2777 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2777 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art

as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2777 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38827] VGR2777 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM266 precursor RNA, VGAM267 precursor RNA, VGAM268 precursor RNA, VGAM269 precursor RNA, VGAM270 precursor RNA, VGAM271 precursor RNA, VGAM272 precursor RNA and VGAM273 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR, VGAM5 PRECURSOR, VGAM6 PRECURSOR, VGAM7 PRECURSOR and VGAM8 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[38828] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM266

RNA, VGAM267 RNA, VGAM268 RNA, VGAM269 RNA, VGAM270 RNA, VGAM271 RNA, VGAM272 RNA and VGAM273 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA, VGAM5 RNA, VGAM6 RNA, VGAM7 RNA and VGAM8 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[38829] VGAM266 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM266 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM266 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM266 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[38830] VGAM267 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM267 host target RNA, herein schematically represented by VGAM2

HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM267 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM267 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[38831] VGAM268 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM268 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM268 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM268 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[38832] VGAM269 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM269 host

target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM269 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM269 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[38833] VGAM270 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM270 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM270 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM270 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[38834] VGAM271 RNA, herein schematically represented by VGAM6 binds complimentarily to a host target binding

site located in an untranslated region of VGAM271 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM271 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA into VGAM271 host target protein, herein schematically represented by VGAM6 HOST TARGET PROTEIN, both of Fig. 1.

[38835] VGAM272 RNA, herein schematically represented by VGAM7 binds complimentarily to a host target binding site located in an untranslated region of VGAM272 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM272 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA into VGAM272 host target protein, herein schematically represented by VGAM7 HOST TARGET PROTEIN, both of Fig. 1.

[38836] VGAM273 RNA, herein schematically represented by

VGAM8 binds complimentarily to a host target binding site located in an untranslated region of VGAM273 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM273 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA into VGAM273 host target protein, herein schematically represented by VGAM8 HOST TARGET PROTEIN, both of Fig. 1.

[38837] It is appreciated that a function of VGR2777 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2777 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2777 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2777 gene: VGAM266 host target protein, VGAM267 host target protein, VGAM268 host target protein, VGAM269 host target protein,

VGAM270 host target protein, VGAM271 host target protein, VGAM272 host target protein and VGAM273 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM266, VGAM267, VGAM268, VGAM269, VGAM270, VGAM271, VGAM272 and VGAM273

[38838] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2778(VGR2778) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[38839] VGR2778 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2778 gene was detected is described hereinabove with reference to Figs. 6-15.

[38840] VGR2778 gene encodes VGR2778 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typi-

cally several hundred nucleotides long.

[38841] VGR2778 precursor RNA folds spatially, forming VGR2778 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2778 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2778 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38842] VGR2778 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM274 precursor RNA, VGAM275 precursor RNA, VGAM276 precursor RNA, VGAM277 precursor RNA, VGAM278 precursor RNA, VGAM279 precursor RNA, VGAM280 precursor RNA and VGAM281 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR, VGAM5 PRECURSOR, VGAM6 PRECURSOR, VGAM7 PRECURSOR and VGAM8 PRECURSOR respectively,

each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[38843] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM274 RNA, VGAM275 RNA, VGAM276 RNA, VGAM277 RNA, VGAM278 RNA, VGAM279 RNA, VGAM280 RNA and VGAM281 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA, VGAM5 RNA, VGAM6 RNA, VGAM7 RNA and VGAM8 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[38844] VGAM274 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM274 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM274 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM274 host target protein, herein schematically

represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[38845] VGAM275 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM275 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM275 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM275 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[38846] VGAM276 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM276 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM276 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA

into VGAM276 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[38847] VGAM277 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM277 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM277 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM277 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[38848] VGAM278 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM278 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM278 host target RNA, herein

schematically represented by VGAM5 HOST TARGET RNA into VGAM278 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[38849] VGAM279 RNA, herein schematically represented by VGAM6 binds complimentarily to a host target binding site located in an untranslated region of VGAM279 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM279 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA into VGAM279 host target protein, herein schematically represented by VGAM6 HOST TARGET PROTEIN, both of Fig. 1.

[38850] VGAM280 RNA, herein schematically represented by VGAM7 binds complimentarily to a host target binding site located in an untranslated region of VGAM280 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby in-

hibiting translation of VGAM280 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA into VGAM280 host target protein, herein schematically represented by VGAM7 HOST TARGET PROTEIN, both of Fig. 1.

[38851] VGAM281 RNA, herein schematically represented by VGAM8 binds complimentarily to a host target binding site located in an untranslated region of VGAM281 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM281 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA into VGAM281 host target protein, herein schematically represented by VGAM8 HOST TARGET PROTEIN, both of Fig. 1.

[38852] It is appreciated that a function of VGR2778 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2778 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2778

gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2778 gene: VGAM274 host target protein, VGAM275 host target protein, VGAM276 host target protein, VGAM277 host target protein, VGAM278 host target protein, VGAM279 host target protein, VGAM280 host target protein and VGAM281 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM274, VGAM275, VGAM276, VGAM277, VGAM278, VGAM279, VGAM280 and VGAM281

[38853] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2779(VGR2779) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[38854] VGR2779 gene, herein designated VGR GENE, is a novel

bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2779 gene was detected is described hereinabove with reference to Figs. 6-15.

[38855] VGR2779 gene encodes VGR2779 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38856] VGR2779 precursor RNA folds spatially, forming VGR2779 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2779 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2779 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38857] VGR2779 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM282 precursor RNA, VGAM283 precursor RNA, VGAM284 precursor RNA, VGAM285 precursor

RNA, VGAM286 precursor RNA, VGAM287 precursor RNA, VGAM288 precursor RNA and VGAM289 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR, VGAM5 PRECURSOR, VGAM6 PRECURSOR, VGAM7 PRECURSOR and VGAM8 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[38858] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM282 RNA, VGAM283 RNA, VGAM284 RNA, VGAM285 RNA, VGAM286 RNA, VGAM287 RNA, VGAM288 RNA and VGAM289 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA, VGAM5 RNA, VGAM6 RNA, VGAM7 RNA and VGAM8 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[38859] VGAM282 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM282 host target RNA, herein schematically represented by VGAM1

HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM282 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM282 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[38860] VGAM283 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM283 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM283 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM283 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[38861] VGAM284 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM284 host

target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM284 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM284 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[38862] VGAM285 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM285 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM285 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM285 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[38863] VGAM286 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding

site located in an untranslated region of VGAM286 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM286 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM286 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[38864] VGAM287 RNA, herein schematically represented by VGAM6 binds complimentarily to a host target binding site located in an untranslated region of VGAM287 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM287 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA into VGAM287 host target protein, herein schematically represented by VGAM6 HOST TARGET PROTEIN, both of Fig. 1.

[38865] VGAM288 RNA, herein schematically represented by

VGAM7 binds complimentarily to a host target binding site located in an untranslated region of VGAM288 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM288 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA into VGAM288 host target protein, herein schematically represented by VGAM7 HOST TARGET PROTEIN, both of Fig. 1.

[38866] VGAM289 RNA, herein schematically represented by VGAM8 binds complimentarily to a host target binding site located in an untranslated region of VGAM289 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM289 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA into VGAM289 host target protein, herein schematically represented by VGAM8 HOST TARGET PROTEIN, both of Fig. 1.

[38867] It is appreciated that a function of VGR2779 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2779 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2779 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2779 gene: VGAM282 host target protein, VGAM283 host target protein, VGAM284 host target protein, VGAM285 host target protein, VGAM286 host target protein, VGAM287 host target protein, VGAM288 host target protein and VGAM289 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM282, VGAM283, VGAM284, VGAM285, VGAM286, VGAM287, VGAM288 and VGAM289

[38868] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2780(VGR2780) viral

gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[38869] VGR2780 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2780 gene was detected is described hereinabove with reference to Figs. 6-15.

[38870] VGR2780 gene encodes VGR2780 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38871] VGR2780 precursor RNA folds spatially, forming VGR2780 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2780 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2780 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the

second half thereof, as is well known in the art.

[38872] VGR2780 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM290 precursor RNA, VGAM291 precursor RNA, VGAM292 precursor RNA, VGAM293 precursor RNA, VGAM294 precursor RNA, VGAM295 precursor RNA, VGAM296 precursor RNA and VGAM297 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR, VGAM5 PRECURSOR, VGAM6 PRECURSOR, VGAM7 PRECURSOR and VGAM8 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[38873] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM290 RNA, VGAM291 RNA, VGAM292 RNA, VGAM293 RNA, VGAM294 RNA, VGAM295 RNA, VGAM296 RNA and VGAM297 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA, VGAM5 RNA, VGAM6 RNA, VGAM7 RNA and VGAM8

RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[38874] VGAM290 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM290 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM290 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM290 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[38875] VGAM291 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM291 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM291 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA

into VGAM291 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[38876] VGAM292 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM292 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM292 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM292 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[38877] VGAM293 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM293 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM293 host target RNA, herein

schematically represented by VGAM4 HOST TARGET RNA into VGAM293 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[38878] VGAM294 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM294 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM294 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM294 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[38879] VGAM295 RNA, herein schematically represented by VGAM6 binds complimentarily to a host target binding site located in an untranslated region of VGAM295 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby in-

hibiting translation of VGAM295 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA into VGAM295 host target protein, herein schematically represented by VGAM6 HOST TARGET PROTEIN, both of Fig. 1.

[38880] VGAM296 RNA, herein schematically represented by VGAM7 binds complimentarily to a host target binding site located in an untranslated region of VGAM296 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM296 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA into VGAM296 host target protein, herein schematically represented by VGAM7 HOST TARGET PROTEIN, both of Fig. 1.

[38881] VGAM297 RNA, herein schematically represented by VGAM8 binds complimentarily to a host target binding site located in an untranslated region of VGAM297 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM297 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA into VGAM297 host target protein, herein schematically represented by VGAM8 HOST TARGET PROTEIN, both of Fig. 1.

[38882] It is appreciated that a function of VGR2780 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2780 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2780 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2780 gene: VGAM290 host target protein, VGAM291 host target protein, VGAM292 host target protein, VGAM293 host target protein, VGAM294 host target protein, VGAM295 host target protein, VGAM296 host target protein and VGAM297 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host tar-

get genes is elaborated hereinabove with reference to VGAM290, VGAM291, VGAM292, VGAM293, VGAM294, VGAM295, VGAM296 and VGAM297

[38883] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2781(VGR2781) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[38884] VGR2781 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2781 gene was detected is described hereinabove with reference to Figs. 6-15.

[38885] VGR2781 gene encodes VGR2781 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38886] VGR2781 precursor RNA folds spatially, forming VGR2781 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2781 folded precursor RNA, herein designated VGR FOLDED PRECUR-

SOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2781 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38887] VGR2781 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 6 separate VGAM precursor RNAs, VGAM298 precursor RNA, VGAM299 precursor RNA, VGAM300 precursor RNA, VGAM301 precursor RNA, VGAM302 precursor RNA and VGAM303 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR, VGAM5 PRECURSOR and VGAM6 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[38888] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM298 RNA, VGAM299 RNA, VGAM300 RNA, VGAM301 RNA,

VGAM302 RNA and VGAM303 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA, VGAM5 RNA and VGAM6 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[38889] VGAM298 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM298 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM298 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM298 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[38890] VGAM299 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM299 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM299 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM299 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[38891] VGAM300 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM300 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM300 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM300 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[38892] VGAM301 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM301 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corre-

sponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM301 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM301 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[38893] VGAM302 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM302 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM302 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM302 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[38894] VGAM303 RNA, herein schematically represented by VGAM6 binds complimentarily to a host target binding site located in an untranslated region of VGAM303 host target RNA, herein schematically represented by VGAM6

HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM303 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA into VGAM303 host target protein, herein schematically represented by VGAM6 HOST TARGET PROTEIN, both of Fig. 1.

[38895] It is appreciated that a function of VGR2781 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2781 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2781 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2781 gene: VGAM298 host target protein, VGAM299 host target protein, VGAM300 host target protein, VGAM301 host target protein, VGAM302 host target protein and VGAM303 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN

respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM298, VGAM299, VGAM300, VGAM301, VGAM302 and VGAM303

[38896] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2782(VGR2782) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[38897] VGR2782 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2782 gene was detected is described hereinabove with reference to Figs. 6-15.

[38898] VGR2782 gene encodes VGR2782 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38899] VGR2782 precursor RNA folds spatially, forming VGR2782 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2782 folded precursor RNA, herein designated VGR FOLDED PRECUR-

SOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2782 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38900] VGR2782 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM304 precursor RNA, VGAM305 precursor RNA and VGAM306 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR and VGAM3 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[38901] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM304 RNA, VGAM305 RNA and VGAM306 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA and VGAM3 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[38902] VGAM304 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM304 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM304 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM304 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[38903] VGAM305 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM305 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM305 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM305 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of

Fig. 1.

[38904] VGAM306 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM306 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM306 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM306 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[38905] It is appreciated that a function of VGR2782 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2782 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2782 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2782 gene: VGAM304 host

target protein, VGAM305 host target protein and VGAM306 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM304, VGAM305 and VGAM306

[38906] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2783(VGR2783) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[38907] VGR2783 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2783 gene was detected is described hereinabove with reference to Figs. 6-15.

[38908] VGR2783 gene encodes VGR2783 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38909] VGR2783 precursor RNA folds spatially, forming VGR2783

folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2783 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2783 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38910] VGR2783 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM310 precursor RNA, VGAM311 precursor RNA and VGAM312 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR and VGAM3 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[38911] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM310 RNA, VGAM311 RNA and VGAM312 RNA respectively,

herein schematically represented by VGAM1 RNA, VGAM2 RNA and VGAM3 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[38912] VGAM310 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM310 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM310 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM310 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[38913] VGAM311 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM311 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM311 host target RNA, herein

schematically represented by VGAM2 HOST TARGET RNA into VGAM311 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[38914] VGAM312 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM312 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM312 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM312 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[38915] It is appreciated that a function of VGR2783 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2783 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2783 gene, herein designated VGR GENE, correlate with, and

may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2783 gene: VGAM310 host target protein, VGAM311 host target protein and VGAM312 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM310, VGAM311 and VGAM312

[38916] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2784(VGR2784) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[38917] VGR2784 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2784 gene was detected is described hereinabove with reference to Figs. 6-15.

[38918] VGR2784 gene encodes VGR2784 precursor RNA, herein

designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38919] VGR2784 precursor RNA folds spatially, forming VGR2784 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2784 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2784 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38920] VGR2784 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM315 precursor RNA, VGAM316 precursor RNA, VGAM317 precursor RNA and VGAM318 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR and VGAM4 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[38921] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM315 RNA, VGAM316 RNA, VGAM317 RNA and VGAM318 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA and VGAM4 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[38922] VGAM315 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM315 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM315 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM315 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[38923] VGAM316 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM316 host

target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM316 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM316 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[38924] VGAM317 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM317 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM317 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM317 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[38925] VGAM318 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding

site located in an untranslated region of VGAM318 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM318 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM318 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[38926] It is appreciated that a function of VGR2784 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2784 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2784 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2784 gene: VGAM315 host target protein, VGAM316 host target protein, VGAM317 host target protein and VGAM318 host target protein, herein schematically represented by VGAM1 HOST TARGET

PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM315, VGAM316, VGAM317 and VGAM318

[38927] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2785(VGR2785) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[38928] VGR2785 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2785 gene was detected is described hereinabove with reference to Figs. 6-15.

[38929] VGR2785 gene encodes VGR2785 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38930] VGR2785 precursor RNA folds spatially, forming VGR2785 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2785 folded

precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2785 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38931] VGR2785 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM319 precursor RNA and VGAM320 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[38932] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM319 RNA and VGAM320 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of

Fig. 8.

[38933] VGAM319 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM319 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM319 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM319 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[38934] VGAM320 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM320 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM320 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM320 host target protein, herein schematically

represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[38935] It is appreciated that a function of VGR2785 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2785 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2785 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2785 gene: VGAM319 host target protein and VGAM320 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM319 and VGAM320

[38936] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2786(VGR2786) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function

and utility of which at least one host target gene is known in the art.

[38937] VGR2786 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2786 gene was detected is described hereinabove with reference to Figs. 6-15.

[38938] VGR2786 gene encodes VGR2786 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38939] VGR2786 precursor RNA folds spatially, forming VGR2786 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2786 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2786 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38940] VGR2786 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellu-

lar enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM324 precursor RNA, VGAM325 precursor RNA and VGAM326 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR and VGAM3 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[38941] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM324 RNA, VGAM325 RNA and VGAM326 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA and VGAM3 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[38942] VGAM324 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM324 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM324 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA

into VGAM324 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[38943] VGAM325 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM325 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM325 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM325 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[38944] VGAM326 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM326 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM326 host target RNA, herein

schematically represented by VGAM3 HOST TARGET RNA into VGAM326 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[38945] It is appreciated that a function of VGR2786 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2786 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2786 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2786 gene: VGAM324 host target protein, VGAM325 host target protein and VGAM326 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM324, VGAM325 and VGAM326

[38946] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2787(VGR2787) viral

gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[38947] VGR2787 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2787 gene was detected is described hereinabove with reference to Figs. 6-15.

[38948] VGR2787 gene encodes VGR2787 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38949] VGR2787 precursor RNA folds spatially, forming VGR2787 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2787 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2787 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the

second half thereof, as is well known in the art.

[38950] VGR2787 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM333 precursor RNA and VGAM334 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[38951] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM333 RNA and VGAM334 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[38952] VGAM333 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM333 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM333 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM333 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[38953] VGAM334 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM334 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM334 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM334 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[38954] It is appreciated that a function of VGR2787 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2787 gene include diagnosis, prevention and treatment of viral infection by .

Specific functions, and accordingly utilities, of VGR2787 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2787 gene: VGAM333 host target protein and VGAM334 host target protein, herein schematically represented by VGAM1 HOST TARGET PRO-TEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated herein-above with reference to VGAM333 and VGAM334

[38955] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2788(VGR2788) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[38956] VGR2788 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2788 gene was detected is described hereinabove with reference to Figs. 6-15.

[38957] VGR2788 gene encodes VGR2788 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38958] VGR2788 precursor RNA folds spatially, forming VGR2788 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2788 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2788 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38959] VGR2788 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM335 precursor RNA, VGAM336 precursor RNA, VGAM337 precursor RNA, VGAM338 precursor RNA and VGAM339 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR and VGAM5 PRECURSOR respectively, each of which VGAM precursor RNAs

being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[38960] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM335 RNA, VGAM336 RNA, VGAM337 RNA, VGAM338 RNA and VGAM339 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA and VGAM5 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[38961] VGAM335 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM335 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM335 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM335 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[38962] VGAM336 RNA, herein schematically represented by

VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM336 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM336 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM336 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[38963] VGAM337 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM337 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM337 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM337 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[38964] VGAM338 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM338 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM338 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM338 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[38965] VGAM339 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM339 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM339 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM339 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of

Fig. 1.

[38966] It is appreciated that a function of VGR2788 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2788 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2788 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2788 gene: VGAM335 host target protein, VGAM336 host target protein, VGAM337 host target protein, VGAM338 host target protein and VGAM339 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM335, VGAM336, VGAM337, VGAM338 and VGAM339

[38967] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2789(VGR2789) viral gene, which encodes an operon-like cluster of novel viral

micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[38968] VGR2789 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2789 gene was detected is described hereinabove with reference to Figs. 6-15.

[38969] VGR2789 gene encodes VGR2789 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38970] VGR2789 precursor RNA folds spatially, forming VGR2789 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2789 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2789 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38971] VGR2789 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM340 precursor RNA, VGAM341 precursor RNA, VGAM342 precursor RNA, VGAM343 precursor RNA and VGAM344 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR and VGAM5 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[38972] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM340 RNA, VGAM341 RNA, VGAM342 RNA, VGAM343 RNA and VGAM344 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA and VGAM5 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[38973] VGAM340 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM340 host target RNA, herein schematically represented by VGAM1

HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM340 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM340 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[38974] VGAM341 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM341 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM341 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM341 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[38975] VGAM342 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM342 host

target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM342 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM342 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[38976] VGAM343 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM343 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM343 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM343 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[38977] VGAM344 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding

site located in an untranslated region of VGAM344 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM344 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM344 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[38978] It is appreciated that a function of VGR2789 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2789 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2789 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2789 gene: VGAM340 host target protein, VGAM341 host target protein, VGAM342 host target protein, VGAM343 host target protein and VGAM344 host target protein, herein schematically repre-

sented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM340, VGAM341, VGAM342, VGAM343 and VGAM344

[38979] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2790(VGR2790) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[38980] VGR2790 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2790 gene was detected is described hereinabove with reference to Figs. 6-15.

[38981] VGR2790 gene encodes VGR2790 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38982] VGR2790 precursor RNA folds spatially, forming VGR2790 folded precursor RNA, herein designated VGR FOLDED

PRECURSOR RNA. It is appreciated that VGR2790 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2790 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38983] VGR2790 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM346 precursor RNA and VGAM347 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[38984] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM346 RNA and VGAM347 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively,

each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[38985] VGAM346 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM346 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM346 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM346 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[38986] VGAM347 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM347 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM347 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA

into VGAM347 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[38987] It is appreciated that a function of VGR2790 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2790 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2790 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2790 gene: VGAM346 host target protein and VGAM347 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM346 and VGAM347

[38988] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2791(VGR2791) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates

expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[38989] VGR2791 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2791 gene was detected is described hereinabove with reference to Figs. 6-15.

[38990] VGR2791 gene encodes VGR2791 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38991] VGR2791 precursor RNA folds spatially, forming VGR2791 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2791 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2791 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38992] VGR2791 folded precursor RNA, herein designated VGR

FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM348 precursor RNA and VGAM349 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[38993] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM348 RNA and VGAM349 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[38994] VGAM348 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM348 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM348 host target RNA, herein

schematically represented by VGAM1 HOST TARGET RNA into VGAM348 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[38995] VGAM349 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM349 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM349 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM349 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[38996] It is appreciated that a function of VGR2791 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2791 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2791 gene, herein designated VGR GENE, correlate with, and

may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2791 gene: VGAM348 host target protein and VGAM349 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM348 and VGAM349

[38997] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2792(VGR2792) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[38998] VGR2792 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2792 gene was detected is described hereinabove with reference to Figs. 6-15.

[38999] VGR2792 gene encodes VGR2792 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typi-

cally several hundred nucleotides long.

[39000] VGR2792 precursor RNA folds spatially, forming VGR2792 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2792 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2792 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39001] VGR2792 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM350 precursor RNA, VGAM351 precursor RNA, VGAM352 precursor RNA, VGAM353 precursor RNA, VGAM354 precursor RNA, VGAM355 precursor RNA, VGAM356 precursor RNA and VGAM357 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR, VGAM5 PRECURSOR, VGAM6 PRECURSOR, VGAM7 PRECURSOR and VGAM8 PRECURSOR respectively,

each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39002] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM350 RNA, VGAM351 RNA, VGAM352 RNA, VGAM353 RNA, VGAM354 RNA, VGAM355 RNA, VGAM356 RNA and VGAM357 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA, VGAM5 RNA, VGAM6 RNA, VGAM7 RNA and VGAM8 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39003] VGAM350 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM350 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM350 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM350 host target protein, herein schematically

represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39004] VGAM351 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM351 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM351 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM351 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39005] VGAM352 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM352 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM352 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA

into VGAM352 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[39006] VGAM353 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM353 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM353 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM353 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[39007] VGAM354 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM354 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM354 host target RNA, herein

schematically represented by VGAM5 HOST TARGET RNA into VGAM354 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[39008] VGAM355 RNA, herein schematically represented by VGAM6 binds complimentarily to a host target binding site located in an untranslated region of VGAM355 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM355 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA into VGAM355 host target protein, herein schematically represented by VGAM6 HOST TARGET PROTEIN, both of Fig. 1.

[39009] VGAM356 RNA, herein schematically represented by VGAM7 binds complimentarily to a host target binding site located in an untranslated region of VGAM356 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby in-

hibiting translation of VGAM356 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA into VGAM356 host target protein, herein schematically represented by VGAM7 HOST TARGET PROTEIN, both of Fig. 1.

[39010] VGAM357 RNA, herein schematically represented by VGAM8 binds complimentarily to a host target binding site located in an untranslated region of VGAM357 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM357 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA into VGAM357 host target protein, herein schematically represented by VGAM8 HOST TARGET PROTEIN, both of Fig. 1.

[39011] It is appreciated that a function of VGR2792 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2792 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2792

gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2792 gene: VGAM350 host target protein, VGAM351 host target protein, VGAM352 host target protein, VGAM353 host target protein, VGAM354 host target protein, VGAM355 host target protein, VGAM356 host target protein and VGAM357 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM350, VGAM351, VGAM352, VGAM353, VGAM354, VGAM355, VGAM356 and VGAM357

[39012] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2793(VGR2793) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39013] VGR2793 gene, herein designated VGR GENE, is a novel

bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2793 gene was detected is described hereinabove with reference to Figs. 6-15.

[39014] VGR2793 gene encodes VGR2793 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39015] VGR2793 precursor RNA folds spatially, forming VGR2793 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2793 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2793 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39016] VGR2793 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 7 separate VGAM precursor RNAs, VGAM358 precursor RNA, VGAM359 precursor RNA, VGAM360 precursor RNA, VGAM361 precursor

RNA, VGAM362 precursor RNA, VGAM363 precursor RNA and VGAM364 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR, VGAM5 PRECURSOR, VGAM6 PRECURSOR and VGAM7 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39017] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM358 RNA, VGAM359 RNA, VGAM360 RNA, VGAM361 RNA, VGAM362 RNA, VGAM363 RNA and VGAM364 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA, VGAM5 RNA, VGAM6 RNA and VGAM7 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39018] VGAM358 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM358 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM358 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM358 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39019] VGAM359 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM359 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM359 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM359 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39020] VGAM360 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM360 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corre-

sponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM360 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM360 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[39021] VGAM361 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM361 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM361 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM361 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[39022] VGAM362 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM362 host target RNA, herein schematically represented by VGAM5

HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM362 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM362 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[39023] VGAM363 RNA, herein schematically represented by VGAM6 binds complimentarily to a host target binding site located in an untranslated region of VGAM363 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM363 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA into VGAM363 host target protein, herein schematically represented by VGAM6 HOST TARGET PROTEIN, both of Fig. 1.

[39024] VGAM364 RNA, herein schematically represented by VGAM7 binds complimentarily to a host target binding site located in an untranslated region of VGAM364 host

target RNA, herein schematically represented by VGAM7 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM364 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA into VGAM364 host target protein, herein schematically represented by VGAM7 HOST TARGET PROTEIN, both of Fig. 1.

[39025] It is appreciated that a function of VGR2793 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2793 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2793 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2793 gene: VGAM358 host target protein, VGAM359 host target protein, VGAM360 host target protein, VGAM361 host target protein, VGAM362 host target protein, VGAM363 host target protein and VGAM364 host target protein, herein schemati-

cally represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated herein-above with reference to VGAM358, VGAM359, VGAM360, VGAM361, VGAM362, VGAM363 and VGAM364

[39026] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2794(VGR2794) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39027] VGR2794 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2794 gene was detected is described hereinabove with reference to Figs. 6-15.

[39028] VGR2794 gene encodes VGR2794 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typi-cally several hundred nucleotides long.

[39029] VGR2794 precursor RNA folds spatially, forming VGR2794 folded precursor RNA, herein designated VGR FOLDED

PRECURSOR RNA. It is appreciated that VGR2794 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2794 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39030] VGR2794 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM365 precursor RNA, VGAM366 precursor RNA, VGAM367 precursor RNA and VGAM368 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR and VGAM4 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39031] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM365 RNA, VGAM366 RNA, VGAM367 RNA and VGAM368 RNA

respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA and VGAM4 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39032] VGAM365 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM365 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM365 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM365 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39033] VGAM366 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM366 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby in-

hibiting translation of VGAM366 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM366 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39034] VGAM367 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM367 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM367 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM367 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[39035] VGAM368 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM368 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM368 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM368 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[39036] It is appreciated that a function of VGR2794 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2794 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2794 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2794 gene: VGAM365 host target protein, VGAM366 host target protein, VGAM367 host target protein and VGAM368 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM365, VGAM366, VGAM367 and VGAM368

[39037] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2795(VGR2795) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39038] VGR2795 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2795 gene was detected is described hereinabove with reference to Figs. 6-15.

[39039] VGR2795 gene encodes VGR2795 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39040] VGR2795 precursor RNA folds spatially, forming VGR2795 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2795 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2795 precur-

sor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39041] VGR2795 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 7 separate VGAM precursor RNAs, VGAM369 precursor RNA, VGAM370 precursor RNA, VGAM371 precursor RNA, VGAM372 precursor RNA, VGAM373 precursor RNA, VGAM374 precursor RNA and VGAM375 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR, VGAM5 PRECURSOR, VGAM6 PRECURSOR and VGAM7 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39042] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM369 RNA, VGAM370 RNA, VGAM371 RNA, VGAM372 RNA, VGAM373 RNA, VGAM374 RNA and VGAM375 RNA respectively, herein schematically represented by VGAM1

RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA, VGAM5 RNA, VGAM6 RNA and VGAM7 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39043] VGAM369 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM369 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM369 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM369 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39044] VGAM370 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM370 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM370 host target RNA, herein

schematically represented by VGAM2 HOST TARGET RNA into VGAM370 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39045] VGAM371 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM371 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM371 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM371 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[39046] VGAM372 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM372 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby in-

hibiting translation of VGAM372 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM372 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[39047] VGAM373 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM373 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM373 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM373 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[39048] VGAM374 RNA, herein schematically represented by VGAM6 binds complimentarily to a host target binding site located in an untranslated region of VGAM374 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM374 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA into VGAM374 host target protein, herein schematically represented by VGAM6 HOST TARGET PROTEIN, both of Fig. 1.

[39049] VGAM375 RNA, herein schematically represented by VGAM7 binds complimentarily to a host target binding site located in an untranslated region of VGAM375 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM375 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA into VGAM375 host target protein, herein schematically represented by VGAM7 HOST TARGET PROTEIN, both of Fig. 1.

[39050] It is appreciated that a function of VGR2795 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2795 gene include diagnosis, prevention and treatment of viral infection by .

Specific functions, and accordingly utilities, of VGR2795 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2795 gene: VGAM369 host target protein, VGAM370 host target protein, VGAM371 host target protein, VGAM372 host target protein, VGAM373 host target protein, VGAM374 host target protein and VGAM375 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM369, VGAM370, VGAM371, VGAM372, VGAM373, VGAM374 and VGAM375

[39051] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2796(VGR2796) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39052] VGR2796 gene, herein designated VGR GENE, is a novel

bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2796 gene was detected is described hereinabove with reference to Figs. 6-15.

[39053] VGR2796 gene encodes VGR2796 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39054] VGR2796 precursor RNA folds spatially, forming VGR2796 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2796 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2796 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39055] VGR2796 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM376 precursor RNA and VGAM377 precursor RNA, herein schematically represented by VGAM1

PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39056] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM376 RNA and VGAM377 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39057] VGAM376 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM376 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM376 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM376 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39058] VGAM377 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM377 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM377 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM377 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39059] It is appreciated that a function of VGR2796 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2796 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2796 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2796 gene: VGAM376 host target protein and VGAM377 host target protein, herein

schematically represented by VGAM1 HOST TARGET PROTEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM376 and VGAM377

[39060] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2797(VGR2797) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39061] VGR2797 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2797 gene was detected is described hereinabove with reference to Figs. 6-15.

[39062] VGR2797 gene encodes VGR2797 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39063] VGR2797 precursor RNA folds spatially, forming VGR2797 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2797 folded

precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2797 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39064] VGR2797 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM378 precursor RNA, VGAM379 precursor RNA, VGAM380 precursor RNA and VGAM381 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR and VGAM4 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39065] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM378 RNA, VGAM379 RNA, VGAM380 RNA and VGAM381 RNA respectively, herein schematically represented by VGAM1

RNA, VGAM2 RNA, VGAM3 RNA and VGAM4 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39066] VGAM378 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM378 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM378 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM378 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39067] VGAM379 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM379 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM379 host target RNA, herein

schematically represented by VGAM2 HOST TARGET RNA into VGAM379 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39068] VGAM380 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM380 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM380 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM380 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[39069] VGAM381 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM381 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby in-

hibiting translation of VGAM381 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM381 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[39070] It is appreciated that a function of VGR2797 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2797 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2797 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2797 gene: VGAM378 host target protein, VGAM379 host target protein, VGAM380 host target protein and VGAM381 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM378, VGAM379, VGAM380 and VGAM381

[39071] Fig. 9 further provides a conceptual description of novel

bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2798(VGR2798) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39072] VGR2798 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2798 gene was detected is described hereinabove with reference to Figs. 6-15.

[39073] VGR2798 gene encodes VGR2798 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39074] VGR2798 precursor RNA folds spatially, forming VGR2798 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2798 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2798 precursor RNA comprises a plurality of segments, the first half

of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39075] VGR2798 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM382 precursor RNA, VGAM383 precursor RNA, VGAM384 precursor RNA, VGAM385 precursor RNA and VGAM386 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR and VGAM5 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39076] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM382 RNA, VGAM383 RNA, VGAM384 RNA, VGAM385 RNA and VGAM386 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA and VGAM5 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39077] VGAM382 RNA, herein schematically represented by

VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM382 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM382 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM382 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39078] VGAM383 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM383 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM383 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM383 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39079] VGAM384 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM384 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM384 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM384 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[39080] VGAM385 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM385 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM385 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM385 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of

Fig. 1.

[39081] VGAM386 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM386 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM386 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM386 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[39082] It is appreciated that a function of VGR2798 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2798 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2798 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2798 gene: VGAM382 host

target protein, VGAM383 host target protein, VGAM384 host target protein, VGAM385 host target protein and VGAM386 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM382, VGAM383, VGAM384, VGAM385 and VGAM386

[39083] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2799(VGR2799) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39084] VGR2799 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2799 gene was detected is described hereinabove with reference to Figs. 6-15.

[39085] VGR2799 gene encodes VGR2799 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typi-

cally several hundred nucleotides long.

[39086] VGR2799 precursor RNA folds spatially, forming VGR2799 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2799 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2799 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39087] VGR2799 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM387 precursor RNA, VGAM388 precursor RNA, VGAM389 precursor RNA, VGAM390 precursor RNA and VGAM391 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR and VGAM5 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39088] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM387 RNA, VGAM388 RNA, VGAM389 RNA, VGAM390 RNA and VGAM391 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA and VGAM5 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39089] VGAM387 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM387 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM387 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM387 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39090] VGAM388 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM388 host

target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM388 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM388 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39091] VGAM389 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM389 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM389 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM389 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[39092] VGAM390 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding

site located in an untranslated region of VGAM390 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM390 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM390 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[39093] VGAM391 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM391 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM391 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM391 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[39094] It is appreciated that a function of VGR2799 gene, herein

designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2799 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2799 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2799 gene: VGAM387 host target protein, VGAM388 host target protein, VGAM389 host target protein, VGAM390 host target protein and VGAM391 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM387, VGAM388, VGAM389, VGAM390 and VGAM391

[39095] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2800(VGR2800) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function

and utility of which at least one host target gene is known in the art.

[39096] VGR2800 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2800 gene was detected is described hereinabove with reference to Figs. 6-15.

[39097] VGR2800 gene encodes VGR2800 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39098] VGR2800 precursor RNA folds spatially, forming VGR2800 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2800 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2800 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39099] VGR2800 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellu-

lar enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM393 precursor RNA, VGAM394 precursor RNA, VGAM395 precursor RNA, VGAM396 precursor RNA, VGAM397 precursor RNA, VGAM398 precursor RNA, VGAM399 precursor RNA and VGAM400 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR, VGAM5 PRECURSOR, VGAM6 PRECURSOR, VGAM7 PRECURSOR and VGAM8 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39100] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM393 RNA, VGAM394 RNA, VGAM395 RNA, VGAM396 RNA, VGAM397 RNA, VGAM398 RNA, VGAM399 RNA and VGAM400 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA, VGAM5 RNA, VGAM6 RNA, VGAM7 RNA and VGAM8 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39101] VGAM393 RNA, herein schematically represented by

VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM393 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM393 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM393 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39102] VGAM394 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM394 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM394 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM394 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39103] VGAM395 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM395 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM395 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM395 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[39104] VGAM396 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM396 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM396 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM396 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of

Fig. 1.

[39105] VGAM397 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM397 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM397 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM397 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[39106] VGAM398 RNA, herein schematically represented by VGAM6 binds complimentarily to a host target binding site located in an untranslated region of VGAM398 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM398 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA into VGAM398 host target protein, herein schematically

represented by VGAM6 HOST TARGET PROTEIN, both of Fig. 1.

[39107] VGAM399 RNA, herein schematically represented by VGAM7 binds complimentarily to a host target binding site located in an untranslated region of VGAM399 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM399 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA into VGAM399 host target protein, herein schematically represented by VGAM7 HOST TARGET PROTEIN, both of Fig. 1.

[39108] VGAM400 RNA, herein schematically represented by VGAM8 binds complimentarily to a host target binding site located in an untranslated region of VGAM400 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM400 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA

into VGAM400 host target protein, herein schematically represented by VGAM8 HOST TARGET PROTEIN, both of Fig. 1.

[39109] It is appreciated that a function of VGR2800 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2800 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2800 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2800 gene: VGAM393 host target protein, VGAM394 host target protein, VGAM395 host target protein, VGAM396 host target protein, VGAM397 host target protein, VGAM398 host target protein, VGAM399 host target protein and VGAM400 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM393, VGAM394, VGAM395, VGAM396, VGAM397, VGAM398, VGAM399 and VGAM400

[39110] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2801(VGR2801) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39111] VGR2801 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2801 gene was detected is described hereinabove with reference to Figs. 6-15.

[39112] VGR2801 gene encodes VGR2801 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39113] VGR2801 precursor RNA folds spatially, forming VGR2801 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2801 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2801 precur-

sor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39114] VGR2801 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 6 separate VGAM precursor RNAs, VGAM401 precursor RNA, VGAM402 precursor RNA, VGAM403 precursor RNA, VGAM404 precursor RNA, VGAM405 precursor RNA and VGAM406 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR, VGAM5 PRECURSOR and VGAM6 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39115] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM401 RNA, VGAM402 RNA, VGAM403 RNA, VGAM404 RNA, VGAM405 RNA and VGAM406 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA, VGAM5 RNA and VGAM6 RNA

respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39116] VGAM401 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM401 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM401 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM401 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39117] VGAM402 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM402 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM402 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA

into VGAM402 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39118] VGAM403 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM403 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM403 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM403 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[39119] VGAM404 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM404 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM404 host target RNA, herein

schematically represented by VGAM4 HOST TARGET RNA into VGAM404 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[39120] VGAM405 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM405 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM405 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM405 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[39121] VGAM406 RNA, herein schematically represented by VGAM6 binds complimentarily to a host target binding site located in an untranslated region of VGAM406 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby in-

hibiting translation of VGAM406 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA into VGAM406 host target protein, herein schematically represented by VGAM6 HOST TARGET PROTEIN, both of Fig. 1.

[39122] It is appreciated that a function of VGR2801 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2801 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2801 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2801 gene: VGAM401 host target protein, VGAM402 host target protein, VGAM403 host target protein, VGAM404 host target protein, VGAM405 host target protein and VGAM406 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM401, VGAM402, VGAM403, VGAM404, VGAM405 and VGAM406

[39123] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2802(VGR2802) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39124] VGR2802 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2802 gene was detected is described hereinabove with reference to Figs. 6-15.

[39125] VGR2802 gene encodes VGR2802 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39126] VGR2802 precursor RNA folds spatially, forming VGR2802 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2802 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2802 precur-

sor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39127] VGR2802 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM407 precursor RNA, VGAM408 precursor RNA and VGAM409 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR and VGAM3 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39128] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM407 RNA, VGAM408 RNA and VGAM409 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA and VGAM3 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39129] VGAM407 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM407 host

target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM407 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM407 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39130] VGAM408 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM408 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM408 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM408 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39131] VGAM409 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding

site located in an untranslated region of VGAM409 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM409 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM409 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[39132] It is appreciated that a function of VGR2802 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2802 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2802 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2802 gene: VGAM407 host target protein, VGAM408 host target protein and VGAM409 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM

HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM407, VGAM408 and VGAM409

[39133] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2803(VGR2803) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39134] VGR2803 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2803 gene was detected is described hereinabove with reference to Figs. 6-15.

[39135] VGR2803 gene encodes VGR2803 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39136] VGR2803 precursor RNA folds spatially, forming VGR2803 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2803 folded precursor RNA, herein designated VGR FOLDED PRECUR-

SOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2803 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39137] VGR2803 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM410 precursor RNA, VGAM411 precursor RNA and VGAM412 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR and VGAM3 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39138] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM410 RNA, VGAM411 RNA and VGAM412 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA and VGAM3 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39139] VGAM410 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM410 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM410 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM410 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39140] VGAM411 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM411 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM411 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM411 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of

Fig. 1.

[39141] VGAM412 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM412 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM412 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM412 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[39142] It is appreciated that a function of VGR2803 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2803 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2803 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2803 gene: VGAM410 host

target protein, VGAM411 host target protein and VGAM412 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM410, VGAM411 and VGAM412

[39143] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2804(VGR2804) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39144] VGR2804 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2804 gene was detected is described hereinabove with reference to Figs. 6-15.

[39145] VGR2804 gene encodes VGR2804 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39146] VGR2804 precursor RNA folds spatially, forming VGR2804

folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2804 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2804 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39147] VGR2804 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 7 separate VGAM precursor RNAs, VGAM413 precursor RNA, VGAM414 precursor RNA, VGAM415 precursor RNA, VGAM416 precursor RNA, VGAM417 precursor RNA, VGAM418 precursor RNA and VGAM419 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR, VGAM5 PRECURSOR, VGAM6 PRECURSOR and VGAM7 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39148] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM413 RNA, VGAM414 RNA, VGAM415 RNA, VGAM416 RNA, VGAM417 RNA, VGAM418 RNA and VGAM419 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA, VGAM5 RNA, VGAM6 RNA and VGAM7 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39149] VGAM413 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM413 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM413 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM413 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39150] VGAM414 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding

site located in an untranslated region of VGAM414 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM414 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM414 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39151] VGAM415 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM415 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM415 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM415 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[39152] VGAM416 RNA, herein schematically represented by

VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM416 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM416 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM416 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[39153] VGAM417 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM417 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM417 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM417 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[39154] VGAM418 RNA, herein schematically represented by VGAM6 binds complimentarily to a host target binding site located in an untranslated region of VGAM418 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM418 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA into VGAM418 host target protein, herein schematically represented by VGAM6 HOST TARGET PROTEIN, both of Fig. 1.

[39155] VGAM419 RNA, herein schematically represented by VGAM7 binds complimentarily to a host target binding site located in an untranslated region of VGAM419 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM419 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA into VGAM419 host target protein, herein schematically represented by VGAM7 HOST TARGET PROTEIN, both of

Fig. 1.

[39156] It is appreciated that a function of VGR2804 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2804 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2804 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2804 gene: VGAM413 host target protein, VGAM414 host target protein, VGAM415 host target protein, VGAM416 host target protein, VGAM417 host target protein, VGAM418 host target protein and VGAM419 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM413, VGAM414, VGAM415, VGAM416, VGAM417, VGAM418 and VGAM419

[39157] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2805(VGR2805) viral

gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39158] VGR2805 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2805 gene was detected is described hereinabove with reference to Figs. 6-15.

[39159] VGR2805 gene encodes VGR2805 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39160] VGR2805 precursor RNA folds spatially, forming VGR2805 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2805 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2805 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the

second half thereof, as is well known in the art.

[39161] VGR2805 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM420 precursor RNA and VGAM421 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39162] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM420 RNA and VGAM421 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39163] VGAM420 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM420 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM420 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM420 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39164] VGAM421 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM421 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM421 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM421 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39165] It is appreciated that a function of VGR2805 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2805 gene include diagnosis, prevention and treatment of viral infection by .

Specific functions, and accordingly utilities, of VGR2805 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2805 gene: VGAM420 host target protein and VGAM421 host target protein, herein schematically represented by VGAM1 HOST TARGET PRO-TEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated herein-above with reference to VGAM420 and VGAM421

[39166] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2806(VGR2806) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39167] VGR2806 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2806 gene was detected is described hereinabove with reference to Figs. 6-15.

[39168] VGR2806 gene encodes VGR2806 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39169] VGR2806 precursor RNA folds spatially, forming VGR2806 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2806 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2806 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39170] VGR2806 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM422 precursor RNA and VGAM423 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39171] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM422 RNA and VGAM423 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39172] VGAM422 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM422 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM422 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM422 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39173] VGAM423 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM423 host target RNA, herein schematically represented by VGAM2

HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM423 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM423 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39174] It is appreciated that a function of VGR2806 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2806 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2806 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2806 gene: VGAM422 host target protein and VGAM423 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM422 and VGAM423

[39175] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2807(VGR2807) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39176] VGR2807 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2807 gene was detected is described hereinabove with reference to Figs. 6-15.

[39177] VGR2807 gene encodes VGR2807 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39178] VGR2807 precursor RNA folds spatially, forming VGR2807 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2807 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2807 precur-

sor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39179] VGR2807 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM424 precursor RNA, VGAM425 precursor RNA, VGAM426 precursor RNA, VGAM427 precursor RNA and VGAM428 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR and VGAM5 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39180] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM424 RNA, VGAM425 RNA, VGAM426 RNA, VGAM427 RNA and VGAM428 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA and VGAM5 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39181] VGAM424 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM424 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM424 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM424 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39182] VGAM425 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM425 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM425 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM425 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of

Fig. 1.

[39183] VGAM426 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM426 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM426 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM426 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[39184] VGAM427 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM427 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM427 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM427 host target protein, herein schematically

represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[39185] VGAM428 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM428 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM428 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM428 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[39186] It is appreciated that a function of VGR2807 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2807 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2807 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in

the operon-like cluster of VGR2807 gene: VGAM424 host target protein, VGAM425 host target protein, VGAM426 host target protein, VGAM427 host target protein and VGAM428 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM424, VGAM425, VGAM426, VGAM427 and VGAM428

[39187] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2808(VGR2808) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39188] VGR2808 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2808 gene was detected is described hereinabove with reference to Figs. 6-15.

[39189] VGR2808 gene encodes VGR2808 precursor RNA, herein

designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39190] VGR2808 precursor RNA folds spatially, forming VGR2808 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2808 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2808 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39191] VGR2808 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM429 precursor RNA, VGAM430 precursor RNA, VGAM431 precursor RNA, VGAM432 precursor RNA and VGAM433 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR and VGAM5 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to

VGAM PRECURSOR RNA of Fig. 8.

[39192] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM429 RNA, VGAM430 RNA, VGAM431 RNA, VGAM432 RNA and VGAM433 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA and VGAM5 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39193] VGAM429 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM429 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM429 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM429 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39194] VGAM430 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding

site located in an untranslated region of VGAM430 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM430 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM430 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39195] VGAM431 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM431 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM431 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM431 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[39196] VGAM432 RNA, herein schematically represented by

VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM432 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM432 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM432 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[39197] VGAM433 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM433 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM433 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM433 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[39198] It is appreciated that a function of VGR2808 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2808 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2808 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2808 gene: VGAM429 host target protein, VGAM430 host target protein, VGAM431 host target protein, VGAM432 host target protein and VGAM433 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM429, VGAM430, VGAM431, VGAM432 and VGAM433

[39199] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2809(VGR2809) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates

expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39200] VGR2809 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2809 gene was detected is described hereinabove with reference to Figs. 6-15.

[39201] VGR2809 gene encodes VGR2809 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39202] VGR2809 precursor RNA folds spatially, forming VGR2809 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2809 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2809 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39203] VGR2809 folded precursor RNA, herein designated VGR

FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM434 precursor RNA, VGAM435 precursor RNA and VGAM436 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR and VGAM3 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39204] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM434 RNA, VGAM435 RNA and VGAM436 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA and VGAM3 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39205] VGAM434 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM434 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM434 host target RNA, herein

schematically represented by VGAM1 HOST TARGET RNA into VGAM434 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39206] VGAM435 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM435 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM435 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM435 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39207] VGAM436 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM436 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby in-

hibiting translation of VGAM436 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM436 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[39208] It is appreciated that a function of VGR2809 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2809 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2809 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2809 gene: VGAM434 host target protein, VGAM435 host target protein and VGAM436 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM434, VGAM435 and VGAM436

[39209] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred

to here as Viral Genomic Record 2810(VGR2810) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39210] VGR2810 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2810 gene was detected is described hereinabove with reference to Figs. 6-15.

[39211] VGR2810 gene encodes VGR2810 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39212] VGR2810 precursor RNA folds spatially, forming VGR2810 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2810 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2810 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which

is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39213] VGR2810 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM437 precursor RNA, VGAM438 precursor RNA and VGAM439 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR and VGAM3 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39214] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM437 RNA, VGAM438 RNA and VGAM439 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA and VGAM3 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39215] VGAM437 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM437 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corre-

sponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM437 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM437 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39216] VGAM438 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM438 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM438 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM438 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39217] VGAM439 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM439 host target RNA, herein schematically represented by VGAM3

HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM439 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM439 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[39218] It is appreciated that a function of VGR2810 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2810 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2810 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2810 gene: VGAM437 host target protein, VGAM438 host target protein and VGAM439 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with refer-

ence to VGAM437, VGAM438 and VGAM439

[39219] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2811(VGR2811) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39220] VGR2811 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2811 gene was detected is described hereinabove with reference to Figs. 6-15.

[39221] VGR2811 gene encodes VGR2811 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39222] VGR2811 precursor RNA folds spatially, forming VGR2811 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2811 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to

the fact that the nucleotide sequence of VGR2811 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39223] VGR2811 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM441 precursor RNA and VGAM442 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39224] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM441 RNA and VGAM442 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39225] VGAM441 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding

site located in an untranslated region of VGAM441 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM441 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM441 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39226] VGAM442 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM442 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM442 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM442 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39227] It is appreciated that a function of VGR2811 gene, herein

designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2811 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2811 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2811 gene: VGAM441 host target protein and VGAM442 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM441 and VGAM442

[39228] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2812(VGR2812) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39229] VGR2812 gene, herein designated VGR GENE, is a novel

bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2812 gene was detected is described hereinabove with reference to Figs. 6-15.

[39230] VGR2812 gene encodes VGR2812 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39231] VGR2812 precursor RNA folds spatially, forming VGR2812 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2812 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2812 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39232] VGR2812 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM443 precursor RNA and VGAM444 precursor RNA, herein schematically represented by VGAM1

PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39233] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM443 RNA and VGAM444 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39234] VGAM443 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM443 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM443 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM443 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39235] VGAM444 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM444 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM444 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM444 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39236] It is appreciated that a function of VGR2812 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2812 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2812 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2812 gene: VGAM443 host target protein and VGAM444 host target protein, herein

schematically represented by VGAM1 HOST TARGET PROTEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM443 and VGAM444

[39237] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2813(VGR2813) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39238] VGR2813 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2813 gene was detected is described hereinabove with reference to Figs. 6-15.

[39239] VGR2813 gene encodes VGR2813 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39240] VGR2813 precursor RNA folds spatially, forming VGR2813 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2813 folded

precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2813 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39241] VGR2813 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM445 precursor RNA and VGAM446 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39242] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM445 RNA and VGAM446 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of

Fig. 8.

[39243] VGAM445 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM445 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM445 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM445 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39244] VGAM446 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM446 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM446 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM446 host target protein, herein schematically

represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39245] It is appreciated that a function of VGR2813 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2813 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2813 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2813 gene: VGAM445 host target protein and VGAM446 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM445 and VGAM446

[39246] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2814(VGR2814) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function

and utility of which at least one host target gene is known in the art.

[39247] VGR2814 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2814 gene was detected is described hereinabove with reference to Figs. 6-15.

[39248] VGR2814 gene encodes VGR2814 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39249] VGR2814 precursor RNA folds spatially, forming VGR2814 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2814 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2814 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39250] VGR2814 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellu-

lar enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM447 precursor RNA and VGAM448 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39251] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM447 RNA and VGAM448 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39252] VGAM447 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM447 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM447 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA

into VGAM447 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39253] VGAM448 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM448 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM448 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM448 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39254] It is appreciated that a function of VGR2814 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2814 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2814 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target

genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2814 gene: VGAM447 host target protein and VGAM448 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM447 and VGAM448

[39255] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2815(VGR2815) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39256] VGR2815 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2815 gene was detected is described hereinabove with reference to Figs. 6-15.

[39257] VGR2815 gene encodes VGR2815 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39258] VGR2815 precursor RNA folds spatially, forming VGR2815 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2815 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2815 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39259] VGR2815 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM450 precursor RNA, VGAM451 precursor RNA and VGAM452 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR and VGAM3 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39260] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM450

RNA, VGAM451 RNA and VGAM452 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA and VGAM3 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39261] VGAM450 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM450 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM450 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM450 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39262] VGAM451 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM451 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby in-

hibiting translation of VGAM451 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM451 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39263] VGAM452 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM452 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM452 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM452 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[39264] It is appreciated that a function of VGR2815 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2815 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2815

gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2815 gene: VGAM450 host target protein, VGAM451 host target protein and VGAM452 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM450, VGAM451 and VGAM452

[39265] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2816(VGR2816) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39266] VGR2816 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2816 gene was detected is described hereinabove with reference to Figs. 6-15.

[39267] VGR2816 gene encodes VGR2816 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39268] VGR2816 precursor RNA folds spatially, forming VGR2816 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2816 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2816 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39269] VGR2816 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM453 precursor RNA, VGAM454 precursor RNA and VGAM455 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR and VGAM3 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39270] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM453 RNA, VGAM454 RNA and VGAM455 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA and VGAM3 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39271] VGAM453 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM453 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM453 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM453 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39272] VGAM454 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM454 host target RNA, herein schematically represented by VGAM2

HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM454 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM454 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39273] VGAM455 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM455 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM455 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM455 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[39274] It is appreciated that a function of VGR2816 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attack-

ing a host. Accordingly, utilities of VGR2816 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2816 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2816 gene: VGAM453 host target protein, VGAM454 host target protein and VGAM455 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM453, VGAM454 and VGAM455

[39275] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2817(VGR2817) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39276] VGR2817 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding,

RNA viral gene. The method by which VGR2817 gene was detected is described hereinabove with reference to Figs. 6-15.

[39277] VGR2817 gene encodes VGR2817 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39278] VGR2817 precursor RNA folds spatially, forming VGR2817 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2817 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2817 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39279] VGR2817 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM456 precursor RNA and VGAM457 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of

which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39280] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM456 RNA and VGAM457 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39281] VGAM456 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM456 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM456 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM456 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39282] VGAM457 RNA, herein schematically represented by

VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM457 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM457 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM457 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39283] It is appreciated that a function of VGR2817 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2817 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2817 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2817 gene: VGAM456 host target protein and VGAM457 host target protein, herein schematically represented by VGAM1 HOST TARGET PRO-

TEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated herein-above with reference to VGAM456 and VGAM457

[39284] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2818(VGR2818) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39285] VGR2818 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2818 gene was detected is described hereinabove with reference to Figs. 6-15.

[39286] VGR2818 gene encodes VGR2818 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typi-cally several hundred nucleotides long.

[39287] VGR2818 precursor RNA folds spatially, forming VGR2818 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2818 folded precursor RNA, herein designated VGR FOLDED PRECUR-

SOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2818 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39288] VGR2818 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM458 precursor RNA and VGAM459 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39289] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM458 RNA and VGAM459 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39290] VGAM458 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM458 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM458 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM458 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39291] VGAM459 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM459 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM459 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM459 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of

Fig. 1.

[39292] It is appreciated that a function of VGR2818 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2818 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2818 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2818 gene: VGAM458 host target protein and VGAM459 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM458 and VGAM459

[39293] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2819(VGR2819) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known

in the art.

[39294] VGR2819 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2819 gene was detected is described hereinabove with reference to Figs. 6-15.

[39295] VGR2819 gene encodes VGR2819 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39296] VGR2819 precursor RNA folds spatially, forming VGR2819 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2819 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2819 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39297] VGR2819 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate VGAM pre-

cursor RNAs, VGAM462 precursor RNA, VGAM463 precursor RNA and VGAM464 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR and VGAM3 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39298] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM462 RNA, VGAM463 RNA and VGAM464 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA and VGAM3 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39299] VGAM462 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM462 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM462 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM462 host target protein, herein schematically

represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39300] VGAM463 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM463 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM463 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM463 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39301] VGAM464 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM464 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM464 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA

into VGAM464 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[39302] It is appreciated that a function of VGR2819 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2819 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2819 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2819 gene: VGAM462 host target protein, VGAM463 host target protein and VGAM464 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM462, VGAM463 and VGAM464

[39303] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2820(VGR2820) viral gene, which encodes an operon-like cluster of novel viral

micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39304] VGR2820 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2820 gene was detected is described hereinabove with reference to Figs. 6-15.

[39305] VGR2820 gene encodes VGR2820 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39306] VGR2820 precursor RNA folds spatially, forming VGR2820 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2820 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2820 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39307] VGR2820 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM466 precursor RNA and VGAM467 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39308] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM466 RNA and VGAM467 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39309] VGAM466 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM466 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby in-

hibiting translation of VGAM466 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM466 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39310] VGAM467 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM467 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM467 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM467 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39311] It is appreciated that a function of VGR2820 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2820 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2820

gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2820 gene: VGAM466 host target protein and VGAM467 host target protein, herein schematically represented by VGAM1 HOST TARGET PRO-TEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated herein-above with reference to VGAM466 and VGAM467

[39312] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2821(VGR2821) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39313] VGR2821 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2821 gene was detected is described hereinabove with reference to Figs. 6-15.

[39314] VGR2821 gene encodes VGR2821 precursor RNA, herein

designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39315] VGR2821 precursor RNA folds spatially, forming VGR2821 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2821 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2821 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39316] VGR2821 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM472 precursor RNA, VGAM473 precursor RNA, VGAM474 precursor RNA, VGAM475 precursor RNA and VGAM476 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR and VGAM5 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to

VGAM PRECURSOR RNA of Fig. 8.

[39317] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM472 RNA, VGAM473 RNA, VGAM474 RNA, VGAM475 RNA and VGAM476 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA and VGAM5 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39318] VGAM472 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM472 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM472 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM472 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39319] VGAM473 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding

site located in an untranslated region of VGAM473 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM473 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM473 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39320] VGAM474 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM474 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM474 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM474 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[39321] VGAM475 RNA, herein schematically represented by

VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM475 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM475 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM475 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[39322] VGAM476 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM476 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM476 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM476 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[39323] It is appreciated that a function of VGR2821 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2821 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2821 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2821 gene: VGAM472 host target protein, VGAM473 host target protein, VGAM474 host target protein, VGAM475 host target protein and VGAM476 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM472, VGAM473, VGAM474, VGAM475 and VGAM476

[39324] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2822(VGR2822) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates

expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39325] VGR2822 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2822 gene was detected is described hereinabove with reference to Figs. 6-15.

[39326] VGR2822 gene encodes VGR2822 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39327] VGR2822 precursor RNA folds spatially, forming VGR2822 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2822 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2822 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39328] VGR2822 folded precursor RNA, herein designated VGR

FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM477 precursor RNA, VGAM478 precursor RNA, VGAM479 precursor RNA, VGAM480 precursor RNA, VGAM481 precursor RNA, VGAM482 precursor RNA, VGAM483 precursor RNA and VGAM484 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR, VGAM5 PRECURSOR, VGAM6 PRECURSOR, VGAM7 PRECURSOR and VGAM8 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39329] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM477 RNA, VGAM478 RNA, VGAM479 RNA, VGAM480 RNA, VGAM481 RNA, VGAM482 RNA, VGAM483 RNA and VGAM484 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA, VGAM5 RNA, VGAM6 RNA, VGAM7 RNA and VGAM8 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39330] VGAM477 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM477 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM477 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM477 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39331] VGAM478 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM478 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM478 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM478 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of

Fig. 1.

[39332] VGAM479 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM479 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM479 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM479 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[39333] VGAM480 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM480 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM480 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM480 host target protein, herein schematically

represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[39334] VGAM481 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM481 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM481 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM481 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[39335] VGAM482 RNA, herein schematically represented by VGAM6 binds complimentarily to a host target binding site located in an untranslated region of VGAM482 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM482 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA

into VGAM482 host target protein, herein schematically represented by VGAM6 HOST TARGET PROTEIN, both of Fig. 1.

[39336] VGAM483 RNA, herein schematically represented by VGAM7 binds complimentarily to a host target binding site located in an untranslated region of VGAM483 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM483 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA into VGAM483 host target protein, herein schematically represented by VGAM7 HOST TARGET PROTEIN, both of Fig. 1.

[39337] VGAM484 RNA, herein schematically represented by VGAM8 binds complimentarily to a host target binding site located in an untranslated region of VGAM484 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM484 host target RNA, herein

schematically represented by VGAM8 HOST TARGET RNA into VGAM484 host target protein, herein schematically represented by VGAM8 HOST TARGET PROTEIN, both of Fig. 1.

[39338] It is appreciated that a function of VGR2822 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2822 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2822 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2822 gene: VGAM477 host target protein, VGAM478 host target protein, VGAM479 host target protein, VGAM480 host target protein, VGAM481 host target protein, VGAM482 host target protein, VGAM483 host target protein and VGAM484 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM477, VGAM478, VGAM479, VGAM480, VGAM481,

VGAM482, VGAM483 and VGAM484

[39339] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2823(VGR2823) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39340] VGR2823 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2823 gene was detected is described hereinabove with reference to Figs. 6-15.

[39341] VGR2823 gene encodes VGR2823 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39342] VGR2823 precursor RNA folds spatially, forming VGR2823 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2823 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to

the fact that the nucleotide sequence of VGR2823 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39343] VGR2823 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM485 precursor RNA, VGAM486 precursor RNA, VGAM487 precursor RNA, VGAM488 precursor RNA, VGAM489 precursor RNA, VGAM490 precursor RNA, VGAM491 precursor RNA and VGAM492 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR, VGAM5 PRECURSOR, VGAM6 PRECURSOR, VGAM7 PRECURSOR and VGAM8 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39344] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM485 RNA, VGAM486 RNA, VGAM487 RNA, VGAM488 RNA,

VGAM489 RNA, VGAM490 RNA, VGAM491 RNA and VGAM492 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA, VGAM5 RNA, VGAM6 RNA, VGAM7 RNA and VGAM8 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39345] VGAM485 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM485 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM485 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM485 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39346] VGAM486 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM486 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corre-

sponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM486 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM486 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39347] VGAM487 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM487 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM487 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM487 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[39348] VGAM488 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM488 host target RNA, herein schematically represented by VGAM4

HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM488 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM488 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[39349] VGAM489 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM489 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM489 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM489 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[39350] VGAM490 RNA, herein schematically represented by VGAM6 binds complimentarily to a host target binding site located in an untranslated region of VGAM490 host

target RNA, herein schematically represented by VGAM6 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM490 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA into VGAM490 host target protein, herein schematically represented by VGAM6 HOST TARGET PROTEIN, both of Fig. 1.

[39351] VGAM491 RNA, herein schematically represented by VGAM7 binds complimentarily to a host target binding site located in an untranslated region of VGAM491 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM491 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA into VGAM491 host target protein, herein schematically represented by VGAM7 HOST TARGET PROTEIN, both of Fig. 1.

[39352] VGAM492 RNA, herein schematically represented by VGAM8 binds complimentarily to a host target binding

site located in an untranslated region of VGAM492 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM492 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA into VGAM492 host target protein, herein schematically represented by VGAM8 HOST TARGET PROTEIN, both of Fig. 1.

[39353] It is appreciated that a function of VGR2823 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2823 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2823 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2823 gene: VGAM485 host target protein, VGAM486 host target protein, VGAM487 host target protein, VGAM488 host target protein, VGAM489 host target protein, VGAM490 host target pro-

tein, VGAM491 host target protein and VGAM492 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM485, VGAM486, VGAM487, VGAM488, VGAM489, VGAM490, VGAM491 and VGAM492

[39354] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2824(VGR2824) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39355] VGR2824 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2824 gene was detected is described hereinabove with reference to Figs. 6-15.

[39356] VGR2824 gene encodes VGR2824 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39357] VGR2824 precursor RNA folds spatially, forming VGR2824 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2824 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2824 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39358] VGR2824 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM493 precursor RNA, VGAM494 precursor RNA and VGAM495 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR and VGAM3 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39359] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM493

RNA, VGAM494 RNA and VGAM495 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA and VGAM3 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39360] VGAM493 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM493 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM493 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM493 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39361] VGAM494 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM494 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby in-

hibiting translation of VGAM494 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM494 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39362] VGAM495 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM495 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM495 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM495 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[39363] It is appreciated that a function of VGR2824 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2824 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2824

gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2824 gene: VGAM493 host target protein, VGAM494 host target protein and VGAM495 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM493, VGAM494 and VGAM495

[39364] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2825(VGR2825) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39365] VGR2825 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2825 gene was detected is described hereinabove with reference to Figs. 6-15.

[39366] VGR2825 gene encodes VGR2825 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39367] VGR2825 precursor RNA folds spatially, forming VGR2825 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2825 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2825 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39368] VGR2825 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM496 precursor RNA and VGAM497 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39369] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM496 RNA and VGAM497 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39370] VGAM496 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM496 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM496 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM496 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39371] VGAM497 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM497 host target RNA, herein schematically represented by VGAM2

HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM497 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM497 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39372] It is appreciated that a function of VGR2825 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2825 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2825 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2825 gene: VGAM496 host target protein and VGAM497 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM496 and VGAM497

[39373] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2826(VGR2826) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39374] VGR2826 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2826 gene was detected is described hereinabove with reference to Figs. 6-15.

[39375] VGR2826 gene encodes VGR2826 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39376] VGR2826 precursor RNA folds spatially, forming VGR2826 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2826 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2826 precur-

sor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39377] VGR2826 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM499 precursor RNA and VGAM500 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39378] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM499 RNA and VGAM500 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39379] VGAM499 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM499 host

target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM499 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM499 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39380] VGAM500 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM500 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM500 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM500 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39381] It is appreciated that a function of VGR2826 gene, herein designated VGR GENE, is inhibition of expression of host

target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2826 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2826 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2826 gene: VGAM499 host target protein and VGAM500 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM499 and VGAM500

[39382] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2827(VGR2827) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39383] VGR2827 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding,

RNA viral gene. The method by which VGR2827 gene was detected is described hereinabove with reference to Figs. 6-15.

[39384] VGR2827 gene encodes VGR2827 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39385] VGR2827 precursor RNA folds spatially, forming VGR2827 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2827 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2827 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39386] VGR2827 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM501 precursor RNA and VGAM502 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of

which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39387] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM501 RNA and VGAM502 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39388] VGAM501 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM501 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM501 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM501 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39389] VGAM502 RNA, herein schematically represented by

VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM502 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM502 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM502 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39390] It is appreciated that a function of VGR2827 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2827 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2827 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2827 gene: VGAM501 host target protein and VGAM502 host target protein, herein schematically represented by VGAM1 HOST TARGET PRO-

TEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated herein-above with reference to VGAM501 and VGAM502

[39391] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2828(VGR2828) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39392] VGR2828 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2828 gene was detected is described hereinabove with reference to Figs. 6-15.

[39393] VGR2828 gene encodes VGR2828 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typi-cally several hundred nucleotides long.

[39394] VGR2828 precursor RNA folds spatially, forming VGR2828 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2828 folded precursor RNA, herein designated VGR FOLDED PRECUR-

SOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2828 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39395] VGR2828 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM506 precursor RNA, VGAM507 precursor RNA and VGAM508 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR and VGAM3 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39396] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM506 RNA, VGAM507 RNA and VGAM508 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA and VGAM3 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39397] VGAM506 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM506 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM506 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM506 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39398] VGAM507 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM507 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM507 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM507 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of

Fig. 1.

[39399] VGAM508 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM508 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM508 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM508 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[39400] It is appreciated that a function of VGR2828 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2828 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2828 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2828 gene: VGAM506 host

target protein, VGAM507 host target protein and VGAM508 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM506, VGAM507 and VGAM508

[39401] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2829(VGR2829) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39402] VGR2829 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2829 gene was detected is described hereinabove with reference to Figs. 6-15.

[39403] VGR2829 gene encodes VGR2829 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39404] VGR2829 precursor RNA folds spatially, forming VGR2829

folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2829 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2829 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39405] VGR2829 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM509 precursor RNA and VGAM510 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39406] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM509 RNA and VGAM510 RNA respectively, herein schematically

represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39407] VGAM509 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM509 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM509 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM509 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39408] VGAM510 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM510 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM510 host target RNA, herein

schematically represented by VGAM2 HOST TARGET RNA into VGAM510 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39409] It is appreciated that a function of VGR2829 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2829 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2829 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2829 gene: VGAM509 host target protein and VGAM510 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM509 and VGAM510

[39410] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2830(VGR2830) viral gene, which encodes an operon-like cluster of novel viral

micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39411] VGR2830 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2830 gene was detected is described hereinabove with reference to Figs. 6-15.

[39412] VGR2830 gene encodes VGR2830 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39413] VGR2830 precursor RNA folds spatially, forming VGR2830 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2830 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2830 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39414] VGR2830 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM511 precursor RNA, VGAM512 precursor RNA, VGAM513 precursor RNA, VGAM514 precursor RNA and VGAM515 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR and VGAM5 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39415] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM511 RNA, VGAM512 RNA, VGAM513 RNA, VGAM514 RNA and VGAM515 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA and VGAM5 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39416] VGAM511 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM511 host target RNA, herein schematically represented by VGAM1

HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM511 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM511 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39417] VGAM512 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM512 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM512 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM512 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39418] VGAM513 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM513 host

target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM513 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM513 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[39419] VGAM514 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM514 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM514 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM514 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[39420] VGAM515 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding

site located in an untranslated region of VGAM515 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM515 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM515 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[39421] It is appreciated that a function of VGR2830 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2830 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2830 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2830 gene: VGAM511 host target protein, VGAM512 host target protein, VGAM513 host target protein, VGAM514 host target protein and VGAM515 host target protein, herein schematically repre-

sented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM511, VGAM512, VGAM513, VGAM514 and VGAM515

[39422] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2831(VGR2831) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39423] VGR2831 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2831 gene was detected is described hereinabove with reference to Figs. 6-15.

[39424] VGR2831 gene encodes VGR2831 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39425] VGR2831 precursor RNA folds spatially, forming VGR2831 folded precursor RNA, herein designated VGR FOLDED

PRECURSOR RNA. It is appreciated that VGR2831 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2831 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39426] VGR2831 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM516 precursor RNA and VGAM517 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39427] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM516 RNA and VGAM517 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively,

each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39428] VGAM516 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM516 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM516 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM516 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39429] VGAM517 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM517 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM517 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA

into VGAM517 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39430] It is appreciated that a function of VGR2831 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2831 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2831 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2831 gene: VGAM516 host target protein and VGAM517 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM516 and VGAM517

[39431] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2832(VGR2832) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates

expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39432] VGR2832 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2832 gene was detected is described hereinabove with reference to Figs. 6-15.

[39433] VGR2832 gene encodes VGR2832 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39434] VGR2832 precursor RNA folds spatially, forming VGR2832 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2832 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2832 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39435] VGR2832 folded precursor RNA, herein designated VGR

FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM519 precursor RNA and VGAM520 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39436] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM519 RNA and VGAM520 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39437] VGAM519 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM519 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM519 host target RNA, herein

schematically represented by VGAM1 HOST TARGET RNA into VGAM519 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39438] VGAM520 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM520 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM520 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM520 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39439] It is appreciated that a function of VGR2832 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2832 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2832 gene, herein designated VGR GENE, correlate with, and

may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2832 gene: VGAM519 host target protein and VGAM520 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM519 and VGAM520

[39440] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2833(VGR2833) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39441] VGR2833 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2833 gene was detected is described hereinabove with reference to Figs. 6-15.

[39442] VGR2833 gene encodes VGR2833 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typi-

cally several hundred nucleotides long.

[39443] VGR2833 precursor RNA folds spatially, forming VGR2833 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2833 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2833 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39444] VGR2833 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM521 precursor RNA and VGAM522 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39445] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA

segments of about 22 nucleotides in length, VGAM521 RNA and VGAM522 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39446] VGAM521 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM521 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM521 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM521 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39447] VGAM522 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM522 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM522 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM522 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39448] It is appreciated that a function of VGR2833 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2833 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2833 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2833 gene: VGAM521 host target protein and VGAM522 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM521 and VGAM522

[39449] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred

to here as Viral Genomic Record 2834(VGR2834) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39450] VGR2834 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2834 gene was detected is described hereinabove with reference to Figs. 6-15.

[39451] VGR2834 gene encodes VGR2834 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39452] VGR2834 precursor RNA folds spatially, forming VGR2834 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2834 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2834 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which

is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39453] VGR2834 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM523 precursor RNA and VGAM524 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39454] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM523 RNA and VGAM524 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39455] VGAM523 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM523 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corre-

sponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM523 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM523 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39456] VGAM524 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM524 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM524 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM524 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39457] It is appreciated that a function of VGR2834 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2834 gene include

diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2834 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2834 gene: VGAM523 host target protein and VGAM524 host target protein, herein schematically represented by VGAM1 HOST TARGET PRO-TEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated herein-above with reference to VGAM523 and VGAM524

[39458] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2835(VGR2835) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39459] VGR2835 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2835 gene was detected is described hereinabove with reference to Figs.

6-15.

[39460] VGR2835 gene encodes VGR2835 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39461] VGR2835 precursor RNA folds spatially, forming VGR2835 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2835 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2835 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39462] VGR2835 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM525 precursor RNA and VGAM526 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig.

8.

[39463] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM525 RNA and VGAM526 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39464] VGAM525 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM525 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM525 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM525 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39465] VGAM526 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM526 host

target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM526 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM526 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39466] It is appreciated that a function of VGR2835 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2835 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2835 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2835 gene: VGAM525 host target protein and VGAM526 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated herein-

above with reference to VGAM525 and VGAM526

[39467] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2836(VGR2836) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39468] VGR2836 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2836 gene was detected is described hereinabove with reference to Figs. 6-15.

[39469] VGR2836 gene encodes VGR2836 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39470] VGR2836 precursor RNA folds spatially, forming VGR2836 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2836 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to

the fact that the nucleotide sequence of VGR2836 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39471] VGR2836 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM536 precursor RNA and VGAM537 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39472] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM536 RNA and VGAM537 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39473] VGAM536 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding

site located in an untranslated region of VGAM536 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM536 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM536 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39474] VGAM537 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM537 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM537 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM537 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39475] It is appreciated that a function of VGR2836 gene, herein

designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2836 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2836 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2836 gene: VGAM536 host target protein and VGAM537 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM536 and VGAM537

[39476] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2837(VGR2837) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39477] VGR2837 gene, herein designated VGR GENE, is a novel

bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2837 gene was detected is described hereinabove with reference to Figs. 6-15.

[39478] VGR2837 gene encodes VGR2837 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39479] VGR2837 precursor RNA folds spatially, forming VGR2837 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2837 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2837 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39480] VGR2837 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM539 precursor RNA, VGAM540 precursor RNA and VGAM541 precursor RNA, herein schemati-

cally represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR and VGAM3 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39481] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM539 RNA, VGAM540 RNA and VGAM541 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA and VGAM3 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39482] VGAM539 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM539 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM539 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM539 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39483] VGAM540 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM540 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM540 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM540 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39484] VGAM541 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM541 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM541 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM541 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of

Fig. 1.

[39485] It is appreciated that a function of VGR2837 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2837 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2837 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2837 gene: VGAM539 host target protein, VGAM540 host target protein and VGAM541 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM539, VGAM540 and VGAM541

[39486] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2838(VGR2838) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function

and utility of which at least one host target gene is known in the art.

[39487] VGR2838 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2838 gene was detected is described hereinabove with reference to Figs. 6-15.

[39488] VGR2838 gene encodes VGR2838 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39489] VGR2838 precursor RNA folds spatially, forming VGR2838 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2838 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2838 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39490] VGR2838 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellu-

lar enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM546 precursor RNA and VGAM547 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39491] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM546 RNA and VGAM547 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39492] VGAM546 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM546 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM546 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA

into VGAM546 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39493] VGAM547 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM547 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM547 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM547 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39494] It is appreciated that a function of VGR2838 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2838 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2838 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target

genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2838 gene: VGAM546 host target protein and VGAM547 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated herein-above with reference to VGAM546 and VGAM547

[39495] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2839(VGR2839) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39496] VGR2839 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2839 gene was detected is described hereinabove with reference to Figs. 6-15.

[39497] VGR2839 gene encodes VGR2839 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39498] VGR2839 precursor RNA folds spatially, forming VGR2839 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2839 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2839 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39499] VGR2839 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM550 precursor RNA and VGAM551 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39500] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM550

RNA and VGAM551 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39501] VGAM550 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM550 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM550 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM550 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39502] VGAM551 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM551 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby in-

hibiting translation of VGAM551 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM551 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39503] It is appreciated that a function of VGR2839 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2839 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2839 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2839 gene: VGAM550 host target protein and VGAM551 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM550 and VGAM551

[39504] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2840(VGR2840) viral

gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39505] VGR2840 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2840 gene was detected is described hereinabove with reference to Figs. 6-15.

[39506] VGR2840 gene encodes VGR2840 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39507] VGR2840 precursor RNA folds spatially, forming VGR2840 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2840 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2840 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the

second half thereof, as is well known in the art.

[39508] VGR2840 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM554 precursor RNA, VGAM555 precursor RNA and VGAM556 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR and VGAM3 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39509] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM554 RNA, VGAM555 RNA and VGAM556 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA and VGAM3 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39510] VGAM554 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM554 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM554 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM554 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39511] VGAM555 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM555 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM555 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM555 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39512] VGAM556 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM556 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corre-

sponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM556 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM556 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[39513] It is appreciated that a function of VGR2840 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2840 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2840 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2840 gene: VGAM554 host target protein, VGAM555 host target protein and VGAM556 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM554, VGAM555 and VGAM556

[39514] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2841(VGR2841) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39515] VGR2841 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2841 gene was detected is described hereinabove with reference to Figs. 6-15.

[39516] VGR2841 gene encodes VGR2841 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39517] VGR2841 precursor RNA folds spatially, forming VGR2841 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2841 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2841 precur-

sor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39518] VGR2841 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM562 precursor RNA, VGAM563 precursor RNA and VGAM564 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR and VGAM3 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39519] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM562 RNA, VGAM563 RNA and VGAM564 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA and VGAM3 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39520] VGAM562 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM562 host

target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM562 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM562 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39521] VGAM563 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM563 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM563 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM563 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39522] VGAM564 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding

site located in an untranslated region of VGAM564 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM564 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM564 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[39523] It is appreciated that a function of VGR2841 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2841 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2841 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2841 gene: VGAM562 host target protein, VGAM563 host target protein and VGAM564 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM

HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM562, VGAM563 and VGAM564

[39524] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2842(VGR2842) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39525] VGR2842 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2842 gene was detected is described hereinabove with reference to Figs. 6-15.

[39526] VGR2842 gene encodes VGR2842 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39527] VGR2842 precursor RNA folds spatially, forming VGR2842 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2842 folded precursor RNA, herein designated VGR FOLDED PRECUR-

SOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2842 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39528] VGR2842 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM565 precursor RNA and VGAM566 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39529] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM565 RNA and VGAM566 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39530] VGAM565 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM565 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM565 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM565 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39531] VGAM566 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM566 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM566 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM566 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of

Fig. 1.

[39532] It is appreciated that a function of VGR2842 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2842 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2842 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2842 gene: VGAM565 host target protein and VGAM566 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM565 and VGAM566

[39533] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2843(VGR2843) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known

in the art.

[39534] VGR2843 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2843 gene was detected is described hereinabove with reference to Figs. 6-15.

[39535] VGR2843 gene encodes VGR2843 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39536] VGR2843 precursor RNA folds spatially, forming VGR2843 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2843 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2843 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39537] VGR2843 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate VGAM pre-

cursor RNAs, VGAM567 precursor RNA, VGAM568 precursor RNA, VGAM569 precursor RNA and VGAM570 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR and VGAM4 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39538] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM567 RNA, VGAM568 RNA, VGAM569 RNA and VGAM570 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA and VGAM4 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39539] VGAM567 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM567 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM567 host target RNA, herein

schematically represented by VGAM1 HOST TARGET RNA into VGAM567 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39540] VGAM568 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM568 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM568 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM568 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39541] VGAM569 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM569 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby in-

hibiting translation of VGAM569 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM569 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[39542] VGAM570 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM570 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM570 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM570 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[39543] It is appreciated that a function of VGR2843 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2843 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2843

gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2843 gene: VGAM567 host target protein, VGAM568 host target protein, VGAM569 host target protein and VGAM570 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM567, VGAM568, VGAM569 and VGAM570

[39544] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2844(VGR2844) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39545] VGR2844 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2844 gene was detected is described hereinabove with reference to Figs.

6-15.

[39546] VGR2844 gene encodes VGR2844 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39547] VGR2844 precursor RNA folds spatially, forming VGR2844 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2844 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2844 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39548] VGR2844 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM571 precursor RNA, VGAM572 precursor RNA, VGAM573 precursor RNA and VGAM574 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR and VGAM4 PRECURSOR respectively, each of which VGAM

precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39549] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM571 RNA, VGAM572 RNA, VGAM573 RNA and VGAM574 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA and VGAM4 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39550] VGAM571 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM571 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM571 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM571 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39551] VGAM572 RNA, herein schematically represented by

VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM572 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM572 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM572 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39552] VGAM573 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM573 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM573 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM573 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[39553] VGAM574 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM574 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM574 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM574 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[39554] It is appreciated that a function of VGR2844 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2844 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2844 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2844 gene: VGAM571 host target protein, VGAM572 host target protein, VGAM573

host target protein and VGAM574 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM571, VGAM572, VGAM573 and VGAM574

[39555] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2845(VGR2845) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39556] VGR2845 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2845 gene was detected is described hereinabove with reference to Figs. 6-15.

[39557] VGR2845 gene encodes VGR2845 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39558] VGR2845 precursor RNA folds spatially, forming VGR2845

folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2845 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2845 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39559] VGR2845 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM575 precursor RNA and VGAM576 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39560] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM575 RNA and VGAM576 RNA respectively, herein schematically

represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39561] VGAM575 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM575 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM575 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM575 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39562] VGAM576 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM576 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM576 host target RNA, herein

schematically represented by VGAM2 HOST TARGET RNA into VGAM576 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39563] It is appreciated that a function of VGR2845 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2845 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2845 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2845 gene: VGAM575 host target protein and VGAM576 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM575 and VGAM576

[39564] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2846(VGR2846) viral gene, which encodes an operon-like cluster of novel viral

micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39565] VGR2846 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2846 gene was detected is described hereinabove with reference to Figs. 6-15.

[39566] VGR2846 gene encodes VGR2846 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39567] VGR2846 precursor RNA folds spatially, forming VGR2846 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2846 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2846 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39568] VGR2846 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM577 precursor RNA and VGAM578 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39569] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM577 RNA and VGAM578 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39570] VGAM577 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM577 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby in-

hibiting translation of VGAM577 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM577 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39571] VGAM578 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM578 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM578 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM578 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39572] It is appreciated that a function of VGR2846 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2846 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2846

gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2846 gene: VGAM577 host target protein and VGAM578 host target protein, herein schematically represented by VGAM1 HOST TARGET PRO-TEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated herein-above with reference to VGAM577 and VGAM578

[39573] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2847(VGR2847) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39574] VGR2847 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2847 gene was detected is described hereinabove with reference to Figs. 6-15.

[39575] VGR2847 gene encodes VGR2847 precursor RNA, herein

designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39576] VGR2847 precursor RNA folds spatially, forming VGR2847 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2847 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2847 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39577] VGR2847 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM580 precursor RNA and VGAM581 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39578] The above mentioned VGAM precursor RNAs are diced by

DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM580 RNA and VGAM581 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39579] VGAM580 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM580 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM580 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM580 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39580] VGAM581 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM581 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corre-

sponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM581 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM581 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39581] It is appreciated that a function of VGR2847 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2847 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2847 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2847 gene: VGAM580 host target protein and VGAM581 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM580 and VGAM581

[39582] Fig. 9 further provides a conceptual description of novel

bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2848(VGR2848) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39583] VGR2848 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2848 gene was detected is described hereinabove with reference to Figs. 6-15.

[39584] VGR2848 gene encodes VGR2848 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39585] VGR2848 precursor RNA folds spatially, forming VGR2848 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2848 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2848 precursor RNA comprises a plurality of segments, the first half

of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39586] VGR2848 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM585 precursor RNA, VGAM586 precursor RNA and VGAM587 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR and VGAM3 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39587] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM585 RNA, VGAM586 RNA and VGAM587 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA and VGAM3 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39588] VGAM585 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM585 host target RNA, herein schematically represented by VGAM1

HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM585 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM585 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39589] VGAM586 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM586 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM586 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM586 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39590] VGAM587 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM587 host

target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM587 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM587 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[39591] It is appreciated that a function of VGR2848 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2848 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2848 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2848 gene: VGAM585 host target protein, VGAM586 host target protein and VGAM587 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these

host target genes is elaborated hereinabove with reference to VGAM585, VGAM586 and VGAM587

[39592] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2849(VGR2849) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39593] VGR2849 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2849 gene was detected is described hereinabove with reference to Figs. 6-15.

[39594] VGR2849 gene encodes VGR2849 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39595] VGR2849 precursor RNA folds spatially, forming VGR2849 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2849 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art

as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2849 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39596] VGR2849 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM588 precursor RNA, VGAM589 precursor RNA and VGAM590 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR and VGAM3 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39597] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM588 RNA, VGAM589 RNA and VGAM590 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA and VGAM3 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39598] VGAM588 RNA, herein schematically represented by

VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM588 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM588 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM588 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39599] VGAM589 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM589 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM589 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM589 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39600] VGAM590 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM590 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM590 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM590 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[39601] It is appreciated that a function of VGR2849 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2849 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2849 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2849 gene: VGAM588 host target protein, VGAM589 host target protein and

VGAM590 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM588, VGAM589 and VGAM590

[39602] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2850(VGR2850) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39603] VGR2850 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2850 gene was detected is described hereinabove with reference to Figs. 6-15.

[39604] VGR2850 gene encodes VGR2850 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39605] VGR2850 precursor RNA folds spatially, forming VGR2850 folded precursor RNA, herein designated VGR FOLDED

PRECURSOR RNA. It is appreciated that VGR2850 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2850 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39606] VGR2850 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM591 precursor RNA and VGAM592 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39607] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM591 RNA and VGAM592 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively,

each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39608] VGAM591 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM591 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM591 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM591 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39609] VGAM592 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM592 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM592 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA

into VGAM592 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39610] It is appreciated that a function of VGR2850 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2850 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2850 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2850 gene: VGAM591 host target protein and VGAM592 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM591 and VGAM592

[39611] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2851(VGR2851) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates

expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39612] VGR2851 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2851 gene was detected is described hereinabove with reference to Figs. 6-15.

[39613] VGR2851 gene encodes VGR2851 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39614] VGR2851 precursor RNA folds spatially, forming VGR2851 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2851 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2851 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39615] VGR2851 folded precursor RNA, herein designated VGR

FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM594 precursor RNA, VGAM595 precursor RNA and VGAM596 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR and VGAM3 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39616] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM594 RNA, VGAM595 RNA and VGAM596 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA and VGAM3 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39617] VGAM594 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM594 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM594 host target RNA, herein

schematically represented by VGAM1 HOST TARGET RNA into VGAM594 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39618] VGAM595 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM595 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM595 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM595 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39619] VGAM596 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM596 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby in-

hibiting translation of VGAM596 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM596 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[39620] It is appreciated that a function of VGR2851 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2851 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2851 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2851 gene: VGAM594 host target protein, VGAM595 host target protein and VGAM596 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM594, VGAM595 and VGAM596

[39621] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred

to here as Viral Genomic Record 2852(VGR2852) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39622] VGR2852 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2852 gene was detected is described hereinabove with reference to Figs. 6-15.

[39623] VGR2852 gene encodes VGR2852 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39624] VGR2852 precursor RNA folds spatially, forming VGR2852 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2852 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2852 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which

is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39625] VGR2852 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM597 precursor RNA, VGAM598 precursor RNA, VGAM599 precursor RNA, VGAM600 precursor RNA, VGAM601 precursor RNA, VGAM602 precursor RNA, VGAM603 precursor RNA and VGAM604 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR, VGAM5 PRECURSOR, VGAM6 PRECURSOR, VGAM7 PRECURSOR and VGAM8 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39626] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM597 RNA, VGAM598 RNA, VGAM599 RNA, VGAM600 RNA, VGAM601 RNA, VGAM602 RNA, VGAM603 RNA and VGAM604 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4

RNA, VGAM5 RNA, VGAM6 RNA, VGAM7 RNA and VGAM8 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39627] VGAM597 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM597 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM597 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM597 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39628] VGAM598 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM598 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM598 host target RNA, herein

schematically represented by VGAM2 HOST TARGET RNA into VGAM598 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39629] VGAM599 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM599 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM599 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM599 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[39630] VGAM600 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM600 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby in-

hibiting translation of VGAM600 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM600 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[39631] VGAM601 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM601 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM601 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM601 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[39632] VGAM602 RNA, herein schematically represented by VGAM6 binds complimentarily to a host target binding site located in an untranslated region of VGAM602 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM602 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA into VGAM602 host target protein, herein schematically represented by VGAM6 HOST TARGET PROTEIN, both of Fig. 1.

[39633] VGAM603 RNA, herein schematically represented by VGAM7 binds complimentarily to a host target binding site located in an untranslated region of VGAM603 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM603 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA into VGAM603 host target protein, herein schematically represented by VGAM7 HOST TARGET PROTEIN, both of Fig. 1.

[39634] VGAM604 RNA, herein schematically represented by VGAM8 binds complimentarily to a host target binding site located in an untranslated region of VGAM604 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA, which host target binding site corre-

sponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM604 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA into VGAM604 host target protein, herein schematically represented by VGAM8 HOST TARGET PROTEIN, both of Fig. 1.

[39635] It is appreciated that a function of VGR2852 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2852 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2852 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2852 gene: VGAM597 host target protein, VGAM598 host target protein, VGAM599 host target protein, VGAM600 host target protein, VGAM601 host target protein, VGAM602 host target protein, VGAM603 host target protein and VGAM604 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TAR-

GET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM597, VGAM598, VGAM599, VGAM600, VGAM601, VGAM602, VGAM603 and VGAM604

[39636] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2853(VGR2853) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39637] VGR2853 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2853 gene was detected is described hereinabove with reference to Figs. 6-15.

[39638] VGR2853 gene encodes VGR2853 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39639] VGR2853 precursor RNA folds spatially, forming VGR2853 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2853 folded

precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2853 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39640] VGR2853 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM605 precursor RNA and VGAM606 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39641] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM605 RNA and VGAM606 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of

Fig. 8.

[39642] VGAM605 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM605 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM605 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM605 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39643] VGAM606 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM606 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM606 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM606 host target protein, herein schematically

represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39644] It is appreciated that a function of VGR2853 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2853 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2853 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2853 gene: VGAM605 host target protein and VGAM606 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM605 and VGAM606

[39645] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2854(VGR2854) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function

and utility of which at least one host target gene is known in the art.

[39646] VGR2854 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2854 gene was detected is described hereinabove with reference to Figs. 6-15.

[39647] VGR2854 gene encodes VGR2854 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39648] VGR2854 precursor RNA folds spatially, forming VGR2854 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2854 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2854 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39649] VGR2854 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellu-

lar enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM607 precursor RNA, VGAM608 precursor RNA, VGAM609 precursor RNA and VGAM610 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR and VGAM4 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39650] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM607 RNA, VGAM608 RNA, VGAM609 RNA and VGAM610 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA and VGAM4 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39651] VGAM607 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM607 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby in-

hibiting translation of VGAM607 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM607 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39652] VGAM608 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM608 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM608 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM608 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39653] VGAM609 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM609 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM609 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM609 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[39654] VGAM610 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM610 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM610 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM610 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[39655] It is appreciated that a function of VGR2854 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2854 gene include diagnosis, prevention and treatment of viral infection by .

Specific functions, and accordingly utilities, of VGR2854 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2854 gene: VGAM607 host target protein, VGAM608 host target protein, VGAM609 host target protein and VGAM610 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM607, VGAM608, VGAM609 and VGAM610

[39656] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2855(VGR2855) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39657] VGR2855 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2855 gene was

detected is described hereinabove with reference to Figs. 6-15.

[39658] VGR2855 gene encodes VGR2855 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39659] VGR2855 precursor RNA folds spatially, forming VGR2855 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2855 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2855 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39660] VGR2855 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM613 precursor RNA and VGAM614 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA

segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39661] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM613 RNA and VGAM614 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39662] VGAM613 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM613 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM613 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM613 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39663] VGAM614 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding

site located in an untranslated region of VGAM614 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM614 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM614 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39664] It is appreciated that a function of VGR2855 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2855 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2855 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2855 gene: VGAM613 host target protein and VGAM614 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN andVGAM HOST TARGET PROTEIN respectively. The

function of these host target genes is elaborated herein-above with reference to VGAM613 and VGAM614

[39665] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2856(VGR2856) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39666] VGR2856 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2856 gene was detected is described hereinabove with reference to Figs. 6-15.

[39667] VGR2856 gene encodes VGR2856 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39668] VGR2856 precursor RNA folds spatially, forming VGR2856 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2856 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art

as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2856 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39669] VGR2856 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM615 precursor RNA and VGAM616 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39670] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM615 RNA and VGAM616 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39671] VGAM615 RNA, herein schematically represented by

VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM615 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM615 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM615 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39672] VGAM616 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM616 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM616 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM616 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39673] It is appreciated that a function of VGR2856 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2856 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2856 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2856 gene: VGAM615 host target protein and VGAM616 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM615 and VGAM616

[39674] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2857(VGR2857) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39675] VGR2857 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2857 gene was detected is described hereinabove with reference to Figs. 6-15.

[39676] VGR2857 gene encodes VGR2857 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39677] VGR2857 precursor RNA folds spatially, forming VGR2857 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2857 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2857 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39678] VGR2857 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM619 precursor RNA, VGAM620 precur-

sor RNA, VGAM621 precursor RNA, VGAM622 precursor RNA, VGAM623 precursor RNA, VGAM624 precursor RNA, VGAM625 precursor RNA and VGAM626 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR, VGAM5 PRECURSOR, VGAM6 PRECURSOR, VGAM7 PRECURSOR and VGAM8 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39679] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM619 RNA, VGAM620 RNA, VGAM621 RNA, VGAM622 RNA, VGAM623 RNA, VGAM624 RNA, VGAM625 RNA and VGAM626 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA, VGAM5 RNA, VGAM6 RNA, VGAM7 RNA and VGAM8 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39680] VGAM619 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM619 host

target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM619 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM619 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39681] VGAM620 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM620 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM620 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM620 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39682] VGAM621 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding

site located in an untranslated region of VGAM621 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM621 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM621 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[39683] VGAM622 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM622 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM622 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM622 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[39684] VGAM623 RNA, herein schematically represented by

VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM623 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM623 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM623 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[39685] VGAM624 RNA, herein schematically represented by VGAM6 binds complimentarily to a host target binding site located in an untranslated region of VGAM624 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM624 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA into VGAM624 host target protein, herein schematically represented by VGAM6 HOST TARGET PROTEIN, both of Fig. 1.

[39686] VGAM625 RNA, herein schematically represented by VGAM7 binds complimentarily to a host target binding site located in an untranslated region of VGAM625 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM625 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA into VGAM625 host target protein, herein schematically represented by VGAM7 HOST TARGET PROTEIN, both of Fig. 1.

[39687] VGAM626 RNA, herein schematically represented by VGAM8 binds complimentarily to a host target binding site located in an untranslated region of VGAM626 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM626 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA into VGAM626 host target protein, herein schematically represented by VGAM8 HOST TARGET PROTEIN, both of

Fig. 1.

[39688] It is appreciated that a function of VGR2857 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2857 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2857 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2857 gene: VGAM619 host target protein, VGAM620 host target protein, VGAM621 host target protein, VGAM622 host target protein, VGAM623 host target protein, VGAM624 host target protein, VGAM625 host target protein and VGAM626 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM619, VGAM620, VGAM621, VGAM622, VGAM623, VGAM624, VGAM625 and VGAM626

[39689] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred

to here as Viral Genomic Record 2858(VGR2858) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39690] VGR2858 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2858 gene was detected is described hereinabove with reference to Figs. 6-15.

[39691] VGR2858 gene encodes VGR2858 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39692] VGR2858 precursor RNA folds spatially, forming VGR2858 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2858 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2858 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which

is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39693] VGR2858 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM627 precursor RNA, VGAM628 precursor RNA, VGAM629 precursor RNA and VGAM630 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR and VGAM4 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39694] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM627 RNA, VGAM628 RNA, VGAM629 RNA and VGAM630 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA and VGAM4 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39695] VGAM627 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM627 host

target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM627 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM627 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39696] VGAM628 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM628 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM628 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM628 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39697] VGAM629 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding

site located in an untranslated region of VGAM629 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM629 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM629 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[39698] VGAM630 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM630 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM630 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM630 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[39699] It is appreciated that a function of VGR2858 gene, herein

designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2858 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2858 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2858 gene: VGAM627 host target protein, VGAM628 host target protein, VGAM629 host target protein and VGAM630 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM627, VGAM628, VGAM629 and VGAM630

[39700] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2859(VGR2859) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known

in the art.

[39701] VGR2859 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2859 gene was detected is described hereinabove with reference to Figs. 6-15.

[39702] VGR2859 gene encodes VGR2859 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39703] VGR2859 precursor RNA folds spatially, forming VGR2859 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2859 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2859 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39704] VGR2859 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM pre-

cursor RNAs, VGAM631 precursor RNA and VGAM632 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39705] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM631 RNA and VGAM632 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39706] VGAM631 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM631 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM631 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM631 host target protein, herein schematically

represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39707] VGAM632 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM632 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM632 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM632 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39708] It is appreciated that a function of VGR2859 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2859 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2859 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in

the operon-like cluster of VGR2859 gene: VGAM631 host target protein and VGAM632 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM631 and VGAM632

[39709] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2860(VGR2860) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39710] VGR2860 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2860 gene was detected is described hereinabove with reference to Figs. 6-15.

[39711] VGR2860 gene encodes VGR2860 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39712] VGR2860 precursor RNA folds spatially, forming VGR2860

folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2860 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2860 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39713] VGR2860 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM633 precursor RNA and VGAM634 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39714] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM633 RNA and VGAM634 RNA respectively, herein schematically

represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39715] VGAM633 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM633 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM633 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM633 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39716] VGAM634 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM634 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM634 host target RNA, herein

schematically represented by VGAM2 HOST TARGET RNA into VGAM634 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39717] It is appreciated that a function of VGR2860 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2860 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2860 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2860 gene: VGAM633 host target protein and VGAM634 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM633 and VGAM634

[39718] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2861(VGR2861) viral gene, which encodes an operon-like cluster of novel viral

micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39719] VGR2861 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2861 gene was detected is described hereinabove with reference to Figs. 6-15.

[39720] VGR2861 gene encodes VGR2861 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39721] VGR2861 precursor RNA folds spatially, forming VGR2861 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2861 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2861 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39722] VGR2861 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM635 precursor RNA and VGAM636 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39723] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM635 RNA and VGAM636 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39724] VGAM635 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM635 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby in-

hibiting translation of VGAM635 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM635 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39725] VGAM636 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM636 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM636 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM636 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39726] It is appreciated that a function of VGR2861 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2861 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2861

gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2861 gene: VGAM635 host target protein and VGAM636 host target protein, herein schematically represented by VGAM1 HOST TARGET PRO-TEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated herein-above with reference to VGAM635 and VGAM636

[39727] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2862(VGR2862) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39728] VGR2862 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2862 gene was detected is described hereinabove with reference to Figs. 6-15.

[39729] VGR2862 gene encodes VGR2862 precursor RNA, herein

designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39730] VGR2862 precursor RNA folds spatially, forming VGR2862 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2862 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2862 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39731] VGR2862 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM638 precursor RNA, VGAM639 precursor RNA and VGAM640 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR and VGAM3 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39732] The above mentioned VGAM precursor RNAs are diced by

DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM638 RNA, VGAM639 RNA and VGAM640 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA and VGAM3 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39733] VGAM638 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM638 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM638 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM638 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39734] VGAM639 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM639 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corre-

sponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM639 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM639 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39735] VGAM640 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM640 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM640 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM640 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[39736] It is appreciated that a function of VGR2862 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2862 gene include

diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2862 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2862 gene: VGAM638 host target protein, VGAM639 host target protein and VGAM640 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM638, VGAM639 and VGAM640

[39737] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2863(VGR2863) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39738] VGR2863 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2863 gene was

detected is described hereinabove with reference to Figs. 6-15.

[39739] VGR2863 gene encodes VGR2863 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39740] VGR2863 precursor RNA folds spatially, forming VGR2863 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2863 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2863 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39741] VGR2863 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM644 precursor RNA and VGAM645 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA

segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39742] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM644 RNA and VGAM645 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39743] VGAM644 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM644 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM644 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM644 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39744] VGAM645 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding

site located in an untranslated region of VGAM645 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM645 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM645 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39745] It is appreciated that a function of VGR2863 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2863 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2863 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2863 gene: VGAM644 host target protein and VGAM645 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN andVGAM HOST TARGET PROTEIN respectively. The

function of these host target genes is elaborated herein-above with reference to VGAM644 and VGAM645

[39746] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2864(VGR2864) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39747] VGR2864 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2864 gene was detected is described hereinabove with reference to Figs. 6-15.

[39748] VGR2864 gene encodes VGR2864 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39749] VGR2864 precursor RNA folds spatially, forming VGR2864 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2864 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art

as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2864 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39750] VGR2864 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM647 precursor RNA, VGAM648 precursor RNA and VGAM649 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR and VGAM3 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39751] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM647 RNA, VGAM648 RNA and VGAM649 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA and VGAM3 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39752] VGAM647 RNA, herein schematically represented by

VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM647 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM647 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM647 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39753] VGAM648 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM648 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM648 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM648 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39754] VGAM649 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM649 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM649 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM649 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[39755] It is appreciated that a function of VGR2864 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2864 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2864 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2864 gene: VGAM647 host target protein, VGAM648 host target protein and

VGAM649 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM647, VGAM648 and VGAM649

[39756] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2865(VGR2865) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39757] VGR2865 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2865 gene was detected is described hereinabove with reference to Figs. 6-15.

[39758] VGR2865 gene encodes VGR2865 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39759] VGR2865 precursor RNA folds spatially, forming VGR2865 folded precursor RNA, herein designated VGR FOLDED

PRECURSOR RNA. It is appreciated that VGR2865 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2865 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39760] VGR2865 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM652 precursor RNA and VGAM653 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39761] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM652 RNA and VGAM653 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39762] VGAM652 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM652 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby in-

hibiting translation of VGAM652 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM652 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39763] VGAM653 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM653 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM653 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM653 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39764] It is appreciated that a function of VGR2865 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2865 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2865

gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2865 gene: VGAM652 host target protein and VGAM653 host target protein, herein schematically represented by VGAM1 HOST TARGET PRO-TEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated herein-above with reference to VGAM652 and VGAM653

[39765] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2866(VGR2866) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39766] VGR2866 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2866 gene was detected is described hereinabove with reference to Figs. 6-15.

[39767] VGR2866 gene encodes VGR2866 precursor RNA, herein

designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39768] VGR2866 precursor RNA folds spatially, forming VGR2866 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2866 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2866 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39769] VGR2866 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM654 precursor RNA, VGAM655 precursor RNA, VGAM656 precursor RNA and VGAM657 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR and VGAM4 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39770] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM654 RNA, VGAM655 RNA, VGAM656 RNA and VGAM657 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA and VGAM4 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39771] VGAM654 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM654 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM654 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM654 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39772] VGAM655 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM655 host

target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM655 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM655 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39773] VGAM656 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM656 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM656 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM656 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[39774] VGAM657 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding

site located in an untranslated region of VGAM657 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM657 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM657 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[39775] It is appreciated that a function of VGR2866 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2866 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2866 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2866 gene: VGAM654 host target protein, VGAM655 host target protein, VGAM656 host target protein and VGAM657 host target protein, herein schematically represented by VGAM1 HOST TARGET

PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM654, VGAM655, VGAM656 and VGAM657

[39776] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2867(VGR2867) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39777] VGR2867 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2867 gene was detected is described hereinabove with reference to Figs. 6-15.

[39778] VGR2867 gene encodes VGR2867 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39779] VGR2867 precursor RNA folds spatially, forming VGR2867 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2867 folded

precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2867 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39780] VGR2867 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM658 precursor RNA, VGAM659 precursor RNA and VGAM660 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR and VGAM3 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39781] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM658 RNA, VGAM659 RNA and VGAM660 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA and VGAM3 RNA respectively, each of which VGAM

RNAs corresponding to VGAM RNA of Fig. 8.

[39782] VGAM658 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM658 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM658 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM658 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39783] VGAM659 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM659 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM659 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM659 host target protein, herein schematically

represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39784] VGAM660 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM660 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM660 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM660 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[39785] It is appreciated that a function of VGR2867 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2867 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2867 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in

the operon-like cluster of VGR2867 gene: VGAM658 host target protein, VGAM659 host target protein and VGAM660 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM658, VGAM659 and VGAM660

[39786] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2868(VGR2868) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39787] VGR2868 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2868 gene was detected is described hereinabove with reference to Figs. 6-15.

[39788] VGR2868 gene encodes VGR2868 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39789] VGR2868 precursor RNA folds spatially, forming VGR2868 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2868 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2868 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39790] VGR2868 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM663 precursor RNA, VGAM664 precursor RNA and VGAM665 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR and VGAM3 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39791] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM663

RNA, VGAM664 RNA and VGAM665 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA and VGAM3 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39792] VGAM663 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM663 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM663 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM663 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39793] VGAM664 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM664 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby in-

hibiting translation of VGAM664 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM664 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39794] VGAM665 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM665 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM665 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM665 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[39795] It is appreciated that a function of VGR2868 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2868 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2868

gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2868 gene: VGAM663 host target protein, VGAM664 host target protein and VGAM665 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM663, VGAM664 and VGAM665

[39796] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2869(VGR2869) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39797] VGR2869 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2869 gene was detected is described hereinabove with reference to Figs. 6-15.

[39798] VGR2869 gene encodes VGR2869 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39799] VGR2869 precursor RNA folds spatially, forming VGR2869 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2869 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2869 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39800] VGR2869 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM671 precursor RNA and VGAM672 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39801] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM671 RNA and VGAM672 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39802] VGAM671 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM671 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM671 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM671 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39803] VGAM672 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM672 host target RNA, herein schematically represented by VGAM2

HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM672 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM672 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39804] It is appreciated that a function of VGR2869 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2869 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2869 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2869 gene: VGAM671 host target protein and VGAM672 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM671 and VGAM672

[39805] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2870(VGR2870) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39806] VGR2870 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2870 gene was detected is described hereinabove with reference to Figs. 6-15.

[39807] VGR2870 gene encodes VGR2870 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39808] VGR2870 precursor RNA folds spatially, forming VGR2870 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2870 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2870 precur-

sor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39809] VGR2870 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM673 precursor RNA, VGAM674 precursor RNA, VGAM675 precursor RNA, VGAM676 precursor RNA, VGAM677 precursor RNA, VGAM678 precursor RNA, VGAM679 precursor RNA and VGAM680 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR, VGAM5 PRECURSOR, VGAM6 PRECURSOR, VGAM7 PRECURSOR and VGAM8 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39810] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM673 RNA, VGAM674 RNA, VGAM675 RNA, VGAM676 RNA, VGAM677 RNA, VGAM678 RNA, VGAM679 RNA and

VGAM680 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA, VGAM5 RNA, VGAM6 RNA, VGAM7 RNA and VGAM8 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39811] VGAM673 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM673 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM673 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM673 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39812] VGAM674 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM674 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM674 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM674 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39813] VGAM675 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM675 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM675 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM675 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[39814] VGAM676 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM676 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corre-

sponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM676 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM676 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[39815] VGAM677 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM677 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM677 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM677 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[39816] VGAM678 RNA, herein schematically represented by VGAM6 binds complimentarily to a host target binding site located in an untranslated region of VGAM678 host target RNA, herein schematically represented by VGAM6

HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM678 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA into VGAM678 host target protein, herein schematically represented by VGAM6 HOST TARGET PROTEIN, both of Fig. 1.

[39817] VGAM679 RNA, herein schematically represented by VGAM7 binds complimentarily to a host target binding site located in an untranslated region of VGAM679 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM679 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA into VGAM679 host target protein, herein schematically represented by VGAM7 HOST TARGET PROTEIN, both of Fig. 1.

[39818] VGAM680 RNA, herein schematically represented by VGAM8 binds complimentarily to a host target binding site located in an untranslated region of VGAM680 host

target RNA, herein schematically represented by VGAM8 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM680 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA into VGAM680 host target protein, herein schematically represented by VGAM8 HOST TARGET PROTEIN, both of Fig. 1.

[39819] It is appreciated that a function of VGR2870 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2870 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2870 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2870 gene: VGAM673 host target protein, VGAM674 host target protein, VGAM675 host target protein, VGAM676 host target protein, VGAM677 host target protein, VGAM678 host target protein, VGAM679 host target protein and VGAM680 host

target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM673, VGAM674, VGAM675, VGAM676, VGAM677, VGAM678, VGAM679 and VGAM680

[39820] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2871(VGR2871) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39821] VGR2871 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2871 gene was detected is described hereinabove with reference to Figs. 6-15.

[39822] VGR2871 gene encodes VGR2871 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39823] VGR2871 precursor RNA folds spatially, forming VGR2871

folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2871 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2871 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39824] VGR2871 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM681 precursor RNA, VGAM682 precursor RNA, VGAM683 precursor RNA, VGAM684 precursor RNA, VGAM685 precursor RNA, VGAM686 precursor RNA, VGAM687 precursor RNA and VGAM688 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR, VGAM5 PRECURSOR, VGAM6 PRECURSOR, VGAM7 PRECURSOR and VGAM8 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECUR-

SOR RNA of Fig. 8.

[39825] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM681 RNA, VGAM682 RNA, VGAM683 RNA, VGAM684 RNA, VGAM685 RNA, VGAM686 RNA, VGAM687 RNA and VGAM688 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA, VGAM5 RNA, VGAM6 RNA, VGAM7 RNA and VGAM8 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39826] VGAM681 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM681 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM681 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM681 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39827] VGAM682 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM682 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM682 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM682 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39828] VGAM683 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM683 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM683 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM683 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of

Fig. 1.

[39829] VGAM684 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM684 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM684 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM684 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[39830] VGAM685 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM685 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM685 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM685 host target protein, herein schematically

represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[39831] VGAM686 RNA, herein schematically represented by VGAM6 binds complimentarily to a host target binding site located in an untranslated region of VGAM686 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM686 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA into VGAM686 host target protein, herein schematically represented by VGAM6 HOST TARGET PROTEIN, both of Fig. 1.

[39832] VGAM687 RNA, herein schematically represented by VGAM7 binds complimentarily to a host target binding site located in an untranslated region of VGAM687 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM687 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA

into VGAM687 host target protein, herein schematically represented by VGAM7 HOST TARGET PROTEIN, both of Fig. 1.

[39833] VGAM688 RNA, herein schematically represented by VGAM8 binds complimentarily to a host target binding site located in an untranslated region of VGAM688 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM688 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA into VGAM688 host target protein, herein schematically represented by VGAM8 HOST TARGET PROTEIN, both of Fig. 1.

[39834] It is appreciated that a function of VGR2871 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2871 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2871 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target

genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2871 gene: VGAM681 host target protein, VGAM682 host target protein, VGAM683 host target protein, VGAM684 host target protein, VGAM685 host target protein, VGAM686 host target protein, VGAM687 host target protein and VGAM688 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM681, VGAM682, VGAM683, VGAM684, VGAM685, VGAM686, VGAM687 and VGAM688

[39835] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2872(VGR2872) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39836] VGR2872 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2872 gene was

detected is described hereinabove with reference to Figs. 6-15.

[39837] VGR2872 gene encodes VGR2872 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39838] VGR2872 precursor RNA folds spatially, forming VGR2872 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2872 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2872 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39839] VGR2872 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM689 precursor RNA, VGAM690 precursor RNA, VGAM691 precursor RNA, VGAM692 precursor RNA, VGAM693 precursor RNA, VGAM694 precursor RNA, VGAM695 precursor RNA and VGAM696 precursor RNA,

herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR, VGAM5 PRECURSOR, VGAM6 PRECURSOR, VGAM7 PRECURSOR and VGAM8 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39840] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM689 RNA, VGAM690 RNA, VGAM691 RNA, VGAM692 RNA, VGAM693 RNA, VGAM694 RNA, VGAM695 RNA and VGAM696 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA, VGAM5 RNA, VGAM6 RNA, VGAM7 RNA and VGAM8 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39841] VGAM689 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM689 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM689 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM689 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39842] VGAM690 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM690 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM690 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM690 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39843] VGAM691 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM691 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corre-

sponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM691 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM691 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[39844] VGAM692 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM692 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM692 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM692 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[39845] VGAM693 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM693 host target RNA, herein schematically represented by VGAM5

HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM693 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM693 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[39846] VGAM694 RNA, herein schematically represented by VGAM6 binds complimentarily to a host target binding site located in an untranslated region of VGAM694 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM694 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA into VGAM694 host target protein, herein schematically represented by VGAM6 HOST TARGET PROTEIN, both of Fig. 1.

[39847] VGAM695 RNA, herein schematically represented by VGAM7 binds complimentarily to a host target binding site located in an untranslated region of VGAM695 host

target RNA, herein schematically represented by VGAM7 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM695 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA into VGAM695 host target protein, herein schematically represented by VGAM7 HOST TARGET PROTEIN, both of Fig. 1.

[39848] VGAM696 RNA, herein schematically represented by VGAM8 binds complimentarily to a host target binding site located in an untranslated region of VGAM696 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM696 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA into VGAM696 host target protein, herein schematically represented by VGAM8 HOST TARGET PROTEIN, both of Fig. 1.

[39849] It is appreciated that a function of VGR2872 gene, herein designated VGR GENE, is inhibition of expression of host

target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2872 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2872 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2872 gene: VGAM689 host target protein, VGAM690 host target protein, VGAM691 host target protein, VGAM692 host target protein, VGAM693 host target protein, VGAM694 host target protein, VGAM695 host target protein and VGAM696 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM689, VGAM690, VGAM691, VGAM692, VGAM693, VGAM694, VGAM695 and VGAM696

[39850] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2873(VGR2873) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates

expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39851] VGR2873 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2873 gene was detected is described hereinabove with reference to Figs. 6-15.

[39852] VGR2873 gene encodes VGR2873 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39853] VGR2873 precursor RNA folds spatially, forming VGR2873 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2873 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2873 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39854] VGR2873 folded precursor RNA, herein designated VGR

FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM697 precursor RNA, VGAM698 precursor RNA, VGAM699 precursor RNA and VGAM700 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR and VGAM4 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39855] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM697 RNA, VGAM698 RNA, VGAM699 RNA and VGAM700 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA and VGAM4 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39856] VGAM697 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM697 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM697 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM697 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39857] VGAM698 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM698 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM698 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM698 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39858] VGAM699 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM699 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corre-

sponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM699 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM699 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[39859] VGAM700 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM700 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM700 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM700 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[39860] It is appreciated that a function of VGR2873 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2873 gene include

diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2873 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2873 gene: VGAM697 host target protein, VGAM698 host target protein, VGAM699 host target protein and VGAM700 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM697, VGAM698, VGAM699 and VGAM700

[39861] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2874(VGR2874) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39862] VGR2874 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding,

RNA viral gene. The method by which VGR2874 gene was detected is described hereinabove with reference to Figs. 6-15.

[39863] VGR2874 gene encodes VGR2874 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39864] VGR2874 precursor RNA folds spatially, forming VGR2874 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2874 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2874 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39865] VGR2874 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 6 separate VGAM precursor RNAs, VGAM701 precursor RNA, VGAM702 precursor RNA, VGAM703 precursor RNA, VGAM704 precursor RNA, VGAM705 precursor RNA and VGAM706 precursor

RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR, VGAM5 PRECURSOR and VGAM6 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39866] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM701 RNA, VGAM702 RNA, VGAM703 RNA, VGAM704 RNA, VGAM705 RNA and VGAM706 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA, VGAM5 RNA and VGAM6 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39867] VGAM701 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM701 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM701 host target RNA, herein

schematically represented by VGAM1 HOST TARGET RNA into VGAM701 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39868] VGAM702 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM702 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM702 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM702 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39869] VGAM703 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM703 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby in-

hibiting translation of VGAM703 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM703 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[39870] VGAM704 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM704 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM704 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM704 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[39871] VGAM705 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM705 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM705 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM705 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[39872] VGAM706 RNA, herein schematically represented by VGAM6 binds complimentarily to a host target binding site located in an untranslated region of VGAM706 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM706 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA into VGAM706 host target protein, herein schematically represented by VGAM6 HOST TARGET PROTEIN, both of Fig. 1.

[39873] It is appreciated that a function of VGR2874 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2874 gene include diagnosis, prevention and treatment of viral infection by .

Specific functions, and accordingly utilities, of VGR2874 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2874 gene: VGAM701 host target protein, VGAM702 host target protein, VGAM703 host target protein, VGAM704 host target protein, VGAM705 host target protein and VGAM706 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM701, VGAM702, VGAM703, VGAM704, VGAM705 and VGAM706

[39874] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2875(VGR2875) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39875] VGR2875 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding,

RNA viral gene. The method by which VGR2875 gene was detected is described hereinabove with reference to Figs. 6-15.

[39876] VGR2875 gene encodes VGR2875 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39877] VGR2875 precursor RNA folds spatially, forming VGR2875 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2875 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2875 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39878] VGR2875 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM710 precursor RNA, VGAM711 precursor RNA and VGAM712 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECUR-

SOR and VGAM3 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39879] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM710 RNA, VGAM711 RNA and VGAM712 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA and VGAM3 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39880] VGAM710 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM710 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM710 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM710 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39881] VGAM711 RNA, herein schematically represented by

VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM711 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM711 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM711 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39882] VGAM712 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM712 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM712 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM712 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[39883] It is appreciated that a function of VGR2875 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2875 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2875 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2875 gene: VGAM710 host target protein, VGAM711 host target protein and VGAM712 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM710, VGAM711 and VGAM712

[39884] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2876(VGR2876) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known

in the art.

[39885] VGR2876 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2876 gene was detected is described hereinabove with reference to Figs. 6-15.

[39886] VGR2876 gene encodes VGR2876 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39887] VGR2876 precursor RNA folds spatially, forming VGR2876 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2876 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2876 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39888] VGR2876 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM pre-

cursor RNAs, VGAM713 precursor RNA and VGAM714 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39889] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM713 RNA and VGAM714 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39890] VGAM713 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM713 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM713 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM713 host target protein, herein schematically

represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39891] VGAM714 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM714 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM714 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM714 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39892] It is appreciated that a function of VGR2876 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2876 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2876 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in

the operon-like cluster of VGR2876 gene: VGAM713 host target protein and VGAM714 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM713 and VGAM714

[39893] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2877(VGR2877) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39894] VGR2877 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2877 gene was detected is described hereinabove with reference to Figs. 6-15.

[39895] VGR2877 gene encodes VGR2877 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39896] VGR2877 precursor RNA folds spatially, forming VGR2877

folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2877 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2877 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39897] VGR2877 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM715 precursor RNA, VGAM716 precursor RNA, VGAM717 precursor RNA and VGAM718 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR and VGAM4 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39898] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM715

RNA, VGAM716 RNA, VGAM717 RNA and VGAM718 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA and VGAM4 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39899] VGAM715 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM715 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM715 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM715 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39900] VGAM716 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM716 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM716 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM716 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39901] VGAM717 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM717 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM717 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM717 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[39902] VGAM718 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM718 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corre-

sponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM718 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM718 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[39903] It is appreciated that a function of VGR2877 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2877 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2877 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2877 gene: VGAM715 host target protein, VGAM716 host target protein, VGAM717 host target protein and VGAM718 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM715, VGAM716,

VGAM717 and VGAM718

[39904] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2878(VGR2878) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39905] VGR2878 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2878 gene was detected is described hereinabove with reference to Figs. 6-15.

[39906] VGR2878 gene encodes VGR2878 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39907] VGR2878 precursor RNA folds spatially, forming VGR2878 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2878 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to

the fact that the nucleotide sequence of VGR2878 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39908] VGR2878 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM719 precursor RNA and VGAM720 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39909] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM719 RNA and VGAM720 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39910] VGAM719 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding

site located in an untranslated region of VGAM719 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM719 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM719 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39911] VGAM720 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM720 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM720 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM720 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39912] It is appreciated that a function of VGR2878 gene, herein

designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2878 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2878 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2878 gene: VGAM719 host target protein and VGAM720 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated herein-above with reference to VGAM719 and VGAM720

[39913] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2879(VGR2879) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39914] VGR2879 gene, herein designated VGR GENE, is a novel

bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2879 gene was detected is described hereinabove with reference to Figs. 6-15.

[39915] VGR2879 gene encodes VGR2879 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39916] VGR2879 precursor RNA folds spatially, forming VGR2879 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2879 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2879 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39917] VGR2879 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM721 precursor RNA, VGAM722 precursor RNA, VGAM723 precursor RNA, VGAM724 precursor

RNA and VGAM725 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR and VGAM5 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39918] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM721 RNA, VGAM722 RNA, VGAM723 RNA, VGAM724 RNA and VGAM725 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA and VGAM5 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39919] VGAM721 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM721 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM721 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA

into VGAM721 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39920] VGAM722 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM722 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM722 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM722 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39921] VGAM723 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM723 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM723 host target RNA, herein

schematically represented by VGAM3 HOST TARGET RNA into VGAM723 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[39922] VGAM724 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM724 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM724 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM724 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[39923] VGAM725 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM725 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby in-

hibiting translation of VGAM725 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM725 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[39924] It is appreciated that a function of VGR2879 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2879 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2879 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2879 gene: VGAM721 host target protein, VGAM722 host target protein, VGAM723 host target protein, VGAM724 host target protein and VGAM725 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM721, VGAM722, VGAM723, VGAM724 and VGAM725

[39925] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2880(VGR2880) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39926] VGR2880 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2880 gene was detected is described hereinabove with reference to Figs. 6-15.

[39927] VGR2880 gene encodes VGR2880 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39928] VGR2880 precursor RNA folds spatially, forming VGR2880 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2880 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2880 precur-

sor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39929] VGR2880 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM727 precursor RNA and VGAM728 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39930] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM727 RNA and VGAM728 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39931] VGAM727 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM727 host

target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM727 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM727 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39932] VGAM728 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM728 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM728 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM728 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39933] It is appreciated that a function of VGR2880 gene, herein designated VGR GENE, is inhibition of expression of host

target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2880 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2880 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2880 gene: VGAM727 host target protein and VGAM728 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM727 and VGAM728

[39934] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2881(VGR2881) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39935] VGR2881 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding,

RNA viral gene. The method by which VGR2881 gene was detected is described hereinabove with reference to Figs. 6-15.

[39936] VGR2881 gene encodes VGR2881 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39937] VGR2881 precursor RNA folds spatially, forming VGR2881 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2881 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2881 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39938] VGR2881 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM729 precursor RNA, VGAM730 precursor RNA, VGAM731 precursor RNA and VGAM732 precursor RNA, herein schematically represented by VGAM1 PRE-

CURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR and VGAM4 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39939] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM729 RNA, VGAM730 RNA, VGAM731 RNA and VGAM732 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA and VGAM4 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39940] VGAM729 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM729 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM729 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM729 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of

Fig. 1.

[39941] VGAM730 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM730 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM730 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM730 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39942] VGAM731 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM731 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM731 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM731 host target protein, herein schematically

represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[39943] VGAM732 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM732 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM732 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM732 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[39944] It is appreciated that a function of VGR2881 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2881 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2881 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in

the operon-like cluster of VGR2881 gene: VGAM729 host target protein, VGAM730 host target protein, VGAM731 host target protein and VGAM732 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM729, VGAM730, VGAM731 and VGAM732

[39945] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2882(VGR2882) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39946] VGR2882 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2882 gene was detected is described hereinabove with reference to Figs. 6-15.

[39947] VGR2882 gene encodes VGR2882 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typi-

cally several hundred nucleotides long.

[39948] VGR2882 precursor RNA folds spatially, forming VGR2882 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2882 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2882 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39949] VGR2882 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 6 separate VGAM precursor RNAs, VGAM733 precursor RNA, VGAM734 precursor RNA, VGAM735 precursor RNA, VGAM736 precursor RNA, VGAM737 precursor RNA and VGAM738 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR, VGAM5 PRECURSOR and VGAM6 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to

VGAM PRECURSOR RNA of Fig. 8.

[39950] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM733 RNA, VGAM734 RNA, VGAM735 RNA, VGAM736 RNA, VGAM737 RNA and VGAM738 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA, VGAM5 RNA and VGAM6 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39951] VGAM733 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM733 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM733 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM733 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39952] VGAM734 RNA, herein schematically represented by

VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM734 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM734 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM734 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39953] VGAM735 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM735 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM735 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM735 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[39954] VGAM736 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM736 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM736 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM736 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[39955] VGAM737 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM737 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM737 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM737 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of

Fig. 1.

[39956] VGAM738 RNA, herein schematically represented by VGAM6 binds complimentarily to a host target binding site located in an untranslated region of VGAM738 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM738 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA into VGAM738 host target protein, herein schematically represented by VGAM6 HOST TARGET PROTEIN, both of Fig. 1.

[39957] It is appreciated that a function of VGR2882 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2882 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2882 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2882 gene: VGAM733 host

target protein, VGAM734 host target protein, VGAM735 host target protein, VGAM736 host target protein, VGAM737 host target protein and VGAM738 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM733, VGAM734, VGAM735, VGAM736, VGAM737 and VGAM738

[39958] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2883(VGR2883) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39959] VGR2883 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2883 gene was detected is described hereinabove with reference to Figs. 6-15.

[39960] VGR2883 gene encodes VGR2883 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typi-

cally several hundred nucleotides long.

[39961] VGR2883 precursor RNA folds spatially, forming VGR2883 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2883 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2883 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39962] VGR2883 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM739 precursor RNA, VGAM740 precursor RNA, VGAM741 precursor RNA and VGAM742 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR and VGAM4 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39963] The above mentioned VGAM precursor RNAs are diced by

DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM739 RNA, VGAM740 RNA, VGAM741 RNA and VGAM742 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA and VGAM4 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39964] VGAM739 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM739 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM739 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM739 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39965] VGAM740 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM740 host target RNA, herein schematically represented by VGAM2

HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM740 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM740 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39966] VGAM741 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM741 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM741 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM741 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[39967] VGAM742 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM742 host

target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM742 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM742 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[39968] It is appreciated that a function of VGR2883 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2883 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2883 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2883 gene: VGAM739 host target protein, VGAM740 host target protein, VGAM741 host target protein and VGAM742 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respec-

tively. The function of these host target genes is elaborated hereinabove with reference to VGAM739, VGAM740, VGAM741 and VGAM742

[39969] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2884(VGR2884) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39970] VGR2884 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2884 gene was detected is described hereinabove with reference to Figs. 6-15.

[39971] VGR2884 gene encodes VGR2884 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39972] VGR2884 precursor RNA folds spatially, forming VGR2884 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2884 folded precursor RNA, herein designated VGR FOLDED PRECUR-

SOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2884 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39973] VGR2884 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM744 precursor RNA, VGAM745 precursor RNA, VGAM746 precursor RNA, VGAM747 precursor RNA, VGAM748 precursor RNA, VGAM749 precursor RNA, VGAM750 precursor RNA and VGAM751 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR, VGAM5 PRECURSOR, VGAM6 PRECURSOR, VGAM7 PRECURSOR and VGAM8 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39974] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA

segments of about 22 nucleotides in length, VGAM744 RNA, VGAM745 RNA, VGAM746 RNA, VGAM747 RNA, VGAM748 RNA, VGAM749 RNA, VGAM750 RNA and VGAM751 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA, VGAM5 RNA, VGAM6 RNA, VGAM7 RNA and VGAM8 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39975] VGAM744 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM744 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM744 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM744 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39976] VGAM745 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM745 host

target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM745 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM745 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39977] VGAM746 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM746 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM746 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM746 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[39978] VGAM747 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding

site located in an untranslated region of VGAM747 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM747 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM747 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[39979] VGAM748 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM748 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM748 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM748 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[39980] VGAM749 RNA, herein schematically represented by

VGAM6 binds complimentarily to a host target binding site located in an untranslated region of VGAM749 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM749 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA into VGAM749 host target protein, herein schematically represented by VGAM6 HOST TARGET PROTEIN, both of Fig. 1.

[39981] VGAM750 RNA, herein schematically represented by VGAM7 binds complimentarily to a host target binding site located in an untranslated region of VGAM750 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM750 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA into VGAM750 host target protein, herein schematically represented by VGAM7 HOST TARGET PROTEIN, both of Fig. 1.

[39982] VGAM751 RNA, herein schematically represented by VGAM8 binds complimentarily to a host target binding site located in an untranslated region of VGAM751 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM751 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA into VGAM751 host target protein, herein schematically represented by VGAM8 HOST TARGET PROTEIN, both of Fig. 1.

[39983] It is appreciated that a function of VGR2884 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2884 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2884 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2884 gene: VGAM744 host target protein, VGAM745 host target protein, VGAM746

host target protein, VGAM747 host target protein, VGAM748 host target protein, VGAM749 host target protein, VGAM750 host target protein and VGAM751 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM744, VGAM745, VGAM746, VGAM747, VGAM748, VGAM749, VGAM750 and VGAM751

[39984] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2885(VGR2885) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[39985] VGR2885 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2885 gene was detected is described hereinabove with reference to Figs. 6-15.

[39986] VGR2885 gene encodes VGR2885 precursor RNA, herein

designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39987] VGR2885 precursor RNA folds spatially, forming VGR2885 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2885 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2885 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39988] VGR2885 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM752 precursor RNA, VGAM753 precursor RNA, VGAM754 precursor RNA, VGAM755 precursor RNA, VGAM756 precursor RNA, VGAM757 precursor RNA, VGAM758 precursor RNA and VGAM759 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR, VGAM5 PRECURSOR, VGAM6 PRECURSOR,

VGAM7 PRECURSOR and VGAM8 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[39989] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM752 RNA, VGAM753 RNA, VGAM754 RNA, VGAM755 RNA, VGAM756 RNA, VGAM757 RNA, VGAM758 RNA and VGAM759 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA, VGAM5 RNA, VGAM6 RNA, VGAM7 RNA and VGAM8 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[39990] VGAM752 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM752 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM752 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA

into VGAM752 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[39991] VGAM753 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM753 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM753 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM753 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[39992] VGAM754 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM754 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM754 host target RNA, herein

schematically represented by VGAM3 HOST TARGET RNA into VGAM754 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[39993] VGAM755 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM755 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM755 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM755 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[39994] VGAM756 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM756 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby in-

hibiting translation of VGAM756 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM756 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[39995] VGAM757 RNA, herein schematically represented by VGAM6 binds complimentarily to a host target binding site located in an untranslated region of VGAM757 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM757 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA into VGAM757 host target protein, herein schematically represented by VGAM6 HOST TARGET PROTEIN, both of Fig. 1.

[39996] VGAM758 RNA, herein schematically represented by VGAM7 binds complimentarily to a host target binding site located in an untranslated region of VGAM758 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM758 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA into VGAM758 host target protein, herein schematically represented by VGAM7 HOST TARGET PROTEIN, both of Fig. 1.

[39997] VGAM759 RNA, herein schematically represented by VGAM8 binds complimentarily to a host target binding site located in an untranslated region of VGAM759 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM759 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA into VGAM759 host target protein, herein schematically represented by VGAM8 HOST TARGET PROTEIN, both of Fig. 1.

[39998] It is appreciated that a function of VGR2885 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2885 gene include diagnosis, prevention and treatment of viral infection by .

Specific functions, and accordingly utilities, of VGR2885 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2885 gene: VGAM752 host target protein, VGAM753 host target protein, VGAM754 host target protein, VGAM755 host target protein, VGAM756 host target protein, VGAM757 host target protein, VGAM758 host target protein and VGAM759 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM752, VGAM753, VGAM754, VGAM755, VGAM756, VGAM757, VGAM758 and VGAM759

[39999] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2886(VGR2886) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40000] VGR2886 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2886 gene was detected is described hereinabove with reference to Figs. 6-15.

[40001] VGR2886 gene encodes VGR2886 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40002] VGR2886 precursor RNA folds spatially, forming VGR2886 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2886 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2886 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40003] VGR2886 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM760 precursor RNA, VGAM761 precur-

sor RNA, VGAM762 precursor RNA, VGAM763 precursor RNA, VGAM764 precursor RNA, VGAM765 precursor RNA, VGAM766 precursor RNA and VGAM767 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR, VGAM5 PRECURSOR, VGAM6 PRECURSOR, VGAM7 PRECURSOR and VGAM8 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40004] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM760 RNA, VGAM761 RNA, VGAM762 RNA, VGAM763 RNA, VGAM764 RNA, VGAM765 RNA, VGAM766 RNA and VGAM767 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA, VGAM5 RNA, VGAM6 RNA, VGAM7 RNA and VGAM8 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40005] VGAM760 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM760 host

target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM760 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM760 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40006] VGAM761 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM761 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM761 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM761 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40007] VGAM762 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding

site located in an untranslated region of VGAM762 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM762 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM762 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[40008] VGAM763 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM763 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM763 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM763 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[40009] VGAM764 RNA, herein schematically represented by

VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM764 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM764 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM764 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[40010] VGAM765 RNA, herein schematically represented by VGAM6 binds complimentarily to a host target binding site located in an untranslated region of VGAM765 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM765 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA into VGAM765 host target protein, herein schematically represented by VGAM6 HOST TARGET PROTEIN, both of Fig. 1.

[40011] VGAM766 RNA, herein schematically represented by VGAM7 binds complimentarily to a host target binding site located in an untranslated region of VGAM766 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM766 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA into VGAM766 host target protein, herein schematically represented by VGAM7 HOST TARGET PROTEIN, both of Fig. 1.

[40012] VGAM767 RNA, herein schematically represented by VGAM8 binds complimentarily to a host target binding site located in an untranslated region of VGAM767 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM767 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA into VGAM767 host target protein, herein schematically represented by VGAM8 HOST TARGET PROTEIN, both of

Fig. 1.

[40013] It is appreciated that a function of VGR2886 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2886 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2886 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2886 gene: VGAM760 host target protein, VGAM761 host target protein, VGAM762 host target protein, VGAM763 host target protein, VGAM764 host target protein, VGAM765 host target protein, VGAM766 host target protein and VGAM767 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM760, VGAM761, VGAM762, VGAM763, VGAM764, VGAM765, VGAM766 and VGAM767

[40014] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred

to here as Viral Genomic Record 2887(VGR2887) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40015] VGR2887 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2887 gene was detected is described hereinabove with reference to Figs. 6-15.

[40016] VGR2887 gene encodes VGR2887 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40017] VGR2887 precursor RNA folds spatially, forming VGR2887 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2887 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2887 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which

is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40018] VGR2887 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM768 precursor RNA and VGAM769 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40019] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM768 RNA and VGAM769 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40020] VGAM768 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM768 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corre-

sponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM768 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM768 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40021] VGAM769 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM769 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM769 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM769 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40022] It is appreciated that a function of VGR2887 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2887 gene include

diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2887 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2887 gene: VGAM768 host target protein and VGAM769 host target protein, herein schematically represented by VGAM1 HOST TARGET PRO-TEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated herein-above with reference to VGAM768 and VGAM769

[40023] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2888(VGR2888) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40024] VGR2888 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2888 gene was detected is described hereinabove with reference to Figs.

6-15.

[40025] VGR2888 gene encodes VGR2888 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40026] VGR2888 precursor RNA folds spatially, forming VGR2888 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2888 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2888 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40027] VGR2888 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM771 precursor RNA, VGAM772 precursor RNA, VGAM773 precursor RNA, VGAM774 precursor RNA and VGAM775 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR and VGAM5 PRE-

CURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40028] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM771 RNA, VGAM772 RNA, VGAM773 RNA, VGAM774 RNA and VGAM775 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA and VGAM5 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40029] VGAM771 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM771 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM771 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM771 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40030] VGAM772 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM772 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM772 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM772 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40031] VGAM773 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM773 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM773 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM773 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of

Fig. 1.

[40032] VGAM774 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM774 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM774 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM774 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[40033] VGAM775 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM775 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM775 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM775 host target protein, herein schematically

represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[40034] It is appreciated that a function of VGR2888 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2888 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2888 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2888 gene: VGAM771 host target protein, VGAM772 host target protein, VGAM773 host target protein, VGAM774 host target protein and VGAM775 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM771, VGAM772, VGAM773, VGAM774 and VGAM775

[40035] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2889(VGR2889) viral

gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40036] VGR2889 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2889 gene was detected is described hereinabove with reference to Figs. 6-15.

[40037] VGR2889 gene encodes VGR2889 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40038] VGR2889 precursor RNA folds spatially, forming VGR2889 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2889 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2889 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the

second half thereof, as is well known in the art.

[40039] VGR2889 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM781 precursor RNA, VGAM782 precursor RNA, VGAM783 precursor RNA and VGAM784 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR and VGAM4 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40040] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM781 RNA, VGAM782 RNA, VGAM783 RNA and VGAM784 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA and VGAM4 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40041] VGAM781 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM781 host target RNA, herein schematically represented by VGAM1

HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM781 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM781 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40042] VGAM782 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM782 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM782 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM782 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40043] VGAM783 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM783 host

target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM783 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM783 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[40044] VGAM784 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM784 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM784 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM784 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[40045] It is appreciated that a function of VGR2889 gene, herein designated VGR GENE, is inhibition of expression of host

target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2889 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2889 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2889 gene: VGAM781 host target protein, VGAM782 host target protein, VGAM783 host target protein and VGAM784 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM781, VGAM782, VGAM783 and VGAM784

[40046] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2890(VGR2890) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40047] VGR2890 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2890 gene was detected is described hereinabove with reference to Figs. 6-15.

[40048] VGR2890 gene encodes VGR2890 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40049] VGR2890 precursor RNA folds spatially, forming VGR2890 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2890 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2890 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40050] VGR2890 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM785 precursor RNA, VGAM786 precur-

sor RNA, VGAM787 precursor RNA and VGAM788 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR and VGAM4 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40051] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM785 RNA, VGAM786 RNA, VGAM787 RNA and VGAM788 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA and VGAM4 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40052] VGAM785 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM785 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM785 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA

into VGAM785 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40053] VGAM786 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM786 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM786 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM786 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40054] VGAM787 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM787 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM787 host target RNA, herein

schematically represented by VGAM3 HOST TARGET RNA into VGAM787 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[40055] VGAM788 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM788 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM788 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM788 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[40056] It is appreciated that a function of VGR2890 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2890 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2890 gene, herein designated VGR GENE, correlate with, and

may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2890 gene: VGAM785 host target protein, VGAM786 host target protein, VGAM787 host target protein and VGAM788 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM785, VGAM786, VGAM787 and VGAM788

[40057] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2891(VGR2891) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40058] VGR2891 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2891 gene was detected is described hereinabove with reference to Figs. 6-15.

[40059] VGR2891 gene encodes VGR2891 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40060] VGR2891 precursor RNA folds spatially, forming VGR2891 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2891 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2891 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40061] VGR2891 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM789 precursor RNA, VGAM790 precursor RNA and VGAM791 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR and VGAM3 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40062] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM789 RNA, VGAM790 RNA and VGAM791 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA and VGAM3 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40063] VGAM789 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM789 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM789 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM789 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40064] VGAM790 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM790 host target RNA, herein schematically represented by VGAM2

HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM790 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM790 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40065] VGAM791 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM791 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM791 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM791 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[40066] It is appreciated that a function of VGR2891 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attack-

ing a host. Accordingly, utilities of VGR2891 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2891 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2891 gene: VGAM789 host target protein, VGAM790 host target protein and VGAM791 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM789, VGAM790 and VGAM791

[40067] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2892(VGR2892) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40068] VGR2892 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding,

RNA viral gene. The method by which VGR2892 gene was detected is described hereinabove with reference to Figs. 6-15.

[40069] VGR2892 gene encodes VGR2892 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40070] VGR2892 precursor RNA folds spatially, forming VGR2892 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2892 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2892 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40071] VGR2892 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM792 precursor RNA and VGAM793 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of

which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40072] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM792 RNA and VGAM793 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40073] VGAM792 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM792 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM792 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM792 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40074] VGAM793 RNA, herein schematically represented by

VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM793 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM793 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM793 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40075] It is appreciated that a function of VGR2892 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2892 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2892 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2892 gene: VGAM792 host target protein and VGAM793 host target protein, herein schematically represented by VGAM1 HOST TARGET PRO-

TEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated herein-above with reference to VGAM792 and VGAM793

[40076] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2893(VGR2893) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40077] VGR2893 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2893 gene was detected is described hereinabove with reference to Figs. 6-15.

[40078] VGR2893 gene encodes VGR2893 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typi-cally several hundred nucleotides long.

[40079] VGR2893 precursor RNA folds spatially, forming VGR2893 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2893 folded precursor RNA, herein designated VGR FOLDED PRECUR-

SOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2893 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40080] VGR2893 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM795 precursor RNA and VGAM796 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40081] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM795 RNA and VGAM796 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40082] VGAM795 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM795 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM795 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM795 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40083] VGAM796 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM796 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM796 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM796 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of

Fig. 1.

[40084] It is appreciated that a function of VGR2893 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2893 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2893 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2893 gene: VGAM795 host target protein and VGAM796 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM795 and VGAM796

[40085] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2894(VGR2894) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known

in the art.

[40086] VGR2894 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2894 gene was detected is described hereinabove with reference to Figs. 6-15.

[40087] VGR2894 gene encodes VGR2894 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40088] VGR2894 precursor RNA folds spatially, forming VGR2894 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2894 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2894 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40089] VGR2894 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM pre-

cursor RNAs, VGAM797 precursor RNA and VGAM798 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40090] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM797 RNA and VGAM798 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40091] VGAM797 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM797 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM797 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM797 host target protein, herein schematically

represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40092] VGAM798 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM798 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM798 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM798 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40093] It is appreciated that a function of VGR2894 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2894 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2894 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in

the operon-like cluster of VGR2894 gene: VGAM797 host target protein and VGAM798 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM797 and VGAM798

[40094] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2895(VGR2895) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40095] VGR2895 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2895 gene was detected is described hereinabove with reference to Figs. 6-15.

[40096] VGR2895 gene encodes VGR2895 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40097] VGR2895 precursor RNA folds spatially, forming VGR2895

folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2895 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2895 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40098] VGR2895 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM799 precursor RNA and VGAM800 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40099] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM799 RNA and VGAM800 RNA respectively, herein schematically

represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40100] VGAM799 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM799 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM799 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM799 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40101] VGAM800 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM800 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM800 host target RNA, herein

schematically represented by VGAM2 HOST TARGET RNA into VGAM800 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40102] It is appreciated that a function of VGR2895 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2895 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2895 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2895 gene: VGAM799 host target protein and VGAM800 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM799 and VGAM800

[40103] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2896(VGR2896) viral gene, which encodes an operon-like cluster of novel viral

micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40104] VGR2896 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2896 gene was detected is described hereinabove with reference to Figs. 6-15.

[40105] VGR2896 gene encodes VGR2896 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40106] VGR2896 precursor RNA folds spatially, forming VGR2896 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2896 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2896 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40107] VGR2896 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM801 precursor RNA, VGAM802 precursor RNA and VGAM803 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR and VGAM3 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40108] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM801 RNA, VGAM802 RNA and VGAM803 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA and VGAM3 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40109] VGAM801 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM801 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby in-

hibiting translation of VGAM801 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM801 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40110] VGAM802 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM802 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM802 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM802 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40111] VGAM803 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM803 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM803 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM803 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[40112] It is appreciated that a function of VGR2896 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2896 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2896 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2896 gene: VGAM801 host target protein, VGAM802 host target protein and VGAM803 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM801, VGAM802 and VGAM803

[40113] Fig. 9 further provides a conceptual description of novel

bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2897(VGR2897) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40114] VGR2897 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2897 gene was detected is described hereinabove with reference to Figs. 6-15.

[40115] VGR2897 gene encodes VGR2897 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40116] VGR2897 precursor RNA folds spatially, forming VGR2897 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2897 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2897 precursor RNA comprises a plurality of segments, the first half

of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40117] VGR2897 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM807 precursor RNA, VGAM808 precursor RNA and VGAM809 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR and VGAM3 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40118] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM807 RNA, VGAM808 RNA and VGAM809 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA and VGAM3 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40119] VGAM807 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM807 host target RNA, herein schematically represented by VGAM1

HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM807 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM807 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40120] VGAM808 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM808 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM808 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM808 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40121] VGAM809 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM809 host

target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM809 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM809 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[40122] It is appreciated that a function of VGR2897 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2897 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2897 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2897 gene: VGAM807 host target protein, VGAM808 host target protein and VGAM809 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these

host target genes is elaborated hereinabove with reference to VGAM807, VGAM808 and VGAM809

[40123] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2898(VGR2898) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40124] VGR2898 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2898 gene was detected is described hereinabove with reference to Figs. 6-15.

[40125] VGR2898 gene encodes VGR2898 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40126] VGR2898 precursor RNA folds spatially, forming VGR2898 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2898 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art

as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2898 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40127] VGR2898 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM812 precursor RNA, VGAM813 precursor RNA and VGAM814 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR and VGAM3 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40128] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM812 RNA, VGAM813 RNA and VGAM814 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA and VGAM3 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40129] VGAM812 RNA, herein schematically represented by

VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM812 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM812 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM812 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40130] VGAM813 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM813 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM813 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM813 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40131] VGAM814 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM814 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM814 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM814 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[40132] It is appreciated that a function of VGR2898 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2898 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2898 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2898 gene: VGAM812 host target protein, VGAM813 host target protein and

VGAM814 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM812, VGAM813 and VGAM814

[40133] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2899(VGR2899) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40134] VGR2899 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2899 gene was detected is described hereinabove with reference to Figs. 6-15.

[40135] VGR2899 gene encodes VGR2899 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40136] VGR2899 precursor RNA folds spatially, forming VGR2899 folded precursor RNA, herein designated VGR FOLDED

PRECURSOR RNA. It is appreciated that VGR2899 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2899 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40137] VGR2899 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM815 precursor RNA and VGAM816 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40138] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM815 RNA and VGAM816 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively,

each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40139] VGAM815 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM815 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM815 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM815 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40140] VGAM816 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM816 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM816 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA

into VGAM816 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40141] It is appreciated that a function of VGR2899 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2899 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2899 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2899 gene: VGAM815 host target protein and VGAM816 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM815 and VGAM816

[40142] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2900(VGR2900) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates

expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40143] VGR2900 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2900 gene was detected is described hereinabove with reference to Figs. 6-15.

[40144] VGR2900 gene encodes VGR2900 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40145] VGR2900 precursor RNA folds spatially, forming VGR2900 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2900 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2900 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40146] VGR2900 folded precursor RNA, herein designated VGR

FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM821 precursor RNA and VGAM822 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40147] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM821 RNA and VGAM822 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40148] VGAM821 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM821 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM821 host target RNA, herein

schematically represented by VGAM1 HOST TARGET RNA into VGAM821 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40149] VGAM822 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM822 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM822 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM822 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40150] It is appreciated that a function of VGR2900 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2900 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2900 gene, herein designated VGR GENE, correlate with, and

may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2900 gene: VGAM821 host target protein and VGAM822 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM821 and VGAM822

[40151] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2901(VGR2901) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40152] VGR2901 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2901 gene was detected is described hereinabove with reference to Figs. 6-15.

[40153] VGR2901 gene encodes VGR2901 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typi-

cally several hundred nucleotides long.

[40154] VGR2901 precursor RNA folds spatially, forming VGR2901 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2901 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2901 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40155] VGR2901 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM823 precursor RNA and VGAM824 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40156] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA

segments of about 22 nucleotides in length, VGAM823 RNA and VGAM824 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40157] VGAM823 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM823 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM823 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM823 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40158] VGAM824 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM824 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM824 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM824 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40159] It is appreciated that a function of VGR2901 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2901 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2901 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2901 gene: VGAM823 host target protein and VGAM824 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM823 and VGAM824

[40160] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred

to here as Viral Genomic Record 2902(VGR2902) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40161] VGR2902 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2902 gene was detected is described hereinabove with reference to Figs. 6-15.

[40162] VGR2902 gene encodes VGR2902 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40163] VGR2902 precursor RNA folds spatially, forming VGR2902 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2902 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2902 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which

is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40164] VGR2902 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM826 precursor RNA and VGAM827 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40165] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM826 RNA and VGAM827 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40166] VGAM826 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM826 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corre-

sponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM826 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM826 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40167] VGAM827 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM827 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM827 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM827 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40168] It is appreciated that a function of VGR2902 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2902 gene include

diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2902 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2902 gene: VGAM826 host target protein and VGAM827 host target protein, herein schematically represented by VGAM1 HOST TARGET PRO-TEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated herein-above with reference to VGAM826 and VGAM827

[40169] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2903(VGR2903) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40170] VGR2903 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2903 gene was detected is described hereinabove with reference to Figs.

6-15.

[40171] VGR2903 gene encodes VGR2903 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40172] VGR2903 precursor RNA folds spatially, forming VGR2903 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2903 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2903 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40173] VGR2903 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM828 precursor RNA, VGAM829 precursor RNA and VGAM830 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR and VGAM3 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA seg-

ment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40174] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM828 RNA, VGAM829 RNA and VGAM830 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA and VGAM3 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40175] VGAM828 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM828 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM828 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM828 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40176] VGAM829 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM829 host

target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM829 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM829 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40177] VGAM830 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM830 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM830 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM830 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[40178] It is appreciated that a function of VGR2903 gene, herein designated VGR GENE, is inhibition of expression of host

target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2903 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2903 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2903 gene: VGAM828 host target protein, VGAM829 host target protein and VGAM830 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM828, VGAM829 and VGAM830

[40179] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2904(VGR2904) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40180] VGR2904 gene, herein designated VGR GENE, is a novel

bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2904 gene was detected is described hereinabove with reference to Figs. 6-15.

[40181] VGR2904 gene encodes VGR2904 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40182] VGR2904 precursor RNA folds spatially, forming VGR2904 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2904 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2904 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40183] VGR2904 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM831 precursor RNA and VGAM832 precursor RNA, herein schematically represented by VGAM1

PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40184] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM831 RNA and VGAM832 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40185] VGAM831 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM831 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM831 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM831 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40186] VGAM832 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM832 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM832 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM832 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40187] It is appreciated that a function of VGR2904 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2904 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2904 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2904 gene: VGAM831 host target protein and VGAM832 host target protein, herein

schematically represented by VGAM1 HOST TARGET PROTEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM831 and VGAM832

[40188] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2905(VGR2905) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40189] VGR2905 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2905 gene was detected is described hereinabove with reference to Figs. 6-15.

[40190] VGR2905 gene encodes VGR2905 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40191] VGR2905 precursor RNA folds spatially, forming VGR2905 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2905 folded

precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2905 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40192] VGR2905 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 6 separate VGAM precursor RNAs, VGAM833 precursor RNA, VGAM834 precursor RNA, VGAM835 precursor RNA, VGAM836 precursor RNA, VGAM837 precursor RNA and VGAM838 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR, VGAM5 PRECURSOR and VGAM6 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40193] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM833

RNA, VGAM834 RNA, VGAM835 RNA, VGAM836 RNA, VGAM837 RNA and VGAM838 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA, VGAM5 RNA and VGAM6 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40194] VGAM833 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM833 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM833 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM833 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40195] VGAM834 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM834 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corre-

sponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM834 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM834 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40196] VGAM835 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM835 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM835 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM835 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[40197] VGAM836 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM836 host target RNA, herein schematically represented by VGAM4

HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM836 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM836 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[40198] VGAM837 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM837 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM837 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM837 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[40199] VGAM838 RNA, herein schematically represented by VGAM6 binds complimentarily to a host target binding site located in an untranslated region of VGAM838 host

target RNA, herein schematically represented by VGAM6 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM838 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA into VGAM838 host target protein, herein schematically represented by VGAM6 HOST TARGET PROTEIN, both of Fig. 1.

[40200] It is appreciated that a function of VGR2905 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2905 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2905 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2905 gene: VGAM833 host target protein, VGAM834 host target protein, VGAM835 host target protein, VGAM836 host target protein, VGAM837 host target protein and VGAM838 host target protein, herein schematically represented by VGAM1 HOST

TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM833, VGAM834, VGAM835, VGAM836, VGAM837 and VGAM838

[40201] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2906(VGR2906) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40202] VGR2906 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2906 gene was detected is described hereinabove with reference to Figs. 6-15.

[40203] VGR2906 gene encodes VGR2906 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40204] VGR2906 precursor RNA folds spatially, forming VGR2906 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2906 folded

precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2906 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40205] VGR2906 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM841 precursor RNA and VGAM842 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40206] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM841 RNA and VGAM842 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of

Fig. 8.

[40207] VGAM841 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM841 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM841 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM841 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40208] VGAM842 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM842 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM842 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM842 host target protein, herein schematically

represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40209] It is appreciated that a function of VGR2906 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2906 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2906 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2906 gene: VGAM841 host target protein and VGAM842 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM841 and VGAM842

[40210] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2907(VGR2907) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function

and utility of which at least one host target gene is known in the art.

[40211] VGR2907 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2907 gene was detected is described hereinabove with reference to Figs. 6-15.

[40212] VGR2907 gene encodes VGR2907 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40213] VGR2907 precursor RNA folds spatially, forming VGR2907 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2907 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2907 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40214] VGR2907 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellu-

lar enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM843 precursor RNA and VGAM844 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40215] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM843 RNA and VGAM844 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40216] VGAM843 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM843 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM843 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA

into VGAM843 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40217] VGAM844 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM844 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM844 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM844 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40218] It is appreciated that a function of VGR2907 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2907 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2907 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target

genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2907 gene: VGAM843 host target protein and VGAM844 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM843 and VGAM844

[40219] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2908(VGR2908) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40220] VGR2908 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2908 gene was detected is described hereinabove with reference to Figs. 6-15.

[40221] VGR2908 gene encodes VGR2908 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40222] VGR2908 precursor RNA folds spatially, forming VGR2908 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2908 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2908 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40223] VGR2908 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM845 precursor RNA, VGAM846 precursor RNA, VGAM847 precursor RNA and VGAM848 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR and VGAM4 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40224] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA

segments of about 22 nucleotides in length, VGAM845 RNA, VGAM846 RNA, VGAM847 RNA and VGAM848 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA and VGAM4 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40225] VGAM845 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM845 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM845 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM845 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40226] VGAM846 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM846 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corre-

sponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM846 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM846 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40227] VGAM847 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM847 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM847 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM847 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[40228] VGAM848 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM848 host target RNA, herein schematically represented by VGAM4

HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM848 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM848 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[40229] It is appreciated that a function of VGR2908 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2908 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2908 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2908 gene: VGAM845 host target protein, VGAM846 host target protein, VGAM847 host target protein and VGAM848 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elabo-

rated hereinabove with reference to VGAM845, VGAM846, VGAM847 and VGAM848

[40230] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2909(VGR2909) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40231] VGR2909 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2909 gene was detected is described hereinabove with reference to Figs. 6-15.

[40232] VGR2909 gene encodes VGR2909 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40233] VGR2909 precursor RNA folds spatially, forming VGR2909 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2909 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art

as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2909 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40234] VGR2909 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM849 precursor RNA, VGAM850 precursor RNA and VGAM851 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR and VGAM3 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40235] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM849 RNA, VGAM850 RNA and VGAM851 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA and VGAM3 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40236] VGAM849 RNA, herein schematically represented by

VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM849 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM849 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM849 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40237] VGAM850 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM850 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM850 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM850 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40238] VGAM851 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM851 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM851 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM851 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[40239] It is appreciated that a function of VGR2909 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2909 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2909 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2909 gene: VGAM849 host target protein, VGAM850 host target protein and

VGAM851 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM849, VGAM850 and VGAM851

[40240] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2910(VGR2910) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40241] VGR2910 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2910 gene was detected is described hereinabove with reference to Figs. 6-15.

[40242] VGR2910 gene encodes VGR2910 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40243] VGR2910 precursor RNA folds spatially, forming VGR2910 folded precursor RNA, herein designated VGR FOLDED

PRECURSOR RNA. It is appreciated that VGR2910 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2910 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40244] VGR2910 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM855 precursor RNA and VGAM856 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40245] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM855 RNA and VGAM856 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively,

each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40246] VGAM855 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM855 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM855 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM855 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40247] VGAM856 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM856 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM856 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA

into VGAM856 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40248] It is appreciated that a function of VGR2910 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2910 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2910 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2910 gene: VGAM855 host target protein and VGAM856 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM855 and VGAM856

[40249] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2911(VGR2911) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates

expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40250] VGR2911 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2911 gene was detected is described hereinabove with reference to Figs. 6-15.

[40251] VGR2911 gene encodes VGR2911 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40252] VGR2911 precursor RNA folds spatially, forming VGR2911 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2911 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2911 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40253] VGR2911 folded precursor RNA, herein designated VGR

FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM857 precursor RNA, VGAM858 precursor RNA and VGAM859 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR and VGAM3 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40254] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM857 RNA, VGAM858 RNA and VGAM859 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA and VGAM3 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40255] VGAM857 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM857 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM857 host target RNA, herein

schematically represented by VGAM1 HOST TARGET RNA into VGAM857 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40256] VGAM858 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM858 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM858 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM858 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40257] VGAM859 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM859 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby in-

hibiting translation of VGAM859 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM859 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[40258] It is appreciated that a function of VGR2911 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2911 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2911 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2911 gene: VGAM857 host target protein, VGAM858 host target protein and VGAM859 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM857, VGAM858 and VGAM859

[40259] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred

to here as Viral Genomic Record 2912(VGR2912) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40260] VGR2912 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2912 gene was detected is described hereinabove with reference to Figs. 6-15.

[40261] VGR2912 gene encodes VGR2912 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40262] VGR2912 precursor RNA folds spatially, forming VGR2912 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2912 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2912 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which

is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40263] VGR2912 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM861 precursor RNA, VGAM862 precursor RNA, VGAM863 precursor RNA and VGAM864 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR and VGAM4 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40264] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM861 RNA, VGAM862 RNA, VGAM863 RNA and VGAM864 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA and VGAM4 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40265] VGAM861 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM861 host

target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM861 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM861 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40266] VGAM862 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM862 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM862 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM862 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40267] VGAM863 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding

site located in an untranslated region of VGAM863 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM863 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM863 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[40268] VGAM864 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM864 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM864 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM864 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[40269] It is appreciated that a function of VGR2912 gene, herein

designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2912 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2912 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2912 gene: VGAM861 host target protein, VGAM862 host target protein, VGAM863 host target protein and VGAM864 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM861, VGAM862, VGAM863 and VGAM864

[40270] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2913(VGR2913) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known

in the art.

[40271] VGR2913 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2913 gene was detected is described hereinabove with reference to Figs. 6-15.

[40272] VGR2913 gene encodes VGR2913 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40273] VGR2913 precursor RNA folds spatially, forming VGR2913 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2913 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2913 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40274] VGR2913 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM pre-

cursor RNAs, VGAM865 precursor RNA and VGAM866 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40275] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM865 RNA and VGAM866 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40276] VGAM865 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM865 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM865 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM865 host target protein, herein schematically

represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40277] VGAM866 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM866 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM866 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM866 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40278] It is appreciated that a function of VGR2913 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2913 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2913 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in

the operon-like cluster of VGR2913 gene: VGAM865 host target protein and VGAM866 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM865 and VGAM866

[40279] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2914(VGR2914) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40280] VGR2914 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2914 gene was detected is described hereinabove with reference to Figs. 6-15.

[40281] VGR2914 gene encodes VGR2914 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40282] VGR2914 precursor RNA folds spatially, forming VGR2914

folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2914 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2914 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40283] VGR2914 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM867 precursor RNA and VGAM868 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40284] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM867 RNA and VGAM868 RNA respectively, herein schematically

represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40285] VGAM867 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM867 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM867 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM867 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40286] VGAM868 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM868 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM868 host target RNA, herein

schematically represented by VGAM2 HOST TARGET RNA into VGAM868 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40287] It is appreciated that a function of VGR2914 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2914 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2914 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2914 gene: VGAM867 host target protein and VGAM868 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM867 and VGAM868

[40288] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2915(VGR2915) viral gene, which encodes an operon-like cluster of novel viral

micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40289] VGR2915 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2915 gene was detected is described hereinabove with reference to Figs. 6-15.

[40290] VGR2915 gene encodes VGR2915 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40291] VGR2915 precursor RNA folds spatially, forming VGR2915 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2915 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2915 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40292] VGR2915 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM869 precursor RNA, VGAM870 precursor RNA, VGAM871 precursor RNA, VGAM872 precursor RNA and VGAM873 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR and VGAM5 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40293] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM869 RNA, VGAM870 RNA, VGAM871 RNA, VGAM872 RNA and VGAM873 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA and VGAM5 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40294] VGAM869 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM869 host target RNA, herein schematically represented by VGAM1

HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM869 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM869 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40295] VGAM870 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM870 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM870 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM870 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40296] VGAM871 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM871 host

target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM871 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM871 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[40297] VGAM872 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM872 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM872 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM872 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[40298] VGAM873 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding

site located in an untranslated region of VGAM873 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM873 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM873 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[40299] It is appreciated that a function of VGR2915 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2915 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2915 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2915 gene: VGAM869 host target protein, VGAM870 host target protein, VGAM871 host target protein, VGAM872 host target protein and VGAM873 host target protein, herein schematically repre-

sented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM869, VGAM870, VGAM871, VGAM872 and VGAM873

[40300] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2916(VGR2916) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40301] VGR2916 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2916 gene was detected is described hereinabove with reference to Figs. 6-15.

[40302] VGR2916 gene encodes VGR2916 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40303] VGR2916 precursor RNA folds spatially, forming VGR2916 folded precursor RNA, herein designated VGR FOLDED

PRECURSOR RNA. It is appreciated that VGR2916 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2916 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40304] VGR2916 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM875 precursor RNA, VGAM876 precursor RNA and VGAM877 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR and VGAM3 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40305] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM875 RNA, VGAM876 RNA and VGAM877 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2

RNA and VGAM3 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40306] VGAM875 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM875 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM875 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM875 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40307] VGAM876 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM876 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM876 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA

into VGAM876 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40308] VGAM877 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM877 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM877 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM877 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[40309] It is appreciated that a function of VGR2916 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2916 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2916 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target

genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2916 gene: VGAM875 host target protein, VGAM876 host target protein and VGAM877 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM875, VGAM876 and VGAM877

[40310] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2917(VGR2917) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40311] VGR2917 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2917 gene was detected is described hereinabove with reference to Figs. 6-15.

[40312] VGR2917 gene encodes VGR2917 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typi-

cally several hundred nucleotides long.

[40313] VGR2917 precursor RNA folds spatially, forming VGR2917 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2917 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2917 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40314] VGR2917 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM880 precursor RNA and VGAM881 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40315] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA

segments of about 22 nucleotides in length, VGAM880 RNA and VGAM881 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40316] VGAM880 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM880 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM880 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM880 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40317] VGAM881 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM881 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM881 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM881 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40318] It is appreciated that a function of VGR2917 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2917 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2917 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2917 gene: VGAM880 host target protein and VGAM881 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM880 and VGAM881

[40319] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred

to here as Viral Genomic Record 2918(VGR2918) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40320] VGR2918 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2918 gene was detected is described hereinabove with reference to Figs. 6-15.

[40321] VGR2918 gene encodes VGR2918 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40322] VGR2918 precursor RNA folds spatially, forming VGR2918 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2918 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2918 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which

is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40323] VGR2918 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM886 precursor RNA and VGAM887 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40324] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM886 RNA and VGAM887 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40325] VGAM886 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM886 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corre-

sponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM886 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM886 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40326] VGAM887 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM887 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM887 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM887 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40327] It is appreciated that a function of VGR2918 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2918 gene include

diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2918 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2918 gene: VGAM886 host target protein and VGAM887 host target protein, herein schematically represented by VGAM1 HOST TARGET PRO-TEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated herein-above with reference to VGAM886 and VGAM887

[40328] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2919(VGR2919) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40329] VGR2919 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2919 gene was detected is described hereinabove with reference to Figs.

6-15.

[40330] VGR2919 gene encodes VGR2919 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40331] VGR2919 precursor RNA folds spatially, forming VGR2919 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2919 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2919 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40332] VGR2919 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM888 precursor RNA, VGAM889 precursor RNA, VGAM890 precursor RNA and VGAM891 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR and VGAM4 PRECURSOR respectively, each of which VGAM

precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40333] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM888 RNA, VGAM889 RNA, VGAM890 RNA and VGAM891 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA and VGAM4 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40334] VGAM888 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM888 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM888 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM888 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40335] VGAM889 RNA, herein schematically represented by

VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM889 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM889 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM889 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40336] VGAM890 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM890 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM890 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM890 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[40337] VGAM891 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM891 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM891 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM891 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[40338] It is appreciated that a function of VGR2919 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2919 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2919 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2919 gene: VGAM888 host target protein, VGAM889 host target protein, VGAM890

host target protein and VGAM891 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM888, VGAM889, VGAM890 and VGAM891

[40339] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2920(VGR2920) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40340] VGR2920 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2920 gene was detected is described hereinabove with reference to Figs. 6-15.

[40341] VGR2920 gene encodes VGR2920 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40342] VGR2920 precursor RNA folds spatially, forming VGR2920

folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2920 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2920 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40343] VGR2920 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM892 precursor RNA, VGAM893 precursor RNA and VGAM894 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR and VGAM3 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40344] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM892 RNA, VGAM893 RNA and VGAM894 RNA respectively,

herein schematically represented by VGAM1 RNA, VGAM2 RNA and VGAM3 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40345] VGAM892 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM892 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM892 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM892 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40346] VGAM893 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM893 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM893 host target RNA, herein

schematically represented by VGAM2 HOST TARGET RNA into VGAM893 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40347] VGAM894 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM894 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM894 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM894 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[40348] It is appreciated that a function of VGR2920 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2920 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2920 gene, herein designated VGR GENE, correlate with, and

may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2920 gene: VGAM892 host target protein, VGAM893 host target protein and VGAM894 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM892, VGAM893 and VGAM894

[40349] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2921(VGR2921) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40350] VGR2921 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2921 gene was detected is described hereinabove with reference to Figs. 6-15.

[40351] VGR2921 gene encodes VGR2921 precursor RNA, herein

designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40352] VGR2921 precursor RNA folds spatially, forming VGR2921 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2921 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2921 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40353] VGR2921 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM895 precursor RNA, VGAM896 precursor RNA and VGAM897 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR and VGAM3 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40354] The above mentioned VGAM precursor RNAs are diced by

DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM895 RNA, VGAM896 RNA and VGAM897 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA and VGAM3 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40355] VGAM895 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM895 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM895 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM895 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40356] VGAM896 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM896 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corre-

sponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM896 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM896 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40357] VGAM897 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM897 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM897 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM897 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[40358] It is appreciated that a function of VGR2921 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2921 gene include

diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2921 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2921 gene: VGAM895 host target protein, VGAM896 host target protein and VGAM897 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM895, VGAM896 and VGAM897

[40359] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2922(VGR2922) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40360] VGR2922 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2922 gene was

detected is described hereinabove with reference to Figs. 6-15.

[40361] VGR2922 gene encodes VGR2922 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40362] VGR2922 precursor RNA folds spatially, forming VGR2922 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2922 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2922 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40363] VGR2922 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM901 precursor RNA and VGAM902 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA

segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40364] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM901 RNA and VGAM902 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40365] VGAM901 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM901 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM901 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM901 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40366] VGAM902 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding

site located in an untranslated region of VGAM902 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM902 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM902 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40367] It is appreciated that a function of VGR2922 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2922 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2922 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2922 gene: VGAM901 host target protein and VGAM902 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN andVGAM HOST TARGET PROTEIN respectively. The

function of these host target genes is elaborated herein-above with reference to VGAM901 and VGAM902

[40368] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2923(VGR2923) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40369] VGR2923 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2923 gene was detected is described hereinabove with reference to Figs. 6-15.

[40370] VGR2923 gene encodes VGR2923 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40371] VGR2923 precursor RNA folds spatially, forming VGR2923 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2923 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art

as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2923 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40372] VGR2923 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM903 precursor RNA and VGAM904 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40373] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM903 RNA and VGAM904 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40374] VGAM903 RNA, herein schematically represented by

VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM903 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM903 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM903 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40375] VGAM904 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM904 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM904 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM904 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40376] It is appreciated that a function of VGR2923 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2923 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2923 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2923 gene: VGAM903 host target protein and VGAM904 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM903 and VGAM904

[40377] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2924(VGR2924) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40378] VGR2924 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2924 gene was detected is described hereinabove with reference to Figs. 6-15.

[40379] VGR2924 gene encodes VGR2924 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40380] VGR2924 precursor RNA folds spatially, forming VGR2924 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2924 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2924 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40381] VGR2924 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM905 precursor RNA, VGAM906 precur-

sor RNA, VGAM907 precursor RNA and VGAM908 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR and VGAM4 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40382] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM905 RNA, VGAM906 RNA, VGAM907 RNA and VGAM908 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA and VGAM4 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40383] VGAM905 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM905 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM905 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA

into VGAM905 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40384] VGAM906 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM906 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM906 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM906 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40385] VGAM907 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM907 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM907 host target RNA, herein

schematically represented by VGAM3 HOST TARGET RNA into VGAM907 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[40386] VGAM908 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM908 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM908 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM908 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[40387] It is appreciated that a function of VGR2924 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2924 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2924 gene, herein designated VGR GENE, correlate with, and

may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2924 gene: VGAM905 host target protein, VGAM906 host target protein, VGAM907 host target protein and VGAM908 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM905, VGAM906, VGAM907 and VGAM908

[40388] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2925(VGR2925) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40389] VGR2925 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2925 gene was detected is described hereinabove with reference to Figs. 6-15.

[40390] VGR2925 gene encodes VGR2925 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40391] VGR2925 precursor RNA folds spatially, forming VGR2925 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2925 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2925 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40392] VGR2925 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM909 precursor RNA and VGAM910 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40393] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM909 RNA and VGAM910 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40394] VGAM909 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM909 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM909 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM909 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40395] VGAM910 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM910 host target RNA, herein schematically represented by VGAM2

HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM910 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM910 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40396] It is appreciated that a function of VGR2925 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2925 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2925 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2925 gene: VGAM909 host target protein and VGAM910 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM909 and VGAM910

[40397] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2926(VGR2926) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40398] VGR2926 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2926 gene was detected is described hereinabove with reference to Figs. 6-15.

[40399] VGR2926 gene encodes VGR2926 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40400] VGR2926 precursor RNA folds spatially, forming VGR2926 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2926 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2926 precur-

sor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40401] VGR2926 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM911 precursor RNA and VGAM912 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40402] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM911 RNA and VGAM912 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40403] VGAM911 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM911 host

target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM911 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM911 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40404] VGAM912 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM912 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM912 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM912 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40405] It is appreciated that a function of VGR2926 gene, herein designated VGR GENE, is inhibition of expression of host

target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2926 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2926 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2926 gene: VGAM911 host target protein and VGAM912 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM911 and VGAM912

[40406] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2927(VGR2927) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40407] VGR2927 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding,

RNA viral gene. The method by which VGR2927 gene was detected is described hereinabove with reference to Figs. 6-15.

[40408] VGR2927 gene encodes VGR2927 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40409] VGR2927 precursor RNA folds spatially, forming VGR2927 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2927 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2927 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40410] VGR2927 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM913 precursor RNA and VGAM914 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of

which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40411] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM913 RNA and VGAM914 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40412] VGAM913 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM913 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM913 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM913 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40413] VGAM914 RNA, herein schematically represented by

VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM914 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM914 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM914 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40414] It is appreciated that a function of VGR2927 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2927 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2927 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2927 gene: VGAM913 host target protein and VGAM914 host target protein, herein schematically represented by VGAM1 HOST TARGET PRO-

TEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated herein-above with reference to VGAM913 and VGAM914

[40415] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2928(VGR2928) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40416] VGR2928 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2928 gene was detected is described hereinabove with reference to Figs. 6-15.

[40417] VGR2928 gene encodes VGR2928 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typi-cally several hundred nucleotides long.

[40418] VGR2928 precursor RNA folds spatially, forming VGR2928 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2928 folded precursor RNA, herein designated VGR FOLDED PRECUR-

SOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2928 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40419] VGR2928 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM915 precursor RNA and VGAM916 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40420] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM915 RNA and VGAM916 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40421] VGAM915 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM915 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM915 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM915 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40422] VGAM916 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM916 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM916 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM916 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of

Fig. 1.

[40423] It is appreciated that a function of VGR2928 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2928 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2928 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2928 gene: VGAM915 host target protein and VGAM916 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM915 and VGAM916

[40424] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2929(VGR2929) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known

in the art.

[40425] VGR2929 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2929 gene was detected is described hereinabove with reference to Figs. 6-15.

[40426] VGR2929 gene encodes VGR2929 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40427] VGR2929 precursor RNA folds spatially, forming VGR2929 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2929 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2929 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40428] VGR2929 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM pre-

cursor RNAs, VGAM918 precursor RNA and VGAM919 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40429] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM918 RNA and VGAM919 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40430] VGAM918 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM918 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM918 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM918 host target protein, herein schematically

represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40431] VGAM919 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM919 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM919 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM919 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40432] It is appreciated that a function of VGR2929 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2929 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2929 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in

the operon-like cluster of VGR2929 gene: VGAM918 host target protein and VGAM919 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM918 and VGAM919

[40433] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2930(VGR2930) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40434] VGR2930 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2930 gene was detected is described hereinabove with reference to Figs. 6-15.

[40435] VGR2930 gene encodes VGR2930 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40436] VGR2930 precursor RNA folds spatially, forming VGR2930

folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2930 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2930 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40437] VGR2930 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM921 precursor RNA, VGAM922 precursor RNA and VGAM923 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR and VGAM3 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40438] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM921 RNA, VGAM922 RNA and VGAM923 RNA respectively,

herein schematically represented by VGAM1 RNA, VGAM2 RNA and VGAM3 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40439] VGAM921 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM921 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM921 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM921 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40440] VGAM922 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM922 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM922 host target RNA, herein

schematically represented by VGAM2 HOST TARGET RNA into VGAM922 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40441] VGAM923 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM923 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM923 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM923 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[40442] It is appreciated that a function of VGR2930 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2930 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2930 gene, herein designated VGR GENE, correlate with, and

may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2930 gene: VGAM921 host target protein, VGAM922 host target protein and VGAM923 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM921, VGAM922 and VGAM923

[40443] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2931(VGR2931) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40444] VGR2931 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2931 gene was detected is described hereinabove with reference to Figs. 6-15.

[40445] VGR2931 gene encodes VGR2931 precursor RNA, herein

designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40446] VGR2931 precursor RNA folds spatially, forming VGR2931 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2931 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2931 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40447] VGR2931 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 6 separate VGAM precursor RNAs, VGAM924 precursor RNA, VGAM925 precursor RNA, VGAM926 precursor RNA, VGAM927 precursor RNA, VGAM928 precursor RNA and VGAM929 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR, VGAM5 PRECURSOR and VGAM6 PRECURSOR respectively, each of which VGAM precursor RNAs

being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40448] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM924 RNA, VGAM925 RNA, VGAM926 RNA, VGAM927 RNA, VGAM928 RNA and VGAM929 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA, VGAM5 RNA and VGAM6 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40449] VGAM924 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM924 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM924 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM924 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40450] VGAM925 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM925 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM925 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM925 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40451] VGAM926 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM926 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM926 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM926 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of

Fig. 1.

[40452] VGAM927 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM927 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM927 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM927 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[40453] VGAM928 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM928 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM928 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM928 host target protein, herein schematically

represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[40454] VGAM929 RNA, herein schematically represented by VGAM6 binds complimentarily to a host target binding site located in an untranslated region of VGAM929 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM929 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA into VGAM929 host target protein, herein schematically represented by VGAM6 HOST TARGET PROTEIN, both of Fig. 1.

[40455] It is appreciated that a function of VGR2931 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2931 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2931 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in

the operon-like cluster of VGR2931 gene: VGAM924 host target protein, VGAM925 host target protein, VGAM926 host target protein, VGAM927 host target protein, VGAM928 host target protein and VGAM929 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM924, VGAM925, VGAM926, VGAM927, VGAM928 and VGAM929

[40456] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2932(VGR2932) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40457] VGR2932 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2932 gene was detected is described hereinabove with reference to Figs. 6-15.

[40458] VGR2932 gene encodes VGR2932 precursor RNA, herein

designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40459] VGR2932 precursor RNA folds spatially, forming VGR2932 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2932 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2932 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40460] VGR2932 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM932 precursor RNA, VGAM933 precursor RNA and VGAM934 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR and VGAM3 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40461] The above mentioned VGAM precursor RNAs are diced by

DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM932 RNA, VGAM933 RNA and VGAM934 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA and VGAM3 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40462] VGAM932 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM932 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM932 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM932 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40463] VGAM933 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM933 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corre-

sponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM933 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM933 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40464] VGAM934 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM934 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM934 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM934 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[40465] It is appreciated that a function of VGR2932 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2932 gene include

diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2932 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2932 gene: VGAM932 host target protein, VGAM933 host target protein and VGAM934 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM932, VGAM933 and VGAM934

[40466] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2933(VGR2933) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40467] VGR2933 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2933 gene was

detected is described hereinabove with reference to Figs. 6-15.

[40468] VGR2933 gene encodes VGR2933 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40469] VGR2933 precursor RNA folds spatially, forming VGR2933 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2933 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2933 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40470] VGR2933 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM935 precursor RNA, VGAM936 precursor RNA and VGAM937 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR and VGAM3 PRECURSOR respectively, each of which

VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40471] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM935 RNA, VGAM936 RNA and VGAM937 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA and VGAM3 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40472] VGAM935 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM935 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM935 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM935 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40473] VGAM936 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding

site located in an untranslated region of VGAM936 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM936 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM936 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40474] VGAM937 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM937 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM937 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM937 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[40475] It is appreciated that a function of VGR2933 gene, herein

designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2933 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2933 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2933 gene: VGAM935 host target protein, VGAM936 host target protein and VGAM937 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM935, VGAM936 and VGAM937

[40476] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2934(VGR2934) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40477] VGR2934 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2934 gene was detected is described hereinabove with reference to Figs. 6-15.

[40478] VGR2934 gene encodes VGR2934 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40479] VGR2934 precursor RNA folds spatially, forming VGR2934 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2934 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2934 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40480] VGR2934 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM938 precursor RNA, VGAM939 precur-

sor RNA and VGAM940 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR and VGAM3 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40481] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM938 RNA, VGAM939 RNA and VGAM940 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA and VGAM3 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40482] VGAM938 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM938 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM938 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM938 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of

Fig. 1.

[40483] VGAM939 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM939 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM939 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM939 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40484] VGAM940 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM940 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM940 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM940 host target protein, herein schematically

represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[40485] It is appreciated that a function of VGR2934 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2934 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2934 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2934 gene: VGAM938 host target protein, VGAM939 host target protein and VGAM940 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM938, VGAM939 and VGAM940

[40486] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2935(VGR2935) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates

expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40487] VGR2935 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2935 gene was detected is described hereinabove with reference to Figs. 6-15.

[40488] VGR2935 gene encodes VGR2935 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40489] VGR2935 precursor RNA folds spatially, forming VGR2935 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2935 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2935 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40490] VGR2935 folded precursor RNA, herein designated VGR

FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM941 precursor RNA, VGAM942 precursor RNA and VGAM943 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR and VGAM3 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40491] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM941 RNA, VGAM942 RNA and VGAM943 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA and VGAM3 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40492] VGAM941 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM941 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM941 host target RNA, herein

schematically represented by VGAM1 HOST TARGET RNA into VGAM941 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40493] VGAM942 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM942 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM942 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM942 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40494] VGAM943 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM943 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby in-

hibiting translation of VGAM943 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM943 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[40495] It is appreciated that a function of VGR2935 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2935 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2935 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2935 gene: VGAM941 host target protein, VGAM942 host target protein and VGAM943 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM941, VGAM942 and VGAM943

[40496] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred

to here as Viral Genomic Record 2936(VGR2936) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40497] VGR2936 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2936 gene was detected is described hereinabove with reference to Figs. 6-15.

[40498] VGR2936 gene encodes VGR2936 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40499] VGR2936 precursor RNA folds spatially, forming VGR2936 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2936 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2936 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which

is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40500] VGR2936 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM944 precursor RNA and VGAM945 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40501] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM944 RNA and VGAM945 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40502] VGAM944 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM944 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corre-

sponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM944 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM944 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40503] VGAM945 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM945 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM945 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM945 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40504] It is appreciated that a function of VGR2936 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2936 gene include

diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2936 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2936 gene: VGAM944 host target protein and VGAM945 host target protein, herein schematically represented by VGAM1 HOST TARGET PRO-TEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated herein-above with reference to VGAM944 and VGAM945

[40505] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2937(VGR2937) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40506] VGR2937 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2937 gene was detected is described hereinabove with reference to Figs.

6-15.

[40507] VGR2937 gene encodes VGR2937 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40508] VGR2937 precursor RNA folds spatially, forming VGR2937 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2937 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2937 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40509] VGR2937 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM946 precursor RNA and VGAM947 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig.

8.

[40510] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM946 RNA and VGAM947 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40511] VGAM946 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM946 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM946 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM946 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40512] VGAM947 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM947 host

target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM947 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM947 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40513] It is appreciated that a function of VGR2937 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2937 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2937 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2937 gene: VGAM946 host target protein and VGAM947 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated herein-

above with reference to VGAM946 and VGAM947

[40514] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2938(VGR2938) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40515] VGR2938 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2938 gene was detected is described hereinabove with reference to Figs. 6-15.

[40516] VGR2938 gene encodes VGR2938 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40517] VGR2938 precursor RNA folds spatially, forming VGR2938 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2938 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to

the fact that the nucleotide sequence of VGR2938 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40518] VGR2938 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM948 precursor RNA and VGAM949 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40519] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM948 RNA and VGAM949 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40520] VGAM948 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding

site located in an untranslated region of VGAM948 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM948 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM948 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40521] VGAM949 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM949 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM949 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM949 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40522] It is appreciated that a function of VGR2938 gene, herein

designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2938 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2938 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2938 gene: VGAM948 host target protein and VGAM949 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM948 and VGAM949

[40523] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2939(VGR2939) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40524] VGR2939 gene, herein designated VGR GENE, is a novel

bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2939 gene was detected is described hereinabove with reference to Figs. 6-15.

[40525] VGR2939 gene encodes VGR2939 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40526] VGR2939 precursor RNA folds spatially, forming VGR2939 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2939 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2939 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40527] VGR2939 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM950 precursor RNA, VGAM951 precursor RNA and VGAM952 precursor RNA, herein schemati-

cally represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR and VGAM3 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40528] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM950 RNA, VGAM951 RNA and VGAM952 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA and VGAM3 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40529] VGAM950 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM950 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM950 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM950 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40530] VGAM951 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM951 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM951 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM951 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40531] VGAM952 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM952 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM952 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM952 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of

Fig. 1.

[40532] It is appreciated that a function of VGR2939 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2939 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2939 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2939 gene: VGAM950 host target protein, VGAM951 host target protein and VGAM952 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM950, VGAM951 and VGAM952

[40533] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2940(VGR2940) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function

and utility of which at least one host target gene is known in the art.

[40534] VGR2940 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2940 gene was detected is described hereinabove with reference to Figs. 6-15.

[40535] VGR2940 gene encodes VGR2940 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40536] VGR2940 precursor RNA folds spatially, forming VGR2940 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2940 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2940 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40537] VGR2940 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellu-

lar enzymatic activity into at least 6 separate VGAM precursor RNAs, VGAM953 precursor RNA, VGAM954 precursor RNA, VGAM955 precursor RNA, VGAM956 precursor RNA, VGAM957 precursor RNA and VGAM958 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR, VGAM5 PRECURSOR and VGAM6 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40538] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM953 RNA, VGAM954 RNA, VGAM955 RNA, VGAM956 RNA, VGAM957 RNA and VGAM958 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA, VGAM5 RNA and VGAM6 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40539] VGAM953 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM953 host target RNA, herein schematically represented by VGAM1

HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM953 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM953 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40540] VGAM954 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM954 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM954 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM954 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40541] VGAM955 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM955 host

target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM955 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM955 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[40542] VGAM956 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM956 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM956 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM956 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[40543] VGAM957 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding

site located in an untranslated region of VGAM957 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM957 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM957 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[40544] VGAM958 RNA, herein schematically represented by VGAM6 binds complimentarily to a host target binding site located in an untranslated region of VGAM958 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM958 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA into VGAM958 host target protein, herein schematically represented by VGAM6 HOST TARGET PROTEIN, both of Fig. 1.

[40545] It is appreciated that a function of VGR2940 gene, herein

designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2940 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2940 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2940 gene: VGAM953 host target protein, VGAM954 host target protein, VGAM955 host target protein, VGAM956 host target protein, VGAM957 host target protein and VGAM958 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM953, VGAM954, VGAM955, VGAM956, VGAM957 and VGAM958

[40546] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2941(VGR2941) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function

and utility of which at least one host target gene is known in the art.

[40547] VGR2941 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2941 gene was detected is described hereinabove with reference to Figs. 6-15.

[40548] VGR2941 gene encodes VGR2941 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40549] VGR2941 precursor RNA folds spatially, forming VGR2941 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2941 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2941 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40550] VGR2941 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellu-

lar enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM959 precursor RNA, VGAM960 precursor RNA and VGAM961 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR and VGAM3 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40551] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM959 RNA, VGAM960 RNA and VGAM961 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA and VGAM3 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40552] VGAM959 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM959 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM959 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA

into VGAM959 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40553] VGAM960 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM960 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM960 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM960 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40554] VGAM961 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM961 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM961 host target RNA, herein

schematically represented by VGAM3 HOST TARGET RNA into VGAM961 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[40555] It is appreciated that a function of VGR2941 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2941 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2941 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2941 gene: VGAM959 host target protein, VGAM960 host target protein and VGAM961 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM959, VGAM960 and VGAM961

[40556] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2942(VGR2942) viral

gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40557] VGR2942 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2942 gene was detected is described hereinabove with reference to Figs. 6-15.

[40558] VGR2942 gene encodes VGR2942 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40559] VGR2942 precursor RNA folds spatially, forming VGR2942 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2942 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2942 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the

second half thereof, as is well known in the art.

[40560] VGR2942 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM962 precursor RNA, VGAM963 precursor RNA, VGAM964 precursor RNA, VGAM965 precursor RNA and VGAM966 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR and VGAM5 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40561] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM962 RNA, VGAM963 RNA, VGAM964 RNA, VGAM965 RNA and VGAM966 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA and VGAM5 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40562] VGAM962 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM962 host

target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM962 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM962 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40563] VGAM963 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM963 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM963 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM963 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40564] VGAM964 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding

site located in an untranslated region of VGAM964 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM964 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM964 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[40565] VGAM965 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM965 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM965 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM965 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[40566] VGAM966 RNA, herein schematically represented by

VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM966 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM966 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM966 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[40567] It is appreciated that a function of VGR2942 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2942 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2942 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2942 gene: VGAM962 host target protein, VGAM963 host target protein, VGAM964 host target protein, VGAM965 host target protein and

VGAM966 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM962, VGAM963, VGAM964, VGAM965 and VGAM966

[40568] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2943(VGR2943) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40569] VGR2943 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2943 gene was detected is described hereinabove with reference to Figs. 6-15.

[40570] VGR2943 gene encodes VGR2943 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40571] VGR2943 precursor RNA folds spatially, forming VGR2943

folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2943 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2943 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40572] VGR2943 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM967 precursor RNA, VGAM968 precursor RNA, VGAM969 precursor RNA and VGAM970 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR and VGAM4 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40573] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM967

RNA, VGAM968 RNA, VGAM969 RNA and VGAM970 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA and VGAM4 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40574] VGAM967 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM967 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM967 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM967 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40575] VGAM968 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM968 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM968 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM968 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40576] VGAM969 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM969 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM969 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM969 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[40577] VGAM970 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM970 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corre-

sponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM970 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM970 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[40578] It is appreciated that a function of VGR2943 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2943 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2943 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2943 gene: VGAM967 host target protein, VGAM968 host target protein, VGAM969 host target protein and VGAM970 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM967, VGAM968,

VGAM969 and VGAM970

[40579] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2944(VGR2944) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40580] VGR2944 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2944 gene was detected is described hereinabove with reference to Figs. 6-15.

[40581] VGR2944 gene encodes VGR2944 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40582] VGR2944 precursor RNA folds spatially, forming VGR2944 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2944 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to

the fact that the nucleotide sequence of VGR2944 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40583] VGR2944 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM971 precursor RNA and VGAM972 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40584] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM971 RNA and VGAM972 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40585] VGAM971 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding

site located in an untranslated region of VGAM971 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM971 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM971 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40586] VGAM972 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM972 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM972 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM972 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40587] It is appreciated that a function of VGR2944 gene, herein

designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2944 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2944 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2944 gene: VGAM971 host target protein and VGAM972 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM971 and VGAM972

[40588] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2945(VGR2945) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40589] VGR2945 gene, herein designated VGR GENE, is a novel

bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2945 gene was detected is described hereinabove with reference to Figs. 6-15.

[40590] VGR2945 gene encodes VGR2945 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40591] VGR2945 precursor RNA folds spatially, forming VGR2945 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2945 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2945 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40592] VGR2945 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM975 precursor RNA, VGAM976 precursor RNA, VGAM977 precursor RNA, VGAM978 precursor

RNA and VGAM979 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR and VGAM5 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40593] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM975 RNA, VGAM976 RNA, VGAM977 RNA, VGAM978 RNA and VGAM979 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA and VGAM5 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40594] VGAM975 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM975 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM975 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA

into VGAM975 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40595] VGAM976 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM976 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM976 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM976 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40596] VGAM977 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM977 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM977 host target RNA, herein

schematically represented by VGAM3 HOST TARGET RNA into VGAM977 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[40597] VGAM978 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM978 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM978 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM978 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[40598] VGAM979 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM979 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby in-

hibiting translation of VGAM979 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM979 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[40599] It is appreciated that a function of VGR2945 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2945 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2945 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2945 gene: VGAM975 host target protein, VGAM976 host target protein, VGAM977 host target protein, VGAM978 host target protein and VGAM979 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM975, VGAM976, VGAM977, VGAM978 and VGAM979

[40600] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2946(VGR2946) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40601] VGR2946 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2946 gene was detected is described hereinabove with reference to Figs. 6-15.

[40602] VGR2946 gene encodes VGR2946 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40603] VGR2946 precursor RNA folds spatially, forming VGR2946 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2946 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2946 precur-

sor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40604] VGR2946 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM980 precursor RNA, VGAM981 precursor RNA, VGAM982 precursor RNA, VGAM983 precursor RNA and VGAM984 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR and VGAM5 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40605] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM980 RNA, VGAM981 RNA, VGAM982 RNA, VGAM983 RNA and VGAM984 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA and VGAM5 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40606] VGAM980 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM980 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM980 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM980 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40607] VGAM981 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM981 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM981 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM981 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of

Fig. 1.

[40608] VGAM982 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM982 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM982 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM982 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[40609] VGAM983 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM983 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM983 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM983 host target protein, herein schematically

represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[40610] VGAM984 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM984 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM984 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM984 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[40611] It is appreciated that a function of VGR2946 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2946 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2946 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in

the operon-like cluster of VGR2946 gene: VGAM980 host target protein, VGAM981 host target protein, VGAM982 host target protein, VGAM983 host target protein and VGAM984 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM980, VGAM981, VGAM982, VGAM983 and VGAM984

[40612] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2947(VGR2947) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40613] VGR2947 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2947 gene was detected is described hereinabove with reference to Figs. 6-15.

[40614] VGR2947 gene encodes VGR2947 precursor RNA, herein

designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40615] VGR2947 precursor RNA folds spatially, forming VGR2947 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2947 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2947 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40616] VGR2947 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM986 precursor RNA, VGAM987 precursor RNA, VGAM988 precursor RNA, VGAM989 precursor RNA and VGAM990 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR and VGAM5 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to

VGAM PRECURSOR RNA of Fig. 8.

[40617] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM986 RNA, VGAM987 RNA, VGAM988 RNA, VGAM989 RNA and VGAM990 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA and VGAM5 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40618] VGAM986 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM986 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM986 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM986 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40619] VGAM987 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding

site located in an untranslated region of VGAM987 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM987 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM987 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40620] VGAM988 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM988 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM988 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM988 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[40621] VGAM989 RNA, herein schematically represented by

VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM989 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM989 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM989 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[40622] VGAM990 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM990 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM990 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM990 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[40623] It is appreciated that a function of VGR2947 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2947 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2947 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2947 gene: VGAM986 host target protein, VGAM987 host target protein, VGAM988 host target protein, VGAM989 host target protein and VGAM990 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM986, VGAM987, VGAM988, VGAM989 and VGAM990

[40624] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2948(VGR2948) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates

expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40625] VGR2948 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2948 gene was detected is described hereinabove with reference to Figs. 6-15.

[40626] VGR2948 gene encodes VGR2948 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40627] VGR2948 precursor RNA folds spatially, forming VGR2948 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2948 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2948 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40628] VGR2948 folded precursor RNA, herein designated VGR

FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 6 separate VGAM precursor RNAs, VGAM991 precursor RNA, VGAM992 precursor RNA, VGAM993 precursor RNA, VGAM994 precursor RNA, VGAM995 precursor RNA and VGAM996 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR, VGAM5 PRECURSOR and VGAM6 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40629] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM991 RNA, VGAM992 RNA, VGAM993 RNA, VGAM994 RNA, VGAM995 RNA and VGAM996 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA, VGAM5 RNA and VGAM6 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40630] VGAM991 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM991 host

target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM991 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM991 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40631] VGAM992 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM992 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM992 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM992 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40632] VGAM993 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding

site located in an untranslated region of VGAM993 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM993 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM993 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[40633] VGAM994 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM994 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM994 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM994 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[40634] VGAM995 RNA, herein schematically represented by

VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM995 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM995 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM995 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[40635] VGAM996 RNA, herein schematically represented by VGAM6 binds complimentarily to a host target binding site located in an untranslated region of VGAM996 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM996 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA into VGAM996 host target protein, herein schematically represented by VGAM6 HOST TARGET PROTEIN, both of Fig. 1.

[40636] It is appreciated that a function of VGR2948 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2948 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2948 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2948 gene: VGAM991 host target protein, VGAM992 host target protein, VGAM993 host target protein, VGAM994 host target protein, VGAM995 host target protein and VGAM996 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM991, VGAM992, VGAM993, VGAM994, VGAM995 and VGAM996

[40637] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2949(VGR2949) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates

expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40638] VGR2949 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2949 gene was detected is described hereinabove with reference to Figs. 6-15.

[40639] VGR2949 gene encodes VGR2949 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40640] VGR2949 precursor RNA folds spatially, forming VGR2949 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2949 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2949 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40641] VGR2949 folded precursor RNA, herein designated VGR

FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM997 precursor RNA, VGAM998 precursor RNA, VGAM999 precursor RNA, VGAM1000 precursor RNA and VGAM1001 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR and VGAM5 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40642] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM997 RNA, VGAM998 RNA, VGAM999 RNA, VGAM1000 RNA and VGAM1001 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA and VGAM5 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40643] VGAM997 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM997 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corre-

sponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM997 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM997 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40644] VGAM998 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM998 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM998 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM998 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40645] VGAM999 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM999 host target RNA, herein schematically represented by VGAM3

HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM999 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM999 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[40646] VGAM1000 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM1000 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1000 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM1000 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[40647] VGAM1001 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM1001 host

target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1001 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM1001 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[40648] It is appreciated that a function of VGR2949 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2949 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2949 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2949 gene: VGAM997 host target protein, VGAM998 host target protein, VGAM999 host target protein, VGAM1000 host target protein and VGAM1001 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through

VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM997, VGAM998, VGAM999, VGAM1000 and VGAM1001

[40649] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2950(VGR2950) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40650] VGR2950 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2950 gene was detected is described hereinabove with reference to Figs. 6-15.

[40651] VGR2950 gene encodes VGR2950 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40652] VGR2950 precursor RNA folds spatially, forming VGR2950 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2950 folded

precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2950 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40653] VGR2950 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 7 separate VGAM precursor RNAs, VGAM1002 precursor RNA, VGAM1003 precursor RNA, VGAM1004 precursor RNA, VGAM1005 precursor RNA, VGAM1006 precursor RNA, VGAM1007 precursor RNA and VGAM1008 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR, VGAM5 PRECURSOR, VGAM6 PRECURSOR and VGAM7 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40654] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA

segments of about 22 nucleotides in length, VGAM1002 RNA, VGAM1003 RNA, VGAM1004 RNA, VGAM1005 RNA, VGAM1006 RNA, VGAM1007 RNA and VGAM1008 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA, VGAM5 RNA, VGAM6 RNA and VGAM7 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40655] VGAM1002 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1002 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1002 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1002 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40656] VGAM1003 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1003 host target RNA, herein schematically represented by VGAM2

HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1003 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1003 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40657] VGAM1004 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM1004 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1004 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM1004 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[40658] VGAM1005 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM1005 host

target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1005 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM1005 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[40659] VGAM1006 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM1006 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1006 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM1006 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[40660] VGAM1007 RNA, herein schematically represented by VGAM6 binds complimentarily to a host target binding

site located in an untranslated region of VGAM1007 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1007 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA into VGAM1007 host target protein, herein schematically represented by VGAM6 HOST TARGET PROTEIN, both of Fig. 1.

[40661] VGAM1008 RNA, herein schematically represented by VGAM7 binds complimentarily to a host target binding site located in an untranslated region of VGAM1008 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1008 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA into VGAM1008 host target protein, herein schematically represented by VGAM7 HOST TARGET PROTEIN, both of Fig. 1.

[40662] It is appreciated that a function of VGR2950 gene, herein

designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2950 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2950 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2950 gene: VGAM1002 host target protein, VGAM1003 host target protein, VGAM1004 host target protein, VGAM1005 host target protein, VGAM1006 host target protein, VGAM1007 host target protein and VGAM1008 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1002, VGAM1003, VGAM1004, VGAM1005, VGAM1006, VGAM1007 and VGAM1008

[40663] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2951(VGR2951) viral gene, which encodes an operon-like cluster of novel viral

micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40664] VGR2951 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2951 gene was detected is described hereinabove with reference to Figs. 6-15.

[40665] VGR2951 gene encodes VGR2951 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40666] VGR2951 precursor RNA folds spatially, forming VGR2951 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2951 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2951 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40667] VGR2951 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM1009 precursor RNA, VGAM1010 precursor RNA and VGAM1011 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR and VGAM3 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40668] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1009 RNA, VGAM1010 RNA and VGAM1011 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA and VGAM3 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40669] VGAM1009 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1009 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1009 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1009 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40670] VGAM1010 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1010 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1010 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1010 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40671] VGAM1011 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM1011 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corre-

sponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1011 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM1011 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[40672] It is appreciated that a function of VGR2951 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2951 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2951 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2951 gene: VGAM1009 host target protein, VGAM1010 host target protein and VGAM1011 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1009, VGAM1010 and VGAM1011

[40673] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2952(VGR2952) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40674] VGR2952 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2952 gene was detected is described hereinabove with reference to Figs. 6-15.

[40675] VGR2952 gene encodes VGR2952 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40676] VGR2952 precursor RNA folds spatially, forming VGR2952 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2952 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2952 precur-

sor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40677] VGR2952 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM1012 precursor RNA and VGAM1013 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40678] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1012 RNA and VGAM1013 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40679] VGAM1012 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1012 host

target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1012 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1012 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40680] VGAM1013 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1013 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1013 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1013 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40681] It is appreciated that a function of VGR2952 gene, herein designated VGR GENE, is inhibition of expression of host

target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2952 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2952 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2952 gene: VGAM1012 host target protein and VGAM1013 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1012 and VGAM1013

[40682] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2953(VGR2953) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40683] VGR2953 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding,

RNA viral gene. The method by which VGR2953 gene was detected is described hereinabove with reference to Figs. 6-15.

[40684] VGR2953 gene encodes VGR2953 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40685] VGR2953 precursor RNA folds spatially, forming VGR2953 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2953 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2953 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40686] VGR2953 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM1015 precursor RNA and VGAM1016 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively,

each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40687] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1015 RNA and VGAM1016 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40688] VGAM1015 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1015 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1015 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1015 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40689] VGAM1016 RNA, herein schematically represented by

VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1016 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1016 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1016 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40690] It is appreciated that a function of VGR2953 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2953 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2953 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2953 gene: VGAM1015 host target protein and VGAM1016 host target protein, herein schematically represented by VGAM1 HOST TARGET

PROTEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1015 and VGAM1016

[40691] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2954(VGR2954) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40692] VGR2954 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2954 gene was detected is described hereinabove with reference to Figs. 6-15.

[40693] VGR2954 gene encodes VGR2954 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40694] VGR2954 precursor RNA folds spatially, forming VGR2954 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2954 folded precursor RNA, herein designated VGR FOLDED PRECUR-

SOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2954 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40695] VGR2954 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM1017 precursor RNA, VGAM1018 precursor RNA and VGAM1019 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR and VGAM3 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40696] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1017 RNA, VGAM1018 RNA and VGAM1019 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA and VGAM3 RNA respectively, each of which VGAM

RNAs corresponding to VGAM RNA of Fig. 8.

[40697] VGAM1017 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1017 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1017 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1017 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40698] VGAM1018 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1018 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1018 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1018 host target protein, herein schematically

represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40699] VGAM1019 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM1019 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1019 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM1019 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[40700] It is appreciated that a function of VGR2954 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2954 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2954 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in

the operon-like cluster of VGR2954 gene: VGAM1017 host target protein, VGAM1018 host target protein and VGAM1019 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1017, VGAM1018 and VGAM1019

[40701] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2955(VGR2955) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40702] VGR2955 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2955 gene was detected is described hereinabove with reference to Figs. 6-15.

[40703] VGR2955 gene encodes VGR2955 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40704] VGR2955 precursor RNA folds spatially, forming VGR2955 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2955 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2955 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40705] VGR2955 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 7 separate VGAM precursor RNAs, VGAM1020 precursor RNA, VGAM1021 precursor RNA, VGAM1022 precursor RNA, VGAM1023 precursor RNA, VGAM1024 precursor RNA, VGAM1025 precursor RNA and VGAM1026 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR, VGAM5 PRECURSOR, VGAM6 PRECURSOR and VGAM7 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to

VGAM PRECURSOR RNA of Fig. 8.

[40706] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1020 RNA, VGAM1021 RNA, VGAM1022 RNA, VGAM1023 RNA, VGAM1024 RNA, VGAM1025 RNA and VGAM1026 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA, VGAM5 RNA, VGAM6 RNA and VGAM7 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40707] VGAM1020 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1020 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1020 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1020 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40708] VGAM1021 RNA, herein schematically represented by

VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1021 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1021 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1021 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40709] VGAM1022 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM1022 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1022 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM1022 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[40710] VGAM1023 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM1023 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1023 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM1023 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[40711] VGAM1024 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM1024 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1024 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM1024 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of

Fig. 1.

[40712] VGAM1025 RNA, herein schematically represented by VGAM6 binds complimentarily to a host target binding site located in an untranslated region of VGAM1025 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1025 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA into VGAM1025 host target protein, herein schematically represented by VGAM6 HOST TARGET PROTEIN, both of Fig. 1.

[40713] VGAM1026 RNA, herein schematically represented by VGAM7 binds complimentarily to a host target binding site located in an untranslated region of VGAM1026 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1026 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA into VGAM1026 host target protein, herein schematically

represented by VGAM7 HOST TARGET PROTEIN, both of Fig. 1.

[40714] It is appreciated that a function of VGR2955 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2955 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2955 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2955 gene: VGAM1020 host target protein, VGAM1021 host target protein, VGAM1022 host target protein, VGAM1023 host target protein, VGAM1024 host target protein, VGAM1025 host target protein and VGAM1026 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1020, VGAM1021, VGAM1022, VGAM1023, VGAM1024, VGAM1025 and VGAM1026

[40715] Fig. 9 further provides a conceptual description of novel

bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2956(VGR2956) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40716] VGR2956 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2956 gene was detected is described hereinabove with reference to Figs. 6-15.

[40717] VGR2956 gene encodes VGR2956 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40718] VGR2956 precursor RNA folds spatially, forming VGR2956 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2956 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2956 precursor RNA comprises a plurality of segments, the first half

of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40719] VGR2956 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM1027 precursor RNA and VGAM1028 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40720] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1027 RNA and VGAM1028 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40721] VGAM1027 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1027 host target RNA, herein schematically represented by VGAM1

HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1027 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1027 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40722] VGAM1028 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1028 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1028 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1028 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40723] It is appreciated that a function of VGR2956 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attack-

ing a host. Accordingly, utilities of VGR2956 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2956 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2956 gene: VGAM1027 host target protein and VGAM1028 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1027 and VGAM1028

[40724] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2957(VGR2957) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40725] VGR2957 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2957 gene was

detected is described hereinabove with reference to Figs. 6-15.

[40726] VGR2957 gene encodes VGR2957 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40727] VGR2957 precursor RNA folds spatially, forming VGR2957 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2957 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2957 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40728] VGR2957 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM1030 precursor RNA and VGAM1031 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin

shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40729] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1030 RNA and VGAM1031 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40730] VGAM1030 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1030 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1030 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1030 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40731] VGAM1031 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding

site located in an untranslated region of VGAM1031 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1031 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1031 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40732] It is appreciated that a function of VGR2957 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2957 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2957 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2957 gene: VGAM1030 host target protein and VGAM1031 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN andVGAM HOST TARGET PROTEIN respectively.

The function of these host target genes is elaborated hereinabove with reference to VGAM1030 and VGAM1031

[40733] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2958(VGR2958) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40734] VGR2958 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2958 gene was detected is described hereinabove with reference to Figs. 6-15.

[40735] VGR2958 gene encodes VGR2958 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40736] VGR2958 precursor RNA folds spatially, forming VGR2958 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2958 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art

as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2958 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40737] VGR2958 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM1032 precursor RNA, VGAM1033 precursor RNA, VGAM1034 precursor RNA, VGAM1035 precursor RNA and VGAM1036 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR and VGAM5 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40738] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1032 RNA, VGAM1033 RNA, VGAM1034 RNA, VGAM1035 RNA and VGAM1036 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA,

VGAM4 RNA and VGAM5 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40739] VGAM1032 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1032 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1032 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1032 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40740] VGAM1033 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1033 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1033 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA

into VGAM1033 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40741] VGAM1034 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM1034 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1034 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM1034 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[40742] VGAM1035 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM1035 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1035 host target RNA, herein

schematically represented by VGAM4 HOST TARGET RNA into VGAM1035 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[40743] VGAM1036 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM1036 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1036 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM1036 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[40744] It is appreciated that a function of VGR2958 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2958 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2958 gene, herein designated VGR GENE, correlate with, and

may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2958 gene: VGAM1032 host target protein, VGAM1033 host target protein, VGAM1034 host target protein, VGAM1035 host target protein and VGAM1036 host target protein, herein schematically represented by VGAM1 HOST TARGET PRO-TEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1032, VGAM1033, VGAM1034, VGAM1035 and VGAM1036

[40745] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2959(VGR2959) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40746] VGR2959 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2959 gene was detected is described hereinabove with reference to Figs.

6-15.

[40747] VGR2959 gene encodes VGR2959 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40748] VGR2959 precursor RNA folds spatially, forming VGR2959 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2959 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2959 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40749] VGR2959 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM1037 precursor RNA, VGAM1038 precursor RNA, VGAM1039 precursor RNA and VGAM1040 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR and VGAM4 PRECURSOR respectively, each of

which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40750] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1037 RNA, VGAM1038 RNA, VGAM1039 RNA and VGAM1040 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA and VGAM4 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40751] VGAM1037 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1037 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1037 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1037 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40752] VGAM1038 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1038 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1038 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1038 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40753] VGAM1039 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM1039 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1039 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM1039 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of

Fig. 1.

[40754] VGAM1040 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM1040 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1040 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM1040 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[40755] It is appreciated that a function of VGR2959 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2959 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2959 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2959 gene: VGAM1037

host target protein, VGAM1038 host target protein, VGAM1039 host target protein and VGAM1040 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1037, VGAM1038, VGAM1039 and VGAM1040

[40756] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2960(VGR2960) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40757] VGR2960 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2960 gene was detected is described hereinabove with reference to Figs. 6-15.

[40758] VGR2960 gene encodes VGR2960 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40759] VGR2960 precursor RNA folds spatially, forming VGR2960 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2960 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2960 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40760] VGR2960 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM1041 precursor RNA, VGAM1042 precursor RNA and VGAM1043 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR and VGAM3 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40761] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA

segments of about 22 nucleotides in length, VGAM1041 RNA, VGAM1042 RNA and VGAM1043 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA and VGAM3 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40762] VGAM1041 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1041 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1041 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1041 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40763] VGAM1042 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1042 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1042 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1042 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40764] VGAM1043 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM1043 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1043 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM1043 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[40765] It is appreciated that a function of VGR2960 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2960 gene include diagnosis, prevention and treatment of viral infection by .

Specific functions, and accordingly utilities, of VGR2960 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2960 gene: VGAM1041 host target protein, VGAM1042 host target protein and VGAM1043 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1041, VGAM1042 and VGAM1043

[40766] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2961(VGR2961) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40767] VGR2961 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2961 gene was detected is described hereinabove with reference to Figs.

6-15.

[40768] VGR2961 gene encodes VGR2961 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40769] VGR2961 precursor RNA folds spatially, forming VGR2961 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2961 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2961 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40770] VGR2961 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM1044 precursor RNA, VGAM1045 precursor RNA and VGAM1046 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR and VGAM3 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA

segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40771] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1044 RNA, VGAM1045 RNA and VGAM1046 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA and VGAM3 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40772] VGAM1044 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1044 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1044 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1044 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40773] VGAM1045 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding

site located in an untranslated region of VGAM1045 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1045 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1045 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40774] VGAM1046 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM1046 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1046 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM1046 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[40775] It is appreciated that a function of VGR2961 gene, herein

designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2961 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2961 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2961 gene: VGAM1044 host target protein, VGAM1045 host target protein and VGAM1046 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1044, VGAM1045 and VGAM1046

[40776] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2962(VGR2962) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40777] VGR2962 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2962 gene was detected is described hereinabove with reference to Figs. 6-15.

[40778] VGR2962 gene encodes VGR2962 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40779] VGR2962 precursor RNA folds spatially, forming VGR2962 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2962 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2962 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40780] VGR2962 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM1047 precursor RNA, VGAM1048 precursor RNA and VGAM1049 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR and VGAM3 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40781] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA

segments of about 22 nucleotides in length, VGAM1047 RNA, VGAM1048 RNA and VGAM1049 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA and VGAM3 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40782] VGAM1047 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1047 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1047 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1047 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40783] VGAM1048 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1048 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1048 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1048 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40784] VGAM1049 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM1049 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1049 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM1049 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[40785] It is appreciated that a function of VGR2962 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2962 gene include diagnosis, prevention and treatment of viral infection by .

Specific functions, and accordingly utilities, of VGR2962 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2962 gene: VGAM1047 host target protein, VGAM1048 host target protein and VGAM1049 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1047, VGAM1048 and VGAM1049

[40786] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2963(VGR2963) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40787] VGR2963 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2963 gene was detected is described hereinabove with reference to Figs.

6-15.

[40788] VGR2963 gene encodes VGR2963 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40789] VGR2963 precursor RNA folds spatially, forming VGR2963 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2963 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2963 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40790] VGR2963 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM1050 precursor RNA, VGAM1051 precursor RNA, VGAM1052 precursor RNA and VGAM1053 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR and VGAM4 PRECURSOR respectively, each of

which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40791] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1050 RNA, VGAM1051 RNA, VGAM1052 RNA and VGAM1053 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA and VGAM4 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40792] VGAM1050 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1050 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1050 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1050 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40793] VGAM1051 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1051 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1051 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1051 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40794] VGAM1052 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM1052 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1052 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM1052 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of

Fig. 1.

[40795] VGAM1053 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM1053 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1053 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM1053 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[40796] It is appreciated that a function of VGR2963 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2963 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2963 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2963 gene: VGAM1050

host target protein, VGAM1051 host target protein, VGAM1052 host target protein and VGAM1053 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1050, VGAM1051, VGAM1052 and VGAM1053

[40797] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2964(VGR2964) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40798] VGR2964 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2964 gene was detected is described hereinabove with reference to Figs. 6-15.

[40799] VGR2964 gene encodes VGR2964 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40800] VGR2964 precursor RNA folds spatially, forming VGR2964 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2964 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2964 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40801] VGR2964 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM1055 precursor RNA and VGAM1056 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40802] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1055

RNA and VGAM1056 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40803] VGAM1055 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1055 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1055 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1055 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40804] VGAM1056 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1056 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby in-

hibiting translation of VGAM1056 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1056 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40805] It is appreciated that a function of VGR2964 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2964 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2964 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2964 gene: VGAM1055 host target protein and VGAM1056 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1055 and VGAM1056

[40806] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2965(VGR2965) viral

gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40807] VGR2965 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2965 gene was detected is described hereinabove with reference to Figs. 6-15.

[40808] VGR2965 gene encodes VGR2965 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40809] VGR2965 precursor RNA folds spatially, forming VGR2965 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2965 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2965 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the

second half thereof, as is well known in the art.

[40810] VGR2965 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM1057 precursor RNA, VGAM1058 precursor RNA and VGAM1059 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR and VGAM3 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40811] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1057 RNA, VGAM1058 RNA and VGAM1059 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA and VGAM3 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40812] VGAM1057 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1057 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corre-

sponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1057 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1057 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40813] VGAM1058 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1058 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1058 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1058 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40814] VGAM1059 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM1059 host target RNA, herein schematically represented by VGAM3

HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1059 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM1059 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[40815] It is appreciated that a function of VGR2965 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2965 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2965 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2965 gene: VGAM1057 host target protein, VGAM1058 host target protein and VGAM1059 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with

reference to VGAM1057, VGAM1058 and VGAM1059

[40816] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2966(VGR2966) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40817] VGR2966 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2966 gene was detected is described hereinabove with reference to Figs. 6-15.

[40818] VGR2966 gene encodes VGR2966 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40819] VGR2966 precursor RNA folds spatially, forming VGR2966 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2966 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to

the fact that the nucleotide sequence of VGR2966 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40820] VGR2966 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM1061 precursor RNA and VGAM1062 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40821] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1061 RNA and VGAM1062 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40822] VGAM1061 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding

site located in an untranslated region of VGAM1061 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1061 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1061 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40823] VGAM1062 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1062 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1062 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1062 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40824] It is appreciated that a function of VGR2966 gene, herein

designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2966 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2966 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2966 gene: VGAM1061 host target protein and VGAM1062 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1061 and VGAM1062

[40825] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2967(VGR2967) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40826] VGR2967 gene, herein designated VGR GENE, is a novel

bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2967 gene was detected is described hereinabove with reference to Figs. 6-15.

[40827] VGR2967 gene encodes VGR2967 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40828] VGR2967 precursor RNA folds spatially, forming VGR2967 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2967 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2967 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40829] VGR2967 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM1063 precursor RNA, VGAM1064 precursor RNA, VGAM1065 precursor RNA and VGAM1066

precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR and VGAM4 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40830] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1063 RNA, VGAM1064 RNA, VGAM1065 RNA and VGAM1066 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA and VGAM4 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40831] VGAM1063 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1063 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1063 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA

into VGAM1063 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40832] VGAM1064 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1064 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1064 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1064 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40833] VGAM1065 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM1065 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1065 host target RNA, herein

schematically represented by VGAM3 HOST TARGET RNA into VGAM1065 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[40834] VGAM1066 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM1066 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1066 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM1066 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[40835] It is appreciated that a function of VGR2967 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2967 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2967 gene, herein designated VGR GENE, correlate with, and

may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2967 gene: VGAM1063 host target protein, VGAM1064 host target protein, VGAM1065 host target protein and VGAM1066 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1063, VGAM1064, VGAM1065 and VGAM1066

[40836] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2968(VGR2968) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40837] VGR2968 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2968 gene was detected is described hereinabove with reference to Figs. 6-15.

[40838] VGR2968 gene encodes VGR2968 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40839] VGR2968 precursor RNA folds spatially, forming VGR2968 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2968 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2968 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40840] VGR2968 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM1067 precursor RNA, VGAM1068 precursor RNA, VGAM1069 precursor RNA, VGAM1070 precursor RNA, VGAM1071 precursor RNA, VGAM1072 precursor RNA, VGAM1073 precursor RNA and VGAM1074 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRE-

CURSOR, VGAM4 PRECURSOR, VGAM5 PRECURSOR, VGAM6 PRECURSOR, VGAM7 PRECURSOR and VGAM8 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40841] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1067 RNA, VGAM1068 RNA, VGAM1069 RNA, VGAM1070 RNA, VGAM1071 RNA, VGAM1072 RNA, VGAM1073 RNA and VGAM1074 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA, VGAM5 RNA, VGAM6 RNA, VGAM7 RNA and VGAM8 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40842] VGAM1067 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1067 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1067 host target RNA, herein

schematically represented by VGAM1 HOST TARGET RNA into VGAM1067 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40843] VGAM1068 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1068 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1068 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1068 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40844] VGAM1069 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM1069 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby in-

hibiting translation of VGAM1069 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM1069 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[40845] VGAM1070 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM1070 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1070 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM1070 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[40846] VGAM1071 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM1071 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1071 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM1071 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[40847] VGAM1072 RNA, herein schematically represented by VGAM6 binds complimentarily to a host target binding site located in an untranslated region of VGAM1072 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1072 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA into VGAM1072 host target protein, herein schematically represented by VGAM6 HOST TARGET PROTEIN, both of Fig. 1.

[40848] VGAM1073 RNA, herein schematically represented by VGAM7 binds complimentarily to a host target binding site located in an untranslated region of VGAM1073 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA, which host target binding site corre-

sponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1073 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA into VGAM1073 host target protein, herein schematically represented by VGAM7 HOST TARGET PROTEIN, both of Fig. 1.

[40849] VGAM1074 RNA, herein schematically represented by VGAM8 binds complimentarily to a host target binding site located in an untranslated region of VGAM1074 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1074 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA into VGAM1074 host target protein, herein schematically represented by VGAM8 HOST TARGET PROTEIN, both of Fig. 1.

[40850] It is appreciated that a function of VGR2968 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2968 gene include

diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2968 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2968 gene: VGAM1067 host target protein, VGAM1068 host target protein, VGAM1069 host target protein, VGAM1070 host target protein, VGAM1071 host target protein, VGAM1072 host target protein, VGAM1073 host target protein and VGAM1074 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1067, VGAM1068, VGAM1069, VGAM1070, VGAM1071, VGAM1072, VGAM1073 and VGAM1074

[40851] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2969(VGR2969) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function

and utility of which at least one host target gene is known in the art.

[40852] VGR2969 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2969 gene was detected is described hereinabove with reference to Figs. 6-15.

[40853] VGR2969 gene encodes VGR2969 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40854] VGR2969 precursor RNA folds spatially, forming VGR2969 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2969 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2969 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40855] VGR2969 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellu-

lar enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM1075 precursor RNA, VGAM1076 precursor RNA, VGAM1077 precursor RNA, VGAM1078 precursor RNA, VGAM1079 precursor RNA, VGAM1080 precursor RNA, VGAM1081 precursor RNA and VGAM1082 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR, VGAM5 PRECURSOR, VGAM6 PRECURSOR, VGAM7 PRECURSOR and VGAM8 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40856] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1075 RNA, VGAM1076 RNA, VGAM1077 RNA, VGAM1078 RNA, VGAM1079 RNA, VGAM1080 RNA, VGAM1081 RNA and VGAM1082 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA, VGAM5 RNA, VGAM6 RNA, VGAM7 RNA and VGAM8 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40857] VGAM1075 RNA, herein schematically represented by

VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1075 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1075 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1075 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40858] VGAM1076 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1076 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1076 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1076 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40859] VGAM1077 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM1077 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1077 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM1077 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[40860] VGAM1078 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM1078 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1078 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM1078 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of

Fig. 1.

[40861] VGAM1079 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM1079 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1079 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM1079 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[40862] VGAM1080 RNA, herein schematically represented by VGAM6 binds complimentarily to a host target binding site located in an untranslated region of VGAM1080 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1080 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA into VGAM1080 host target protein, herein schematically

represented by VGAM6 HOST TARGET PROTEIN, both of Fig. 1.

[40863] VGAM1081 RNA, herein schematically represented by VGAM7 binds complimentarily to a host target binding site located in an untranslated region of VGAM1081 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1081 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA into VGAM1081 host target protein, herein schematically represented by VGAM7 HOST TARGET PROTEIN, both of Fig. 1.

[40864] VGAM1082 RNA, herein schematically represented by VGAM8 binds complimentarily to a host target binding site located in an untranslated region of VGAM1082 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1082 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA

into VGAM1082 host target protein, herein schematically represented by VGAM8 HOST TARGET PROTEIN, both of Fig. 1.

[40865] It is appreciated that a function of VGR2969 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2969 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2969 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2969 gene: VGAM1075 host target protein, VGAM1076 host target protein, VGAM1077 host target protein, VGAM1078 host target protein, VGAM1079 host target protein, VGAM1080 host target protein, VGAM1081 host target protein and VGAM1082 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1075, VGAM1076, VGAM1077, VGAM1078, VGAM1079, VGAM1080, VGAM1081 and

[40866] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2970(VGR2970) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40867] VGR2970 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2970 gene was detected is described hereinabove with reference to Figs. 6-15.

[40868] VGR2970 gene encodes VGR2970 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40869] VGR2970 precursor RNA folds spatially, forming VGR2970 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2970 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to

the fact that the nucleotide sequence of VGR2970 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40870] VGR2970 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM1083 precursor RNA, VGAM1084 precursor RNA, VGAM1085 precursor RNA, VGAM1086 precursor RNA, VGAM1087 precursor RNA, VGAM1088 precursor RNA, VGAM1089 precursor RNA and VGAM1090 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR, VGAM5 PRECURSOR, VGAM6 PRECURSOR, VGAM7 PRECURSOR and VGAM8 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40871] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1083 RNA, VGAM1084 RNA, VGAM1085 RNA, VGAM1086 RNA,

VGAM1087 RNA, VGAM1088 RNA, VGAM1089 RNA and VGAM1090 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA, VGAM5 RNA, VGAM6 RNA, VGAM7 RNA and VGAM8 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40872] VGAM1083 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1083 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1083 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1083 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40873] VGAM1084 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1084 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corre-

sponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1084 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1084 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40874] VGAM1085 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM1085 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1085 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM1085 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[40875] VGAM1086 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM1086 host target RNA, herein schematically represented by VGAM4

HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1086 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM1086 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[40876] VGAM1087 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM1087 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1087 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM1087 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[40877] VGAM1088 RNA, herein schematically represented by VGAM6 binds complimentarily to a host target binding site located in an untranslated region of VGAM1088 host

target RNA, herein schematically represented by VGAM6 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1088 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA into VGAM1088 host target protein, herein schematically represented by VGAM6 HOST TARGET PROTEIN, both of Fig. 1.

[40878] VGAM1089 RNA, herein schematically represented by VGAM7 binds complimentarily to a host target binding site located in an untranslated region of VGAM1089 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1089 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA into VGAM1089 host target protein, herein schematically represented by VGAM7 HOST TARGET PROTEIN, both of Fig. 1.

[40879] VGAM1090 RNA, herein schematically represented by VGAM8 binds complimentarily to a host target binding

site located in an untranslated region of VGAM1090 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1090 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA into VGAM1090 host target protein, herein schematically represented by VGAM8 HOST TARGET PROTEIN, both of Fig. 1.

[40880] It is appreciated that a function of VGR2970 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2970 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2970 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2970 gene: VGAM1083 host target protein, VGAM1084 host target protein, VGAM1085 host target protein, VGAM1086 host target protein, VGAM1087 host target protein, VGAM1088 host

target protein, VGAM1089 host target protein and VGAM1090 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1083, VGAM1084, VGAM1085, VGAM1086, VGAM1087, VGAM1088, VGAM1089 and VGAM1090

[40881] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2971(VGR2971) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40882] VGR2971 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2971 gene was detected is described hereinabove with reference to Figs. 6-15.

[40883] VGR2971 gene encodes VGR2971 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typi-

cally several hundred nucleotides long.

[40884] VGR2971 precursor RNA folds spatially, forming VGR2971 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2971 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2971 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40885] VGR2971 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM1091 precursor RNA, VGAM1092 precursor RNA, VGAM1093 precursor RNA, VGAM1094 precursor RNA and VGAM1095 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR and VGAM5 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40886] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1091 RNA, VGAM1092 RNA, VGAM1093 RNA, VGAM1094 RNA and VGAM1095 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA and VGAM5 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40887] VGAM1091 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1091 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1091 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1091 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40888] VGAM1092 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1092 host

target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1092 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1092 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40889] VGAM1093 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM1093 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1093 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM1093 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[40890] VGAM1094 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding

site located in an untranslated region of VGAM1094 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1094 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM1094 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[40891] VGAM1095 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM1095 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1095 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM1095 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[40892] It is appreciated that a function of VGR2971 gene, herein

designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2971 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2971 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2971 gene: VGAM1091 host target protein, VGAM1092 host target protein, VGAM1093 host target protein, VGAM1094 host target protein and VGAM1095 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1091, VGAM1092, VGAM1093, VGAM1094 and VGAM1095

[40893] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2972(VGR2972) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function

and utility of which at least one host target gene is known in the art.

[40894] VGR2972 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2972 gene was detected is described hereinabove with reference to Figs. 6-15.

[40895] VGR2972 gene encodes VGR2972 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40896] VGR2972 precursor RNA folds spatially, forming VGR2972 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2972 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2972 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40897] VGR2972 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellu-

lar enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM1096 precursor RNA, VGAM1097 precursor RNA, VGAM1098 precursor RNA, VGAM1099 precursor RNA, VGAM1100 precursor RNA, VGAM1101 precursor RNA, VGAM1102 precursor RNA and VGAM1103 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR, VGAM5 PRECURSOR, VGAM6 PRECURSOR, VGAM7 PRECURSOR and VGAM8 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40898] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1096 RNA, VGAM1097 RNA, VGAM1098 RNA, VGAM1099 RNA, VGAM1100 RNA, VGAM1101 RNA, VGAM1102 RNA and VGAM1103 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA, VGAM5 RNA, VGAM6 RNA, VGAM7 RNA and VGAM8 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40899] VGAM1096 RNA, herein schematically represented by

VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1096 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1096 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1096 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40900] VGAM1097 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1097 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1097 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1097 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40901] VGAM1098 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM1098 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1098 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM1098 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[40902] VGAM1099 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM1099 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1099 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM1099 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of

Fig. 1.

[40903] VGAM1100 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM1100 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1100 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM1100 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[40904] VGAM1101 RNA, herein schematically represented by VGAM6 binds complimentarily to a host target binding site located in an untranslated region of VGAM1101 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1101 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA into VGAM1101 host target protein, herein schematically

represented by VGAM6 HOST TARGET PROTEIN, both of Fig. 1.

[40905] VGAM1102 RNA, herein schematically represented by VGAM7 binds complimentarily to a host target binding site located in an untranslated region of VGAM1102 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1102 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA into VGAM1102 host target protein, herein schematically represented by VGAM7 HOST TARGET PROTEIN, both of Fig. 1.

[40906] VGAM1103 RNA, herein schematically represented by VGAM8 binds complimentarily to a host target binding site located in an untranslated region of VGAM1103 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1103 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA

into VGAM1103 host target protein, herein schematically represented by VGAM8 HOST TARGET PROTEIN, both of Fig. 1.

[40907] It is appreciated that a function of VGR2972 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2972 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2972 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2972 gene: VGAM1096 host target protein, VGAM1097 host target protein, VGAM1098 host target protein, VGAM1099 host target protein, VGAM1100 host target protein, VGAM1101 host target protein, VGAM1102 host target protein and VGAM1103 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1096, VGAM1097, VGAM1098, VGAM1099, VGAM1100, VGAM1101, VGAM1102 and

[40908] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2973(VGR2973) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40909] VGR2973 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2973 gene was detected is described hereinabove with reference to Figs. 6-15.

[40910] VGR2973 gene encodes VGR2973 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40911] VGR2973 precursor RNA folds spatially, forming VGR2973 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2973 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to

the fact that the nucleotide sequence of VGR2973 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40912] VGR2973 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM1104 precursor RNA, VGAM1105 precursor RNA and VGAM1106 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR and VGAM3 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40913] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1104 RNA, VGAM1105 RNA and VGAM1106 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA and VGAM3 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40914] VGAM1104 RNA, herein schematically represented by

VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1104 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1104 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1104 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40915] VGAM1105 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1105 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1105 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1105 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40916] VGAM1106 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM1106 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1106 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM1106 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[40917] It is appreciated that a function of VGR2973 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2973 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2973 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2973 gene: VGAM1104 host target protein, VGAM1105 host target protein and

VGAM1106 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1104, VGAM1105 and VGAM1106

[40918] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2974(VGR2974) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40919] VGR2974 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2974 gene was detected is described hereinabove with reference to Figs. 6-15.

[40920] VGR2974 gene encodes VGR2974 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40921] VGR2974 precursor RNA folds spatially, forming VGR2974 folded precursor RNA, herein designated VGR FOLDED

PRECURSOR RNA. It is appreciated that VGR2974 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2974 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40922] VGR2974 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM1108 precursor RNA and VGAM1109 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40923] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1108 RNA and VGAM1109 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respec-

tively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40924] VGAM1108 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1108 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1108 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1108 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40925] VGAM1109 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1109 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1109 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA

into VGAM1109 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40926] It is appreciated that a function of VGR2974 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2974 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2974 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2974 gene: VGAM1108 host target protein and VGAM1109 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1108 and VGAM1109

[40927] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2975(VGR2975) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates

expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40928] VGR2975 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2975 gene was detected is described hereinabove with reference to Figs. 6-15.

[40929] VGR2975 gene encodes VGR2975 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40930] VGR2975 precursor RNA folds spatially, forming VGR2975 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2975 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2975 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40931] VGR2975 folded precursor RNA, herein designated VGR

FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM1111 precursor RNA, VGAM1112 precursor RNA, VGAM1113 precursor RNA, VGAM1114 precursor RNA and VGAM1115 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR and VGAM5 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40932] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1111 RNA, VGAM1112 RNA, VGAM1113 RNA, VGAM1114 RNA and VGAM1115 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA and VGAM5 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40933] VGAM1111 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1111 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corre-

sponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1111 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1111 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40934] VGAM1112 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1112 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1112 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1112 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40935] VGAM1113 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM1113 host target RNA, herein schematically represented by VGAM3

HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1113 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM1113 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[40936] VGAM1114 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM1114 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1114 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM1114 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[40937] VGAM1115 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM1115 host

target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1115 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM1115 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[40938] It is appreciated that a function of VGR2975 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2975 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2975 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2975 gene: VGAM1111 host target protein, VGAM1112 host target protein, VGAM1113 host target protein, VGAM1114 host target protein and VGAM1115 host target protein, herein schematically represented by VGAM1 HOST TARGET PRO-

TEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1111, VGAM1112, VGAM1113, VGAM1114 and VGAM1115

[40939] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2976(VGR2976) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40940] VGR2976 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2976 gene was detected is described hereinabove with reference to Figs. 6-15.

[40941] VGR2976 gene encodes VGR2976 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40942] VGR2976 precursor RNA folds spatially, forming VGR2976 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2976 folded

precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2976 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40943] VGR2976 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM1116 precursor RNA, VGAM1117 precursor RNA, VGAM1118 precursor RNA, VGAM1119 precursor RNA and VGAM1120 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR and VGAM5 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40944] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1116 RNA, VGAM1117 RNA, VGAM1118 RNA, VGAM1119 RNA

and VGAM1120 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA and VGAM5 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40945] VGAM1116 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1116 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1116 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1116 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40946] VGAM1117 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1117 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby in-

hibiting translation of VGAM1117 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1117 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40947] VGAM1118 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM1118 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1118 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM1118 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[40948] VGAM1119 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM1119 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1119 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM1119 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[40949] VGAM1120 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM1120 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1120 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM1120 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[40950] It is appreciated that a function of VGR2976 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2976 gene include diagnosis, prevention and treatment of viral infection by .

Specific functions, and accordingly utilities, of VGR2976 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2976 gene: VGAM1116 host target protein, VGAM1117 host target protein, VGAM1118 host target protein, VGAM1119 host target protein and VGAM1120 host target protein, herein schematically represented by VGAM1 HOST TARGET PRO-TEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1116, VGAM1117, VGAM1118, VGAM1119 and VGAM1120

[40951] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2977(VGR2977) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40952] VGR2977 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding,

RNA viral gene. The method by which VGR2977 gene was detected is described hereinabove with reference to Figs. 6-15.

[40953] VGR2977 gene encodes VGR2977 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40954] VGR2977 precursor RNA folds spatially, forming VGR2977 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2977 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2977 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40955] VGR2977 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM1121 precursor RNA, VGAM1122 precursor RNA, VGAM1123 precursor RNA, VGAM1124 precursor RNA and VGAM1125 precursor RNA, herein

schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR and VGAM5 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40956] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1121 RNA, VGAM1122 RNA, VGAM1123 RNA, VGAM1124 RNA and VGAM1125 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA and VGAM5 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40957] VGAM1121 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1121 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1121 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1121 host target protein, herein schematically

represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40958] VGAM1122 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1122 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1122 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1122 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40959] VGAM1123 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM1123 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1123 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA

into VGAM1123 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[40960] VGAM1124 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM1124 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1124 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM1124 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[40961] VGAM1125 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM1125 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1125 host target RNA, herein

schematically represented by VGAM5 HOST TARGET RNA into VGAM1125 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[40962] It is appreciated that a function of VGR2977 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2977 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2977 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2977 gene: VGAM1121 host target protein, VGAM1122 host target protein, VGAM1123 host target protein, VGAM1124 host target protein and VGAM1125 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1121, VGAM1122, VGAM1123, VGAM1124 and VGAM1125

[40963] Fig. 9 further provides a conceptual description of novel

bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2978(VGR2978) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40964] VGR2978 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2978 gene was detected is described hereinabove with reference to Figs. 6-15.

[40965] VGR2978 gene encodes VGR2978 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40966] VGR2978 precursor RNA folds spatially, forming VGR2978 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2978 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2978 precursor RNA comprises a plurality of segments, the first half

of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40967] VGR2978 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 6 separate VGAM precursor RNAs, VGAM1127 precursor RNA, VGAM1128 precursor RNA, VGAM1129 precursor RNA, VGAM1130 precursor RNA, VGAM1131 precursor RNA and VGAM1132 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR, VGAM5 PRECURSOR and VGAM6 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40968] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1127 RNA, VGAM1128 RNA, VGAM1129 RNA, VGAM1130 RNA, VGAM1131 RNA and VGAM1132 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA, VGAM5 RNA and VGAM6 RNA respectively, each of which VGAM RNAs corresponding to

VGAM RNA of Fig. 8.

[40969] VGAM1127 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1127 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1127 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1127 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40970] VGAM1128 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1128 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1128 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1128 host target protein, herein schematically

represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40971] VGAM1129 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM1129 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1129 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM1129 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[40972] VGAM1130 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM1130 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1130 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA

into VGAM1130 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[40973] VGAM1131 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM1131 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1131 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM1131 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[40974] VGAM1132 RNA, herein schematically represented by VGAM6 binds complimentarily to a host target binding site located in an untranslated region of VGAM1132 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1132 host target RNA, herein

schematically represented by VGAM6 HOST TARGET RNA into VGAM1132 host target protein, herein schematically represented by VGAM6 HOST TARGET PROTEIN, both of Fig. 1.

[40975] It is appreciated that a function of VGR2978 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2978 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2978 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2978 gene: VGAM1127 host target protein, VGAM1128 host target protein, VGAM1129 host target protein, VGAM1130 host target protein, VGAM1131 host target protein and VGAM1132 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1127, VGAM1128, VGAM1129, VGAM1130, VGAM1131 and VGAM1132

[40976] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2979(VGR2979) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40977] VGR2979 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2979 gene was detected is described hereinabove with reference to Figs. 6-15.

[40978] VGR2979 gene encodes VGR2979 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40979] VGR2979 precursor RNA folds spatially, forming VGR2979 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2979 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2979 precur-

sor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40980] VGR2979 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM1133 precursor RNA, VGAM1134 precursor RNA and VGAM1135 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR and VGAM3 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40981] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1133 RNA, VGAM1134 RNA and VGAM1135 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA and VGAM3 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40982] VGAM1133 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding

site located in an untranslated region of VGAM1133 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1133 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1133 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40983] VGAM1134 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1134 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1134 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1134 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40984] VGAM1135 RNA, herein schematically represented by

VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM1135 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1135 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM1135 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[40985] It is appreciated that a function of VGR2979 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2979 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2979 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2979 gene: VGAM1133 host target protein, VGAM1134 host target protein and VGAM1135 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1133, VGAM1134 and VGAM1135

[40986] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2980(VGR2980) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40987] VGR2980 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2980 gene was detected is described hereinabove with reference to Figs. 6-15.

[40988] VGR2980 gene encodes VGR2980 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40989] VGR2980 precursor RNA folds spatially, forming VGR2980 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2980 folded

precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2980 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40990] VGR2980 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM1136 precursor RNA, VGAM1137 precursor RNA and VGAM1138 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR and VGAM3 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[40991] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1136 RNA, VGAM1137 RNA and VGAM1138 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2

RNA and VGAM3 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[40992] VGAM1136 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1136 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1136 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1136 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[40993] VGAM1137 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1137 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1137 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA

into VGAM1137 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[40994] VGAM1138 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM1138 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1138 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM1138 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[40995] It is appreciated that a function of VGR2980 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2980 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2980 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target

genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2980 gene: VGAM1136 host target protein, VGAM1137 host target protein and VGAM1138 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1136, VGAM1137 and VGAM1138

[40996] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2981(VGR2981) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[40997] VGR2981 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2981 gene was detected is described hereinabove with reference to Figs. 6-15.

[40998] VGR2981 gene encodes VGR2981 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typi-

cally several hundred nucleotides long.

[40999] VGR2981 precursor RNA folds spatially, forming VGR2981 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2981 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2981 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[41000] VGR2981 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM1139 precursor RNA, VGAM1140 precursor RNA and VGAM1141 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR and VGAM3 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[41001] The above mentioned VGAM precursor RNAs are diced by

DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1139 RNA, VGAM1140 RNA and VGAM1141 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA and VGAM3 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[41002] VGAM1139 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1139 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1139 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1139 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[41003] VGAM1140 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1140 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corre-

sponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1140 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1140 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[41004] VGAM1141 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM1141 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1141 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM1141 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[41005] It is appreciated that a function of VGR2981 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2981 gene include

diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2981 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2981 gene: VGAM1139 host target protein, VGAM1140 host target protein and VGAM1141 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1139, VGAM1140 and VGAM1141

[41006] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2982(VGR2982) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[41007] VGR2982 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2982 gene was

detected is described hereinabove with reference to Figs. 6-15.

[41008] VGR2982 gene encodes VGR2982 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[41009] VGR2982 precursor RNA folds spatially, forming VGR2982 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2982 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2982 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[41010] VGR2982 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM1142 precursor RNA, VGAM1143 precursor RNA, VGAM1144 precursor RNA and VGAM1145 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRE-

CURSOR and VGAM4 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[41011] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1142 RNA, VGAM1143 RNA, VGAM1144 RNA and VGAM1145 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA and VGAM4 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[41012] VGAM1142 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1142 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1142 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1142 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of

Fig. 1.

[41013] VGAM1143 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1143 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1143 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1143 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[41014] VGAM1144 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM1144 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1144 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM1144 host target protein, herein schematically

represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[41015] VGAM1145 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM1145 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1145 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM1145 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[41016] It is appreciated that a function of VGR2982 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2982 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2982 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in

the operon-like cluster of VGR2982 gene: VGAM1142 host target protein, VGAM1143 host target protein, VGAM1144 host target protein and VGAM1145 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1142, VGAM1143, VGAM1144 and VGAM1145

[41017] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2983(VGR2983) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[41018] VGR2983 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2983 gene was detected is described hereinabove with reference to Figs. 6-15.

[41019] VGR2983 gene encodes VGR2983 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typi-

cally several hundred nucleotides long.

[41020] VGR2983 precursor RNA folds spatially, forming VGR2983 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2983 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2983 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[41021] VGR2983 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM1146 precursor RNA and VGAM1147 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[41022] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA

segments of about 22 nucleotides in length, VGAM1146 RNA and VGAM1147 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[41023] VGAM1146 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1146 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1146 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1146 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[41024] VGAM1147 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1147 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1147 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1147 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[41025] It is appreciated that a function of VGR2983 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2983 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2983 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2983 gene: VGAM1146 host target protein and VGAM1147 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1146 and VGAM1147

[41026] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred

to here as Viral Genomic Record 2984(VGR2984) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[41027] VGR2984 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2984 gene was detected is described hereinabove with reference to Figs. 6-15.

[41028] VGR2984 gene encodes VGR2984 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[41029] VGR2984 precursor RNA folds spatially, forming VGR2984 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2984 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2984 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which

is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[41030] VGR2984 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM1148 precursor RNA, VGAM1149 precursor RNA and VGAM1150 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR and VGAM3 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[41031] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1148 RNA, VGAM1149 RNA and VGAM1150 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA and VGAM3 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[41032] VGAM1148 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1148 host target RNA, herein schematically represented by VGAM1

HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1148 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1148 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[41033] VGAM1149 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1149 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1149 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1149 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[41034] VGAM1150 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM1150 host

target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1150 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM1150 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[41035] It is appreciated that a function of VGR2984 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2984 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2984 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2984 gene: VGAM1148 host target protein, VGAM1149 host target protein and VGAM1150 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function

of these host target genes is elaborated hereinabove with reference to VGAM1148, VGAM1149 and VGAM1150

[41036] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2985(VGR2985) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[41037] VGR2985 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2985 gene was detected is described hereinabove with reference to Figs. 6-15.

[41038] VGR2985 gene encodes VGR2985 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[41039] VGR2985 precursor RNA folds spatially, forming VGR2985 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2985 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art

as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2985 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[41040] VGR2985 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM1151 precursor RNA, VGAM1152 precursor RNA, VGAM1153 precursor RNA and VGAM1154 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR and VGAM4 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[41041] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1151 RNA, VGAM1152 RNA, VGAM1153 RNA and VGAM1154 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA and VGAM4 RNA

respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[41042] VGAM1151 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1151 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1151 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1151 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[41043] VGAM1152 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1152 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1152 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA

into VGAM1152 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[41044] VGAM1153 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM1153 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1153 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM1153 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[41045] VGAM1154 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM1154 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1154 host target RNA, herein

schematically represented by VGAM4 HOST TARGET RNA into VGAM1154 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[41046] It is appreciated that a function of VGR2985 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2985 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2985 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2985 gene: VGAM1151 host target protein, VGAM1152 host target protein, VGAM1153 host target protein and VGAM1154 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1151, VGAM1152, VGAM1153 and VGAM1154

[41047] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred

to here as Viral Genomic Record 2986(VGR2986) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[41048] VGR2986 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2986 gene was detected is described hereinabove with reference to Figs. 6-15.

[41049] VGR2986 gene encodes VGR2986 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[41050] VGR2986 precursor RNA folds spatially, forming VGR2986 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2986 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2986 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which

is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[41051] VGR2986 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM1155 precursor RNA, VGAM1156 precursor RNA and VGAM1157 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR and VGAM3 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[41052] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1155 RNA, VGAM1156 RNA and VGAM1157 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA and VGAM3 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[41053] VGAM1155 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1155 host target RNA, herein schematically represented by VGAM1

HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1155 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1155 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[41054] VGAM1156 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1156 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1156 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1156 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[41055] VGAM1157 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM1157 host

target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1157 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM1157 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[41056] It is appreciated that a function of VGR2986 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2986 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2986 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2986 gene: VGAM1155 host target protein, VGAM1156 host target protein and VGAM1157 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function

of these host target genes is elaborated hereinabove with reference to VGAM1155, VGAM1156 and VGAM1157

[41057] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2987(VGR2987) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[41058] VGR2987 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2987 gene was detected is described hereinabove with reference to Figs. 6-15.

[41059] VGR2987 gene encodes VGR2987 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[41060] VGR2987 precursor RNA folds spatially, forming VGR2987 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2987 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art

as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2987 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[41061] VGR2987 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM1159 precursor RNA, VGAM1160 precursor RNA and VGAM1161 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR and VGAM3 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[41062] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1159 RNA, VGAM1160 RNA and VGAM1161 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA and VGAM3 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[41063] VGAM1159 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1159 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1159 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1159 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[41064] VGAM1160 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1160 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1160 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1160 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of

Fig. 1.

[41065] VGAM1161 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM1161 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1161 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM1161 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[41066] It is appreciated that a function of VGR2987 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2987 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2987 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2987 gene: VGAM1159

host target protein, VGAM1160 host target protein and VGAM1161 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1159, VGAM1160 and VGAM1161

[41067] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2988(VGR2988) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[41068] VGR2988 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2988 gene was detected is described hereinabove with reference to Figs. 6-15.

[41069] VGR2988 gene encodes VGR2988 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[41070] VGR2988 precursor RNA folds spatially, forming VGR2988

folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2988 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2988 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[41071] VGR2988 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM1162 precursor RNA, VGAM1163 precursor RNA, VGAM1164 precursor RNA and VGAM1165 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR and VGAM4 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[41072] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA

segments of about 22 nucleotides in length, VGAM1162 RNA, VGAM1163 RNA, VGAM1164 RNA and VGAM1165 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA and VGAM4 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[41073] VGAM1162 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1162 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1162 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1162 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[41074] VGAM1163 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1163 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corre-

sponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1163 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1163 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[41075] VGAM1164 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM1164 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1164 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM1164 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[41076] VGAM1165 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM1165 host target RNA, herein schematically represented by VGAM4

HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1165 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM1165 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[41077] It is appreciated that a function of VGR2988 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2988 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2988 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2988 gene: VGAM1162 host target protein, VGAM1163 host target protein, VGAM1164 host target protein and VGAM1165 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is

elaborated hereinabove with reference to VGAM1162, VGAM1163, VGAM1164 and VGAM1165

[41078] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2989(VGR2989) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[41079] VGR2989 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2989 gene was detected is described hereinabove with reference to Figs. 6-15.

[41080] VGR2989 gene encodes VGR2989 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[41081] VGR2989 precursor RNA folds spatially, forming VGR2989 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2989 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art

as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2989 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[41082] VGR2989 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM1166 precursor RNA and VGAM1167 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[41083] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1166 RNA and VGAM1167 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[41084] VGAM1166 RNA, herein schematically represented by

VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1166 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1166 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1166 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[41085] VGAM1167 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1167 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1167 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1167 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[41086] It is appreciated that a function of VGR2989 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2989 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2989 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2989 gene: VGAM1166 host target protein and VGAM1167 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1166 and VGAM1167

[41087] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2990(VGR2990) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[41088] VGR2990 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2990 gene was detected is described hereinabove with reference to Figs. 6-15.

[41089] VGR2990 gene encodes VGR2990 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[41090] VGR2990 precursor RNA folds spatially, forming VGR2990 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2990 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2990 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[41091] VGR2990 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM1168 precursor RNA and VGAM1169

precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[41092] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1168 RNA and VGAM1169 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[41093] VGAM1168 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1168 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1168 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1168 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of

Fig. 1.

[41094] VGAM1169 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1169 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1169 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1169 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[41095] It is appreciated that a function of VGR2990 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2990 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2990 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2990 gene: VGAM1168

host target protein and VGAM1169 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1168 and VGAM1169

[41096] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2991(VGR2991) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[41097] VGR2991 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2991 gene was detected is described hereinabove with reference to Figs. 6-15.

[41098] VGR2991 gene encodes VGR2991 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[41099] VGR2991 precursor RNA folds spatially, forming VGR2991 folded precursor RNA, herein designated VGR FOLDED

PRECURSOR RNA. It is appreciated that VGR2991 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2991 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[41100] VGR2991 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM1171 precursor RNA, VGAM1172 precursor RNA and VGAM1173 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR and VGAM3 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[41101] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1171 RNA, VGAM1172 RNA and VGAM1173 RNA respectively,

herein schematically represented by VGAM1 RNA, VGAM2 RNA and VGAM3 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[41102] VGAM1171 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1171 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1171 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1171 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[41103] VGAM1172 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1172 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1172 host target RNA, herein

schematically represented by VGAM2 HOST TARGET RNA into VGAM1172 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[41104] VGAM1173 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM1173 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1173 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM1173 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[41105] It is appreciated that a function of VGR2991 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2991 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2991 gene, herein designated VGR GENE, correlate with, and

may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2991 gene: VGAM1171 host target protein, VGAM1172 host target protein and VGAM1173 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1171, VGAM1172 and VGAM1173

[41106] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2992(VGR2992) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[41107] VGR2992 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2992 gene was detected is described hereinabove with reference to Figs. 6-15.

[41108] VGR2992 gene encodes VGR2992 precursor RNA, herein

designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[41109] VGR2992 precursor RNA folds spatially, forming VGR2992 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2992 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2992 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[41110] VGR2992 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM1174 precursor RNA, VGAM1175 precursor RNA and VGAM1176 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR and VGAM3 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[41111] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1174 RNA, VGAM1175 RNA and VGAM1176 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA and VGAM3 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[41112] VGAM1174 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1174 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1174 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1174 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[41113] VGAM1175 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1175 host target RNA, herein schematically represented by VGAM2

HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1175 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1175 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[41114] VGAM1176 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM1176 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1176 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM1176 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[41115] It is appreciated that a function of VGR2992 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attack-

ing a host. Accordingly, utilities of VGR2992 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2992 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2992 gene: VGAM1174 host target protein, VGAM1175 host target protein and VGAM1176 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1174, VGAM1175 and VGAM1176

[41116] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2993(VGR2993) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[41117] VGR2993 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding,

RNA viral gene. The method by which VGR2993 gene was detected is described hereinabove with reference to Figs. 6-15.

[41118] VGR2993 gene encodes VGR2993 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[41119] VGR2993 precursor RNA folds spatially, forming VGR2993 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2993 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2993 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[41120] VGR2993 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM1177 precursor RNA, VGAM1178 precursor RNA, VGAM1179 precursor RNA, VGAM1180 precursor RNA and VGAM1181 precursor RNA, herein

schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR and VGAM5 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[41121] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1177 RNA, VGAM1178 RNA, VGAM1179 RNA, VGAM1180 RNA and VGAM1181 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA and VGAM5 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[41122] VGAM1177 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1177 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1177 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1177 host target protein, herein schematically

represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[41123] VGAM1178 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1178 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1178 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1178 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[41124] VGAM1179 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM1179 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1179 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA

into VGAM1179 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[41125] VGAM1180 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM1180 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1180 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM1180 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[41126] VGAM1181 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM1181 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1181 host target RNA, herein

schematically represented by VGAM5 HOST TARGET RNA into VGAM1181 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[41127] It is appreciated that a function of VGR2993 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2993 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2993 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2993 gene: VGAM1177 host target protein, VGAM1178 host target protein, VGAM1179 host target protein, VGAM1180 host target protein and VGAM1181 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1177, VGAM1178, VGAM1179, VGAM1180 and VGAM1181

[41128] Fig. 9 further provides a conceptual description of novel

bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2994(VGR2994) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[41129] VGR2994 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2994 gene was detected is described hereinabove with reference to Figs. 6-15.

[41130] VGR2994 gene encodes VGR2994 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[41131] VGR2994 precursor RNA folds spatially, forming VGR2994 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2994 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2994 precursor RNA comprises a plurality of segments, the first half

of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[41132] VGR2994 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM1183 precursor RNA, VGAM1184 precursor RNA and VGAM1185 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR and VGAM3 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[41133] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1183 RNA, VGAM1184 RNA and VGAM1185 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA and VGAM3 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[41134] VGAM1183 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1183 host

target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1183 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1183 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[41135] VGAM1184 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1184 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1184 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1184 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[41136] VGAM1185 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding

site located in an untranslated region of VGAM1185 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1185 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM1185 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[41137] It is appreciated that a function of VGR2994 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2994 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2994 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2994 gene: VGAM1183 host target protein, VGAM1184 host target protein and VGAM1185 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through

VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1183, VGAM1184 and VGAM1185

[41138] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2995(VGR2995) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[41139] VGR2995 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2995 gene was detected is described hereinabove with reference to Figs. 6-15.

[41140] VGR2995 gene encodes VGR2995 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[41141] VGR2995 precursor RNA folds spatially, forming VGR2995 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2995 folded precursor RNA, herein designated VGR FOLDED PRECUR-

SOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2995 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[41142] VGR2995 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM1186 precursor RNA, VGAM1187 precursor RNA and VGAM1188 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR and VGAM3 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[41143] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1186 RNA, VGAM1187 RNA and VGAM1188 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA and VGAM3 RNA respectively, each of which VGAM

RNAs corresponding to VGAM RNA of Fig. 8.

[41144] VGAM1186 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1186 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1186 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1186 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[41145] VGAM1187 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1187 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1187 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1187 host target protein, herein schematically

represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[41146] VGAM1188 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM1188 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1188 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM1188 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[41147] It is appreciated that a function of VGR2995 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2995 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2995 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in

the operon-like cluster of VGR2995 gene: VGAM1186 host target protein, VGAM1187 host target protein and VGAM1188 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1186, VGAM1187 and VGAM1188

[41148] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2996(VGR2996) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[41149] VGR2996 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2996 gene was detected is described hereinabove with reference to Figs. 6-15.

[41150] VGR2996 gene encodes VGR2996 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[41151] VGR2996 precursor RNA folds spatially, forming VGR2996 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2996 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2996 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[41152] VGR2996 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM1189 precursor RNA, VGAM1190 precursor RNA and VGAM1191 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR and VGAM3 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[41153] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA

segments of about 22 nucleotides in length, VGAM1189 RNA, VGAM1190 RNA and VGAM1191 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA and VGAM3 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[41154] VGAM1189 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1189 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1189 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1189 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[41155] VGAM1190 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1190 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1190 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1190 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[41156] VGAM1191 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM1191 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1191 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM1191 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[41157] It is appreciated that a function of VGR2996 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2996 gene include diagnosis, prevention and treatment of viral infection by .

Specific functions, and accordingly utilities, of VGR2996 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2996 gene: VGAM1189 host target protein, VGAM1190 host target protein and VGAM1191 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1189, VGAM1190 and VGAM1191

[41158] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2997(VGR2997) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[41159] VGR2997 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2997 gene was detected is described hereinabove with reference to Figs.

6-15.

[41160] VGR2997 gene encodes VGR2997 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[41161] VGR2997 precursor RNA folds spatially, forming VGR2997 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2997 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2997 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[41162] VGR2997 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM1192 precursor RNA, VGAM1193 precursor RNA and VGAM1194 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR and VGAM3 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA

segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[41163] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1192 RNA, VGAM1193 RNA and VGAM1194 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA and VGAM3 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[41164] VGAM1192 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1192 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1192 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1192 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[41165] VGAM1193 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding

site located in an untranslated region of VGAM1193 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1193 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1193 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[41166] VGAM1194 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM1194 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1194 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM1194 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[41167] It is appreciated that a function of VGR2997 gene, herein

designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2997 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2997 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2997 gene: VGAM1192 host target protein, VGAM1193 host target protein and VGAM1194 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1192, VGAM1193 and VGAM1194

[41168] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2998(VGR2998) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[41169] VGR2998 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2998 gene was detected is described hereinabove with reference to Figs. 6-15.

[41170] VGR2998 gene encodes VGR2998 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[41171] VGR2998 precursor RNA folds spatially, forming VGR2998 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2998 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2998 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[41172] VGR2998 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM1195 precursor RNA, VGAM1196 pre-

cursor RNA, VGAM1197 precursor RNA and VGAM1198 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR and VGAM4 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[41173] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1195 RNA, VGAM1196 RNA, VGAM1197 RNA and VGAM1198 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA and VGAM4 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[41174] VGAM1195 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1195 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1195 host target RNA, herein

schematically represented by VGAM1 HOST TARGET RNA into VGAM1195 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[41175] VGAM1196 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1196 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1196 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1196 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[41176] VGAM1197 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM1197 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby in-

hibiting translation of VGAM1197 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM1197 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[41177] VGAM1198 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM1198 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1198 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM1198 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[41178] It is appreciated that a function of VGR2998 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2998 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2998

gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2998 gene: VGAM1195 host target protein, VGAM1196 host target protein, VGAM1197 host target protein and VGAM1198 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1195, VGAM1196, VGAM1197 and VGAM1198

[41179] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2999(VGR2999) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[41180] VGR2999 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2999 gene was detected is described hereinabove with reference to Figs.

6-15.

[41181] VGR2999 gene encodes VGR2999 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[41182] VGR2999 precursor RNA folds spatially, forming VGR2999 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2999 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR2999 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[41183] VGR2999 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM1199 precursor RNA, VGAM1200 precursor RNA, VGAM1201 precursor RNA and VGAM1202 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR and VGAM4 PRECURSOR respectively, each of

which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[41184] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1199 RNA, VGAM1200 RNA, VGAM1201 RNA and VGAM1202 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA and VGAM4 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[41185] VGAM1199 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1199 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1199 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1199 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[41186] VGAM1200 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1200 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1200 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1200 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[41187] VGAM1201 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM1201 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1201 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM1201 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of

Fig. 1.

[41188] VGAM1202 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM1202 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1202 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM1202 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[41189] It is appreciated that a function of VGR2999 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2999 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR2999 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR2999 gene: VGAM1199

host target protein, VGAM1200 host target protein, VGAM1201 host target protein and VGAM1202 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1199, VGAM1200, VGAM1201 and VGAM1202

[41190] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3000(VGR3000) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[41191] VGR3000 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3000 gene was detected is described hereinabove with reference to Figs. 6-15.

[41192] VGR3000 gene encodes VGR3000 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[41193] VGR3000 precursor RNA folds spatially, forming VGR3000 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3000 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR3000 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[41194] VGR3000 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM1203 precursor RNA, VGAM1204 precursor RNA and VGAM1205 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR and VGAM3 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[41195] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA

segments of about 22 nucleotides in length, VGAM1203 RNA, VGAM1204 RNA and VGAM1205 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA and VGAM3 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[41196] VGAM1203 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1203 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1203 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1203 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[41197] VGAM1204 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1204 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1204 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1204 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[41198] VGAM1205 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM1205 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1205 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM1205 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[41199] It is appreciated that a function of VGR3000 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3000 gene include diagnosis, prevention and treatment of viral infection by .

Specific functions, and accordingly utilities, of VGR3000 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR3000 gene: VGAM1203 host target protein, VGAM1204 host target protein and VGAM1205 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1203, VGAM1204 and VGAM1205

[41200] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3001(VGR3001) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[41201] VGR3001 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3001 gene was detected is described hereinabove with reference to Figs.

6-15.

[41202] VGR3001 gene encodes VGR3001 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[41203] VGR3001 precursor RNA folds spatially, forming VGR3001 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3001 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR3001 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[41204] VGR3001 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM1206 precursor RNA, VGAM1207 precursor RNA, VGAM1208 precursor RNA and VGAM1209 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR and VGAM4 PRECURSOR respectively, each of

which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[41205] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1206 RNA, VGAM1207 RNA, VGAM1208 RNA and VGAM1209 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA and VGAM4 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[41206] VGAM1206 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1206 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1206 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1206 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[41207] VGAM1207 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1207 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1207 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1207 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[41208] VGAM1208 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM1208 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1208 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM1208 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of

Fig. 1.

[41209] VGAM1209 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM1209 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1209 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM1209 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[41210] It is appreciated that a function of VGR3001 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3001 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR3001 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR3001 gene: VGAM1206

host target protein, VGAM1207 host target protein, VGAM1208 host target protein and VGAM1209 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1206, VGAM1207, VGAM1208 and VGAM1209

[41211] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3002(VGR3002) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[41212] VGR3002 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3002 gene was detected is described hereinabove with reference to Figs. 6-15.

[41213] VGR3002 gene encodes VGR3002 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[41214] VGR3002 precursor RNA folds spatially, forming VGR3002 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3002 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR3002 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[41215] VGR3002 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM1210 precursor RNA, VGAM1211 precursor RNA and VGAM1212 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR and VGAM3 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[41216] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA

segments of about 22 nucleotides in length, VGAM1210 RNA, VGAM1211 RNA and VGAM1212 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA and VGAM3 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[41217] VGAM1210 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1210 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1210 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1210 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[41218] VGAM1211 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1211 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1211 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1211 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[41219] VGAM1212 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM1212 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1212 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM1212 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[41220] It is appreciated that a function of VGR3002 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3002 gene include diagnosis, prevention and treatment of viral infection by .

Specific functions, and accordingly utilities, of VGR3002 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR3002 gene: VGAM1210 host target protein, VGAM1211 host target protein and VGAM1212 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1210, VGAM1211 and VGAM1212

[41221] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3003(VGR3003) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[41222] VGR3003 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3003 gene was detected is described hereinabove with reference to Figs.

6-15.

[41223] VGR3003 gene encodes VGR3003 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[41224] VGR3003 precursor RNA folds spatially, forming VGR3003 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3003 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR3003 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[41225] VGR3003 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM1214 precursor RNA, VGAM1215 precursor RNA, VGAM1216 precursor RNA and VGAM1217 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR and VGAM4 PRECURSOR respectively, each of

which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[41226] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1214 RNA, VGAM1215 RNA, VGAM1216 RNA and VGAM1217 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA and VGAM4 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[41227] VGAM1214 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1214 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1214 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1214 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[41228] VGAM1215 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1215 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1215 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1215 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[41229] VGAM1216 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM1216 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1216 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM1216 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of

Fig. 1.

[41230] VGAM1217 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM1217 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1217 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM1217 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[41231] It is appreciated that a function of VGR3003 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3003 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR3003 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR3003 gene: VGAM1214

host target protein, VGAM1215 host target protein, VGAM1216 host target protein and VGAM1217 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1214, VGAM1215, VGAM1216 and VGAM1217

[41232] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3004(VGR3004) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[41233] VGR3004 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3004 gene was detected is described hereinabove with reference to Figs. 6-15.

[41234] VGR3004 gene encodes VGR3004 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[41235] VGR3004 precursor RNA folds spatially, forming VGR3004 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3004 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR3004 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[41236] VGR3004 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM1218 precursor RNA and VGAM1219 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[41237] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1218

RNA and VGAM1219 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[41238] VGAM1218 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1218 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1218 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1218 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[41239] VGAM1219 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1219 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby in-

hibiting translation of VGAM1219 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1219 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[41240] It is appreciated that a function of VGR3004 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3004 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR3004 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR3004 gene: VGAM1218 host target protein and VGAM1219 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1218 and VGAM1219

[41241] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3005(VGR3005) viral

gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[41242] VGR3005 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3005 gene was detected is described hereinabove with reference to Figs. 6-15.

[41243] VGR3005 gene encodes VGR3005 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[41244] VGR3005 precursor RNA folds spatially, forming VGR3005 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3005 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR3005 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the

second half thereof, as is well known in the art.

[41245] VGR3005 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM1220 precursor RNA, VGAM1221 precursor RNA and VGAM1222 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR and VGAM3 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[41246] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1220 RNA, VGAM1221 RNA and VGAM1222 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA and VGAM3 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[41247] VGAM1220 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1220 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corre-

sponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1220 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1220 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[41248] VGAM1221 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1221 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1221 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1221 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[41249] VGAM1222 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM1222 host target RNA, herein schematically represented by VGAM3

HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1222 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM1222 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[41250] It is appreciated that a function of VGR3005 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3005 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR3005 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR3005 gene: VGAM1220 host target protein, VGAM1221 host target protein and VGAM1222 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with

reference to VGAM1220, VGAM1221 and VGAM1222

[41251] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3006(VGR3006) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[41252] VGR3006 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3006 gene was detected is described hereinabove with reference to Figs. 6-15.

[41253] VGR3006 gene encodes VGR3006 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[41254] VGR3006 precursor RNA folds spatially, forming VGR3006 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3006 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to

the fact that the nucleotide sequence of VGR3006 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[41255] VGR3006 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM1223 precursor RNA and VGAM1224 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[41256] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1223 RNA and VGAM1224 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[41257] VGAM1223 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding

site located in an untranslated region of VGAM1223 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1223 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1223 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[41258] VGAM1224 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1224 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1224 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1224 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[41259] It is appreciated that a function of VGR3006 gene, herein

designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3006 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR3006 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR3006 gene: VGAM1223 host target protein and VGAM1224 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1223 and VGAM1224

[41260] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3007(VGR3007) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[41261] VGR3007 gene, herein designated VGR GENE, is a novel

bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3007 gene was detected is described hereinabove with reference to Figs. 6-15.

[41262] VGR3007 gene encodes VGR3007 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[41263] VGR3007 precursor RNA folds spatially, forming VGR3007 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3007 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR3007 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[41264] VGR3007 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM1226 precursor RNA, VGAM1227 precursor RNA, VGAM1228 precursor RNA and VGAM1229

precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR and VGAM4 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[41265] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1226 RNA, VGAM1227 RNA, VGAM1228 RNA and VGAM1229 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA and VGAM4 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[41266] VGAM1226 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1226 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1226 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA

into VGAM1226 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[41267] VGAM1227 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1227 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1227 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1227 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[41268] VGAM1228 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM1228 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1228 host target RNA, herein

schematically represented by VGAM3 HOST TARGET RNA into VGAM1228 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[41269] VGAM1229 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM1229 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1229 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM1229 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[41270] It is appreciated that a function of VGR3007 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3007 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR3007 gene, herein designated VGR GENE, correlate with, and

may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR3007 gene: VGAM1226 host target protein, VGAM1227 host target protein, VGAM1228 host target protein and VGAM1229 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1226, VGAM1227, VGAM1228 and VGAM1229

[41271] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3008(VGR3008) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[41272] VGR3008 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3008 gene was detected is described hereinabove with reference to Figs. 6-15.

[41273] VGR3008 gene encodes VGR3008 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[41274] VGR3008 precursor RNA folds spatially, forming VGR3008 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3008 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR3008 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[41275] VGR3008 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM1230 precursor RNA, VGAM1231 precursor RNA, VGAM1232 precursor RNA, VGAM1233 precursor RNA and VGAM1234 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR and VGAM5 PRECURSOR respectively, each of which VGAM

precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[41276] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1230 RNA, VGAM1231 RNA, VGAM1232 RNA, VGAM1233 RNA and VGAM1234 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA and VGAM5 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[41277] VGAM1230 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1230 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1230 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1230 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[41278] VGAM1231 RNA, herein schematically represented by

VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1231 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1231 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1231 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[41279] VGAM1232 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM1232 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1232 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM1232 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[41280] VGAM1233 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM1233 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1233 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM1233 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[41281] VGAM1234 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM1234 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1234 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM1234 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of

Fig. 1.

[41282] It is appreciated that a function of VGR3008 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3008 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR3008 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR3008 gene: VGAM1230 host target protein, VGAM1231 host target protein, VGAM1232 host target protein, VGAM1233 host target protein and VGAM1234 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1230, VGAM1231, VGAM1232, VGAM1233 and VGAM1234

[41283] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3009(VGR3009) viral gene, which encodes an operon-like cluster of novel viral

micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[41284] VGR3009 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3009 gene was detected is described hereinabove with reference to Figs. 6-15.

[41285] VGR3009 gene encodes VGR3009 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[41286] VGR3009 precursor RNA folds spatially, forming VGR3009 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3009 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR3009 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[41287] VGR3009 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 6 separate VGAM precursor RNAs, VGAM1235 precursor RNA, VGAM1236 precursor RNA, VGAM1237 precursor RNA, VGAM1238 precursor RNA, VGAM1239 precursor RNA and VGAM1240 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR, VGAM5 PRECURSOR and VGAM6 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[41288] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1235 RNA, VGAM1236 RNA, VGAM1237 RNA, VGAM1238 RNA, VGAM1239 RNA and VGAM1240 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA, VGAM5 RNA and VGAM6 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[41289] VGAM1235 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding

site located in an untranslated region of VGAM1235 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1235 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1235 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[41290] VGAM1236 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1236 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1236 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1236 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[41291] VGAM1237 RNA, herein schematically represented by

VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM1237 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1237 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM1237 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[41292] VGAM1238 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM1238 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1238 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM1238 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[41293] VGAM1239 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM1239 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1239 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM1239 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[41294] VGAM1240 RNA, herein schematically represented by VGAM6 binds complimentarily to a host target binding site located in an untranslated region of VGAM1240 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1240 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA into VGAM1240 host target protein, herein schematically represented by VGAM6 HOST TARGET PROTEIN, both of

Fig. 1.

[41295] It is appreciated that a function of VGR3009 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3009 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR3009 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR3009 gene: VGAM1235 host target protein, VGAM1236 host target protein, VGAM1237 host target protein, VGAM1238 host target protein, VGAM1239 host target protein and VGAM1240 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1235, VGAM1236, VGAM1237, VGAM1238, VGAM1239 and VGAM1240

[41296] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3010(VGR3010) viral

gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[41297] VGR3010 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3010 gene was detected is described hereinabove with reference to Figs. 6-15.

[41298] VGR3010 gene encodes VGR3010 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[41299] VGR3010 precursor RNA folds spatially, forming VGR3010 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3010 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR3010 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the

second half thereof, as is well known in the art.

[41300] VGR3010 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM1241 precursor RNA and VGAM1242 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[41301] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1241 RNA and VGAM1242 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[41302] VGAM1241 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1241 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1241 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1241 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[41303] VGAM1242 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1242 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1242 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1242 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[41304] It is appreciated that a function of VGR3010 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3010 gene include diagnosis, prevention and treatment of viral infection by .

Specific functions, and accordingly utilities, of VGR3010 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR3010 gene: VGAM1241 host target protein and VGAM1242 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1241 and VGAM1242

[41305] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3011(VGR3011) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[41306] VGR3011 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3011 gene was detected is described hereinabove with reference to Figs. 6-15.

[41307] VGR3011 gene encodes VGR3011 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[41308] VGR3011 precursor RNA folds spatially, forming VGR3011 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3011 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR3011 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[41309] VGR3011 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM1243 precursor RNA, VGAM1244 precursor RNA, VGAM1245 precursor RNA and VGAM1246 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR and VGAM4 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA

segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[41310] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1243 RNA, VGAM1244 RNA, VGAM1245 RNA and VGAM1246 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA and VGAM4 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[41311] VGAM1243 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1243 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1243 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1243 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[41312] VGAM1244 RNA, herein schematically represented by

VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1244 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1244 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1244 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[41313] VGAM1245 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM1245 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1245 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM1245 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[41314] VGAM1246 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM1246 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1246 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM1246 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[41315] It is appreciated that a function of VGR3011 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3011 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR3011 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR3011 gene: VGAM1243 host target protein, VGAM1244 host target protein,

VGAM1245 host target protein and VGAM1246 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1243, VGAM1244, VGAM1245 and VGAM1246

[41316] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3012(VGR3012) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[41317] VGR3012 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3012 gene was detected is described hereinabove with reference to Figs. 6-15.

[41318] VGR3012 gene encodes VGR3012 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[41319] VGR3012 precursor RNA folds spatially, forming VGR3012

folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3012 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR3012 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[41320] VGR3012 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM1247 precursor RNA, VGAM1248 precursor RNA, VGAM1249 precursor RNA, VGAM1250 precursor RNA and VGAM1251 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR and VGAM5 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[41321] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA

segments of about 22 nucleotides in length, VGAM1247 RNA, VGAM1248 RNA, VGAM1249 RNA, VGAM1250 RNA and VGAM1251 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA and VGAM5 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[41322] VGAM1247 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1247 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1247 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1247 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[41323] VGAM1248 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1248 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corre-

sponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1248 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1248 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[41324] VGAM1249 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM1249 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1249 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM1249 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[41325] VGAM1250 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM1250 host target RNA, herein schematically represented by VGAM4

HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1250 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM1250 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[41326] VGAM1251 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM1251 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1251 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM1251 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[41327] It is appreciated that a function of VGR3012 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attack-

ing a host. Accordingly, utilities of VGR3012 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR3012 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR3012 gene: VGAM1247 host target protein, VGAM1248 host target protein, VGAM1249 host target protein, VGAM1250 host target protein and VGAM1251 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1247, VGAM1248, VGAM1249, VGAM1250 and VGAM1251

[41328] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3013(VGR3013) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[41329] VGR3013 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3013 gene was detected is described hereinabove with reference to Figs. 6-15.

[41330] VGR3013 gene encodes VGR3013 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[41331] VGR3013 precursor RNA folds spatially, forming VGR3013 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3013 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR3013 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[41332] VGR3013 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM1252 precursor RNA, VGAM1253 pre-

cursor RNA, VGAM1254 precursor RNA, VGAM1255 precursor RNA and VGAM1256 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR and VGAM5 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[41333] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1252 RNA, VGAM1253 RNA, VGAM1254 RNA, VGAM1255 RNA and VGAM1256 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA and VGAM5 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[41334] VGAM1252 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1252 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1252 host target RNA, herein

schematically represented by VGAM1 HOST TARGET RNA into VGAM1252 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[41335] VGAM1253 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1253 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1253 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1253 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[41336] VGAM1254 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM1254 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby in-

hibiting translation of VGAM1254 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM1254 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[41337] VGAM1255 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM1255 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1255 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM1255 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[41338] VGAM1256 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM1256 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1256 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM1256 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[41339] It is appreciated that a function of VGR3013 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3013 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR3013 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR3013 gene: VGAM1252 host target protein, VGAM1253 host target protein, VGAM1254 host target protein, VGAM1255 host target protein and VGAM1256 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1252, VGAM1253,

VGAM1254, VGAM1255 and VGAM1256

[41340] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3014(VGR3014) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[41341] VGR3014 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3014 gene was detected is described hereinabove with reference to Figs. 6-15.

[41342] VGR3014 gene encodes VGR3014 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[41343] VGR3014 precursor RNA folds spatially, forming VGR3014 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3014 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to

the fact that the nucleotide sequence of VGR3014 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[41344] VGR3014 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM1257 precursor RNA and VGAM1258 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[41345] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1257 RNA and VGAM1258 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[41346] VGAM1257 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding

site located in an untranslated region of VGAM1257 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1257 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1257 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[41347] VGAM1258 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1258 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1258 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1258 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[41348] It is appreciated that a function of VGR3014 gene, herein

designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3014 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR3014 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR3014 gene: VGAM1257 host target protein and VGAM1258 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1257 and VGAM1258

[41349] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3015(VGR3015) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[41350] VGR3015 gene, herein designated VGR GENE, is a novel

bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3015 gene was detected is described hereinabove with reference to Figs. 6-15.

[41351] VGR3015 gene encodes VGR3015 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[41352] VGR3015 precursor RNA folds spatially, forming VGR3015 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3015 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR3015 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[41353] VGR3015 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM1259 precursor RNA, VGAM1260 precursor RNA, VGAM1261 precursor RNA and VGAM1262

precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR and VGAM4 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[41354] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1259 RNA, VGAM1260 RNA, VGAM1261 RNA and VGAM1262 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA and VGAM4 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[41355] VGAM1259 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1259 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1259 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA

into VGAM1259 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[41356] VGAM1260 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1260 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1260 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1260 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[41357] VGAM1261 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM1261 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1261 host target RNA, herein

schematically represented by VGAM3 HOST TARGET RNA into VGAM1261 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[41358] VGAM1262 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM1262 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1262 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM1262 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[41359] It is appreciated that a function of VGR3015 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3015 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR3015 gene, herein designated VGR GENE, correlate with, and

may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR3015 gene: VGAM1259 host target protein, VGAM1260 host target protein, VGAM1261 host target protein and VGAM1262 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1259, VGAM1260, VGAM1261 and VGAM1262

[41360] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3016(VGR3016) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[41361] VGR3016 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3016 gene was detected is described hereinabove with reference to Figs. 6-15.

[41362] VGR3016 gene encodes VGR3016 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[41363] VGR3016 precursor RNA folds spatially, forming VGR3016 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3016 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR3016 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[41364] VGR3016 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM1263 precursor RNA, VGAM1264 precursor RNA, VGAM1265 precursor RNA, VGAM1266 precursor RNA and VGAM1267 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR and VGAM5 PRECURSOR respectively, each of which VGAM

precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[41365] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1263 RNA, VGAM1264 RNA, VGAM1265 RNA, VGAM1266 RNA and VGAM1267 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA and VGAM5 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[41366] VGAM1263 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1263 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1263 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1263 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[41367] VGAM1264 RNA, herein schematically represented by

VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1264 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1264 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1264 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[41368] VGAM1265 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM1265 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1265 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM1265 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[41369] VGAM1266 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM1266 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1266 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM1266 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[41370] VGAM1267 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM1267 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1267 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM1267 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of

Fig. 1.

[41371] It is appreciated that a function of VGR3016 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3016 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR3016 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR3016 gene: VGAM1263 host target protein, VGAM1264 host target protein, VGAM1265 host target protein, VGAM1266 host target protein and VGAM1267 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1263, VGAM1264, VGAM1265, VGAM1266 and VGAM1267

[41372] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3017(VGR3017) viral gene, which encodes an operon-like cluster of novel viral

micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[41373] VGR3017 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3017 gene was detected is described hereinabove with reference to Figs. 6-15.

[41374] VGR3017 gene encodes VGR3017 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[41375] VGR3017 precursor RNA folds spatially, forming VGR3017 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3017 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR3017 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[41376] VGR3017 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM1268 precursor RNA, VGAM1269 precursor RNA, VGAM1270 precursor RNA, VGAM1271 precursor RNA and VGAM1272 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR and VGAM5 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[41377] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1268 RNA, VGAM1269 RNA, VGAM1270 RNA, VGAM1271 RNA and VGAM1272 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA and VGAM5 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[41378] VGAM1268 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1268 host target RNA, herein schematically represented by VGAM1

HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1268 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1268 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[41379] VGAM1269 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1269 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1269 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1269 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[41380] VGAM1270 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM1270 host

target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1270 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM1270 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[41381] VGAM1271 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM1271 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1271 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM1271 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[41382] VGAM1272 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding

site located in an untranslated region of VGAM1272 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1272 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM1272 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[41383] It is appreciated that a function of VGR3017 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3017 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR3017 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR3017 gene: VGAM1268 host target protein, VGAM1269 host target protein, VGAM1270 host target protein, VGAM1271 host target protein and VGAM1272 host target protein, herein

schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1268, VGAM1269, VGAM1270, VGAM1271 and VGAM1272

[41384] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3018(VGR3018) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[41385] VGR3018 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3018 gene was detected is described hereinabove with reference to Figs. 6-15.

[41386] VGR3018 gene encodes VGR3018 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[41387] VGR3018 precursor RNA folds spatially, forming VGR3018 folded precursor RNA, herein designated VGR FOLDED

PRECURSOR RNA. It is appreciated that VGR3018 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR3018 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[41388] VGR3018 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM1273 precursor RNA, VGAM1274 precursor RNA, VGAM1275 precursor RNA and VGAM1276 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR and VGAM4 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[41389] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1273

RNA, VGAM1274 RNA, VGAM1275 RNA and VGAM1276 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA and VGAM4 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[41390] VGAM1273 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1273 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1273 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1273 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[41391] VGAM1274 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1274 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1274 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1274 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[41392] VGAM1275 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM1275 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1275 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM1275 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[41393] VGAM1276 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM1276 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corre-

sponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1276 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM1276 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[41394] It is appreciated that a function of VGR3018 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3018 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR3018 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR3018 gene: VGAM1273 host target protein, VGAM1274 host target protein, VGAM1275 host target protein and VGAM1276 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1273,

VGAM1274, VGAM1275 and VGAM1276

[41395] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3019(VGR3019) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[41396] VGR3019 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3019 gene was detected is described hereinabove with reference to Figs. 6-15.

[41397] VGR3019 gene encodes VGR3019 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[41398] VGR3019 precursor RNA folds spatially, forming VGR3019 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3019 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to

the fact that the nucleotide sequence of VGR3019 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[41399] VGR3019 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM1277 precursor RNA, VGAM1278 precursor RNA, VGAM1279 precursor RNA and VGAM1280 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR and VGAM4 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[41400] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1277 RNA, VGAM1278 RNA, VGAM1279 RNA and VGAM1280 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA and VGAM4 RNA respectively, each of which VGAM RNAs corresponding to

VGAM RNA of Fig. 8.

[41401] VGAM1277 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1277 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1277 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1277 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[41402] VGAM1278 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1278 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1278 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1278 host target protein, herein schematically

represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[41403] VGAM1279 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM1279 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1279 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM1279 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[41404] VGAM1280 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM1280 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1280 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA

into VGAM1280 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[41405] It is appreciated that a function of VGR3019 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3019 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR3019 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR3019 gene: VGAM1277 host target protein, VGAM1278 host target protein, VGAM1279 host target protein and VGAM1280 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1277, VGAM1278, VGAM1279 and VGAM1280

[41406] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3020(VGR3020) viral

gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[41407] VGR3020 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3020 gene was detected is described hereinabove with reference to Figs. 6-15.

[41408] VGR3020 gene encodes VGR3020 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[41409] VGR3020 precursor RNA folds spatially, forming VGR3020 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3020 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR3020 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the

second half thereof, as is well known in the art.

[41410] VGR3020 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 7 separate VGAM precursor RNAs, VGAM1281 precursor RNA, VGAM1282 precursor RNA, VGAM1283 precursor RNA, VGAM1284 precursor RNA, VGAM1285 precursor RNA, VGAM1286 precursor RNA and VGAM1287 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR, VGAM5 PRECURSOR, VGAM6 PRECURSOR and VGAM7 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[41411] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1281 RNA, VGAM1282 RNA, VGAM1283 RNA, VGAM1284 RNA, VGAM1285 RNA, VGAM1286 RNA and VGAM1287 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA, VGAM5 RNA, VGAM6 RNA and VGAM7 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[41412] VGAM1281 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1281 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1281 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1281 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[41413] VGAM1282 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1282 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1282 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1282 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of

Fig. 1.

[41414] VGAM1283 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM1283 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1283 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM1283 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[41415] VGAM1284 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM1284 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1284 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM1284 host target protein, herein schematically

represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[41416] VGAM1285 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM1285 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1285 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM1285 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[41417] VGAM1286 RNA, herein schematically represented by VGAM6 binds complimentarily to a host target binding site located in an untranslated region of VGAM1286 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1286 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA

into VGAM1286 host target protein, herein schematically represented by VGAM6 HOST TARGET PROTEIN, both of Fig. 1.

[41418] VGAM1287 RNA, herein schematically represented by VGAM7 binds complimentarily to a host target binding site located in an untranslated region of VGAM1287 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1287 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA into VGAM1287 host target protein, herein schematically represented by VGAM7 HOST TARGET PROTEIN, both of Fig. 1.

[41419] It is appreciated that a function of VGR3020 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3020 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR3020 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target

genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR3020 gene: VGAM1281 host target protein, VGAM1282 host target protein, VGAM1283 host target protein, VGAM1284 host target protein, VGAM1285 host target protein, VGAM1286 host target protein and VGAM1287 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1281, VGAM1282, VGAM1283, VGAM1284, VGAM1285, VGAM1286 and VGAM1287

[41420] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3021(VGR3021) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[41421] VGR3021 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3021 gene was

detected is described hereinabove with reference to Figs. 6-15.

[41422] VGR3021 gene encodes VGR3021 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[41423] VGR3021 precursor RNA folds spatially, forming VGR3021 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3021 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR3021 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[41424] VGR3021 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM1288 precursor RNA and VGAM1289 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin

shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[41425] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1288 RNA and VGAM1289 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[41426] VGAM1288 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1288 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1288 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1288 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[41427] VGAM1289 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding

site located in an untranslated region of VGAM1289 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1289 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1289 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[41428] It is appreciated that a function of VGR3021 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3021 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR3021 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR3021 gene: VGAM1288 host target protein and VGAM1289 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN andVGAM HOST TARGET PROTEIN respectively.

The function of these host target genes is elaborated hereinabove with reference to VGAM1288 and VGAM1289

[41429] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3022(VGR3022) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[41430] VGR3022 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3022 gene was detected is described hereinabove with reference to Figs. 6-15.

[41431] VGR3022 gene encodes VGR3022 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[41432] VGR3022 precursor RNA folds spatially, forming VGR3022 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3022 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art

as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR3022 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[41433] VGR3022 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM1291 precursor RNA, VGAM1292 precursor RNA and VGAM1293 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR and VGAM3 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[41434] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1291 RNA, VGAM1292 RNA and VGAM1293 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA and VGAM3 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[41435] VGAM1291 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1291 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1291 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1291 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[41436] VGAM1292 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1292 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1292 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1292 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of

Fig. 1.

[41437] VGAM1293 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM1293 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1293 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM1293 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[41438] It is appreciated that a function of VGR3022 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3022 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR3022 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR3022 gene: VGAM1291

host target protein, VGAM1292 host target protein and VGAM1293 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1291, VGAM1292 and VGAM1293

[41439] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3023(VGR3023) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[41440] VGR3023 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3023 gene was detected is described hereinabove with reference to Figs. 6-15.

[41441] VGR3023 gene encodes VGR3023 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[41442] VGR3023 precursor RNA folds spatially, forming VGR3023

folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3023 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR3023 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[41443] VGR3023 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM1294 precursor RNA, VGAM1295 precursor RNA and VGAM1296 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR and VGAM3 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[41444] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1294

RNA, VGAM1295 RNA and VGAM1296 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA and VGAM3 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[41445] VGAM1294 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1294 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1294 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1294 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[41446] VGAM1295 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1295 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby in-

hibiting translation of VGAM1295 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1295 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[41447] VGAM1296 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM1296 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1296 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM1296 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[41448] It is appreciated that a function of VGR3023 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3023 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR3023

gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR3023 gene: VGAM1294 host target protein, VGAM1295 host target protein and VGAM1296 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1294, VGAM1295 and VGAM1296

[41449] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3024(VGR3024) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[41450] VGR3024 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3024 gene was detected is described hereinabove with reference to Figs. 6-15.

[41451] VGR3024 gene encodes VGR3024 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[41452] VGR3024 precursor RNA folds spatially, forming VGR3024 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3024 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR3024 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[41453] VGR3024 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM1297 precursor RNA, VGAM1298 precursor RNA, VGAM1299 precursor RNA, VGAM1300 precursor RNA and VGAM1301 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR and VGAM5 PRECURSOR respectively, each of which VGAM

precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[41454] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1297 RNA, VGAM1298 RNA, VGAM1299 RNA, VGAM1300 RNA and VGAM1301 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA and VGAM5 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[41455] VGAM1297 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1297 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1297 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1297 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[41456] VGAM1298 RNA, herein schematically represented by

VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1298 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1298 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1298 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[41457] VGAM1299 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM1299 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1299 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM1299 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[41458] VGAM1300 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM1300 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1300 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM1300 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[41459] VGAM1301 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM1301 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1301 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM1301 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of

Fig. 1.

[41460] It is appreciated that a function of VGR3024 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3024 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR3024 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR3024 gene: VGAM1297 host target protein, VGAM1298 host target protein, VGAM1299 host target protein, VGAM1300 host target protein and VGAM1301 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1297, VGAM1298, VGAM1299, VGAM1300 and VGAM1301

[41461] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3025(VGR3025) viral gene, which encodes an operon-like cluster of novel viral

micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[41462] VGR3025 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3025 gene was detected is described hereinabove with reference to Figs. 6-15.

[41463] VGR3025 gene encodes VGR3025 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[41464] VGR3025 precursor RNA folds spatially, forming VGR3025 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3025 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR3025 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[41465] VGR3025 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM1302 precursor RNA, VGAM1303 precursor RNA and VGAM1304 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR and VGAM3 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[41466] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1302 RNA, VGAM1303 RNA and VGAM1304 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA and VGAM3 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[41467] VGAM1302 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1302 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1302 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1302 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[41468] VGAM1303 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1303 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1303 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1303 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[41469] VGAM1304 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM1304 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corre-

sponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1304 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM1304 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[41470] It is appreciated that a function of VGR3025 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3025 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR3025 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR3025 gene: VGAM1302 host target protein, VGAM1303 host target protein and VGAM1304 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1302, VGAM1303 and VGAM1304

[41471] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3026(VGR3026) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[41472] VGR3026 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3026 gene was detected is described hereinabove with reference to Figs. 6-15.

[41473] VGR3026 gene encodes VGR3026 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[41474] VGR3026 precursor RNA folds spatially, forming VGR3026 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3026 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR3026 precur-

sor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[41475] VGR3026 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM1305 precursor RNA, VGAM1306 precursor RNA, VGAM1307 precursor RNA and VGAM1308 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR and VGAM4 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[41476] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1305 RNA, VGAM1306 RNA, VGAM1307 RNA and VGAM1308 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA and VGAM4 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[41477] VGAM1305 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1305 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1305 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1305 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[41478] VGAM1306 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1306 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1306 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1306 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of

Fig. 1.

[41479] VGAM1307 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM1307 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1307 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM1307 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[41480] VGAM1308 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM1308 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1308 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM1308 host target protein, herein schematically

represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[41481] It is appreciated that a function of VGR3026 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3026 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR3026 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR3026 gene: VGAM1305 host target protein, VGAM1306 host target protein, VGAM1307 host target protein and VGAM1308 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1305, VGAM1306, VGAM1307 and VGAM1308

[41482] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3027(VGR3027) viral gene, which encodes an operon-like cluster of novel viral

micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[41483] VGR3027 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3027 gene was detected is described hereinabove with reference to Figs. 6-15.

[41484] VGR3027 gene encodes VGR3027 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[41485] VGR3027 precursor RNA folds spatially, forming VGR3027 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3027 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR3027 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[41486] VGR3027 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM1309 precursor RNA and VGAM1310 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[41487] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1309 RNA and VGAM1310 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[41488] VGAM1309 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1309 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby in-

hibiting translation of VGAM1309 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1309 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[41489] VGAM1310 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1310 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1310 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1310 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[41490] It is appreciated that a function of VGR3027 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3027 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR3027

gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR3027 gene: VGAM1309 host target protein and VGAM1310 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1309 and VGAM1310

[41491] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3028(VGR3028) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[41492] VGR3028 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3028 gene was detected is described hereinabove with reference to Figs. 6-15.

[41493] VGR3028 gene encodes VGR3028 precursor RNA, herein

designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[41494] VGR3028 precursor RNA folds spatially, forming VGR3028 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3028 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR3028 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[41495] VGR3028 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 6 separate VGAM precursor RNAs, VGAM1311 precursor RNA, VGAM1312 precursor RNA, VGAM1313 precursor RNA, VGAM1314 precursor RNA, VGAM1315 precursor RNA and VGAM1316 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR, VGAM5 PRECURSOR and VGAM6 PRECURSOR respectively, each of which VGAM

precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[41496] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1311 RNA, VGAM1312 RNA, VGAM1313 RNA, VGAM1314 RNA, VGAM1315 RNA and VGAM1316 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA, VGAM5 RNA and VGAM6 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[41497] VGAM1311 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1311 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1311 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1311 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[41498] VGAM1312 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1312 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1312 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1312 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[41499] VGAM1313 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM1313 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1313 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM1313 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of

Fig. 1.

[41500] VGAM1314 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM1314 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1314 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM1314 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[41501] VGAM1315 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM1315 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1315 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM1315 host target protein, herein schematically

represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[41502] VGAM1316 RNA, herein schematically represented by VGAM6 binds complimentarily to a host target binding site located in an untranslated region of VGAM1316 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1316 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA into VGAM1316 host target protein, herein schematically represented by VGAM6 HOST TARGET PROTEIN, both of Fig. 1.

[41503] It is appreciated that a function of VGR3028 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3028 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR3028 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in

the operon-like cluster of VGR3028 gene: VGAM1311 host target protein, VGAM1312 host target protein, VGAM1313 host target protein, VGAM1314 host target protein, VGAM1315 host target protein and VGAM1316 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1311, VGAM1312, VGAM1313, VGAM1314, VGAM1315 and VGAM1316

[41504] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3029(VGR3029) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[41505] VGR3029 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3029 gene was detected is described hereinabove with reference to Figs. 6-15.

[41506] VGR3029 gene encodes VGR3029 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[41507] VGR3029 precursor RNA folds spatially, forming VGR3029 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3029 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR3029 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[41508] VGR3029 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM1317 precursor RNA, VGAM1318 precursor RNA and VGAM1319 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR and VGAM3 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig.

8.

[41509] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1317 RNA, VGAM1318 RNA and VGAM1319 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA and VGAM3 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[41510] VGAM1317 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1317 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1317 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1317 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[41511] VGAM1318 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1318 host

target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1318 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1318 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[41512] VGAM1319 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM1319 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1319 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM1319 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[41513] It is appreciated that a function of VGR3029 gene, herein designated VGR GENE, is inhibition of expression of host

target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3029 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR3029 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR3029 gene: VGAM1317 host target protein, VGAM1318 host target protein and VGAM1319 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1317, VGAM1318 and VGAM1319

[41514] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3030(VGR3030) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[41515] VGR3030 gene, herein designated VGR GENE, is a novel

bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3030 gene was detected is described hereinabove with reference to Figs. 6-15.

[41516] VGR3030 gene encodes VGR3030 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[41517] VGR3030 precursor RNA folds spatially, forming VGR3030 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3030 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR3030 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[41518] VGR3030 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM1320 precursor RNA and VGAM1321 precursor RNA, herein schematically represented by

VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[41519] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1320 RNA and VGAM1321 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[41520] VGAM1320 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1320 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1320 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1320 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[41521] VGAM1321 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1321 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1321 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1321 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[41522] It is appreciated that a function of VGR3030 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3030 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR3030 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR3030 gene: VGAM1320 host target protein and VGAM1321 host target protein,

herein schematically represented by VGAM1 HOST TARGET PROTEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1320 and VGAM1321

[41523] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3031(VGR3031) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[41524] VGR3031 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3031 gene was detected is described hereinabove with reference to Figs. 6-15.

[41525] VGR3031 gene encodes VGR3031 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[41526] VGR3031 precursor RNA folds spatially, forming VGR3031 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3031 folded

precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR3031 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[41527] VGR3031 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM1322 precursor RNA, VGAM1323 precursor RNA, VGAM1324 precursor RNA and VGAM1325 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR and VGAM4 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[41528] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1322 RNA, VGAM1323 RNA, VGAM1324 RNA and VGAM1325

RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA and VGAM4 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[41529] VGAM1322 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1322 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1322 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1322 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[41530] VGAM1323 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1323 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby in-

hibiting translation of VGAM1323 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1323 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[41531] VGAM1324 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM1324 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1324 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM1324 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[41532] VGAM1325 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM1325 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1325 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM1325 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[41533] It is appreciated that a function of VGR3031 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3031 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR3031 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR3031 gene: VGAM1322 host target protein, VGAM1323 host target protein, VGAM1324 host target protein and VGAM1325 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1322, VGAM1323, VGAM1324 and VGAM1325

[41534] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3032(VGR3032) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[41535] VGR3032 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3032 gene was detected is described hereinabove with reference to Figs. 6-15.

[41536] VGR3032 gene encodes VGR3032 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[41537] VGR3032 precursor RNA folds spatially, forming VGR3032 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3032 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR3032 precur-

sor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[41538] VGR3032 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM1326 precursor RNA, VGAM1327 precursor RNA and VGAM1328 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR and VGAM3 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[41539] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1326 RNA, VGAM1327 RNA and VGAM1328 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA and VGAM3 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[41540] VGAM1326 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding

site located in an untranslated region of VGAM1326 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1326 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1326 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[41541] VGAM1327 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1327 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1327 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1327 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[41542] VGAM1328 RNA, herein schematically represented by

VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM1328 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1328 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM1328 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[41543] It is appreciated that a function of VGR3032 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3032 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR3032 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR3032 gene: VGAM1326 host target protein, VGAM1327 host target protein and VGAM1328 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1326, VGAM1327 and VGAM1328

[41544] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3033(VGR3033) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[41545] VGR3033 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3033 gene was detected is described hereinabove with reference to Figs. 6-15.

[41546] VGR3033 gene encodes VGR3033 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[41547] VGR3033 precursor RNA folds spatially, forming VGR3033 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3033 folded

precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR3033 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[41548] VGR3033 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 6 separate VGAM precursor RNAs, VGAM1330 precursor RNA, VGAM1331 precursor RNA, VGAM1332 precursor RNA, VGAM1333 precursor RNA, VGAM1334 precursor RNA and VGAM1335 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR, VGAM5 PRECURSOR and VGAM6 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[41549] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1330

RNA, VGAM1331 RNA, VGAM1332 RNA, VGAM1333 RNA, VGAM1334 RNA and VGAM1335 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA, VGAM5 RNA and VGAM6 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[41550] VGAM1330 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1330 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1330 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1330 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[41551] VGAM1331 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1331 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corre-

sponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1331 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1331 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[41552] VGAM1332 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM1332 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1332 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM1332 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[41553] VGAM1333 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM1333 host target RNA, herein schematically represented by VGAM4

HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1333 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM1333 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[41554] VGAM1334 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM1334 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1334 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM1334 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[41555] VGAM1335 RNA, herein schematically represented by VGAM6 binds complimentarily to a host target binding site located in an untranslated region of VGAM1335 host

target RNA, herein schematically represented by VGAM6 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1335 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA into VGAM1335 host target protein, herein schematically represented by VGAM6 HOST TARGET PROTEIN, both of Fig. 1.

[41556] It is appreciated that a function of VGR3033 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3033 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR3033 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR3033 gene: VGAM1330 host target protein, VGAM1331 host target protein, VGAM1332 host target protein, VGAM1333 host target protein, VGAM1334 host target protein and VGAM1335 host target protein, herein schematically represented by

VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1330, VGAM1331, VGAM1332, VGAM1333, VGAM1334 and VGAM1335

[41557] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3034(VGR3034) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[41558] VGR3034 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3034 gene was detected is described hereinabove with reference to Figs. 6-15.

[41559] VGR3034 gene encodes VGR3034 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[41560] VGR3034 precursor RNA folds spatially, forming VGR3034 folded precursor RNA, herein designated VGR FOLDED

PRECURSOR RNA. It is appreciated that VGR3034 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR3034 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[41561] VGR3034 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM1336 precursor RNA and VGAM1337 precursor RNA, herein schematically represented by VGAM1 PRECURSOR and VGAM2 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[41562] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1336 RNA and VGAM1337 RNA respectively, herein schematically represented by VGAM1 RNA and VGAM2 RNA respec-

tively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[41563] VGAM1336 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1336 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1336 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1336 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[41564] VGAM1337 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1337 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1337 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA

into VGAM1337 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[41565] It is appreciated that a function of VGR3034 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3034 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR3034 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR3034 gene: VGAM1336 host target protein and VGAM1337 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN andVGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1336 and VGAM1337

[41566] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3035(VGR3035) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates

expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[41567] VGR3035 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3035 gene was detected is described hereinabove with reference to Figs. 6-15.

[41568] VGR3035 gene encodes VGR3035 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[41569] VGR3035 precursor RNA folds spatially, forming VGR3035 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3035 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR3035 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[41570] VGR3035 folded precursor RNA, herein designated VGR

FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM1340 precursor RNA, VGAM1341 precursor RNA, VGAM1342 precursor RNA and VGAM1343 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR and VGAM4 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[41571] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1340 RNA, VGAM1341 RNA, VGAM1342 RNA and VGAM1343 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA and VGAM4 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[41572] VGAM1340 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1340 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corre-

sponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1340 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1340 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[41573] VGAM1341 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1341 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1341 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1341 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[41574] VGAM1342 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM1342 host target RNA, herein schematically represented by VGAM3

HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1342 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM1342 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[41575] VGAM1343 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM1343 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1343 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM1343 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[41576] It is appreciated that a function of VGR3035 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attack-

ing a host. Accordingly, utilities of VGR3035 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR3035 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR3035 gene: VGAM1340 host target protein, VGAM1341 host target protein, VGAM1342 host target protein and VGAM1343 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1340, VGAM1341, VGAM1342 and VGAM1343

[41577] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3036(VGR3036) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[41578] VGR3036 gene, herein designated VGR GENE, is a novel

bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3036 gene was detected is described hereinabove with reference to Figs. 6-15.

[41579] VGR3036 gene encodes VGR3036 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[41580] VGR3036 precursor RNA folds spatially, forming VGR3036 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3036 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR3036 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[41581] VGR3036 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM1346 precursor RNA, VGAM1347 precursor RNA, VGAM1348 precursor RNA, VGAM1349 pre-

cursor RNA, VGAM1350 precursor RNA, VGAM1351 precursor RNA, VGAM1352 precursor RNA and VGAM1353 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR, VGAM5 PRECURSOR, VGAM6 PRECURSOR, VGAM7 PRECURSOR and VGAM8 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[41582] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1346 RNA, VGAM1347 RNA, VGAM1348 RNA, VGAM1349 RNA, VGAM1350 RNA, VGAM1351 RNA, VGAM1352 RNA and VGAM1353 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4 RNA, VGAM5 RNA, VGAM6 RNA, VGAM7 RNA and VGAM8 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[41583] VGAM1346 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1346 host target RNA, herein schematically represented by VGAM1

HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1346 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1346 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[41584] VGAM1347 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1347 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1347 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA into VGAM1347 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[41585] VGAM1348 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM1348 host

target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1348 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM1348 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[41586] VGAM1349 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM1349 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1349 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM1349 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[41587] VGAM1350 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding

site located in an untranslated region of VGAM1350 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1350 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM1350 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[41588] VGAM1351 RNA, herein schematically represented by VGAM6 binds complimentarily to a host target binding site located in an untranslated region of VGAM1351 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1351 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA into VGAM1351 host target protein, herein schematically represented by VGAM6 HOST TARGET PROTEIN, both of Fig. 1.

[41589] VGAM1352 RNA, herein schematically represented by

VGAM7 binds complimentarily to a host target binding site located in an untranslated region of VGAM1352 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1352 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA into VGAM1352 host target protein, herein schematically represented by VGAM7 HOST TARGET PROTEIN, both of Fig. 1.

[41590] VGAM1353 RNA, herein schematically represented by VGAM8 binds complimentarily to a host target binding site located in an untranslated region of VGAM1353 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1353 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA into VGAM1353 host target protein, herein schematically represented by VGAM8 HOST TARGET PROTEIN, both of Fig. 1.

[41591] It is appreciated that a function of VGR3036 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3036 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR3036 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR3036 gene: VGAM1346 host target protein, VGAM1347 host target protein, VGAM1348 host target protein, VGAM1349 host target protein, VGAM1350 host target protein, VGAM1351 host target protein, VGAM1352 host target protein and VGAM1353 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1346, VGAM1347, VGAM1348, VGAM1349, VGAM1350, VGAM1351, VGAM1352 and VGAM1353

[41592] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred

to here as Viral Genomic Record 3037(VGR3037) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[41593] VGR3037 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3037 gene was detected is described hereinabove with reference to Figs. 6-15.

[41594] VGR3037 gene encodes VGR3037 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[41595] VGR3037 precursor RNA folds spatially, forming VGR3037 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3037 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of VGR3037 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which

is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[41596] VGR3037 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM1354 precursor RNA, VGAM1355 precursor RNA, VGAM1356 precursor RNA, VGAM1357 precursor RNA, VGAM1358 precursor RNA, VGAM1359 precursor RNA, VGAM1360 precursor RNA and VGAM1361 precursor RNA, herein schematically represented by VGAM1 PRECURSOR, VGAM2 PRECURSOR, VGAM3 PRECURSOR, VGAM4 PRECURSOR, VGAM5 PRECURSOR, VGAM6 PRECURSOR, VGAM7 PRECURSOR and VGAM8 PRECURSOR respectively, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM PRECURSOR RNA of Fig. 8.

[41597] The above mentioned VGAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1354 RNA, VGAM1355 RNA, VGAM1356 RNA, VGAM1357 RNA, VGAM1358 RNA, VGAM1359 RNA, VGAM1360 RNA and VGAM1361 RNA respectively, herein schematically represented by VGAM1 RNA, VGAM2 RNA, VGAM3 RNA, VGAM4

RNA, VGAM5 RNA, VGAM6 RNA, VGAM7 RNA and VGAM8 RNA respectively, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 8.

[41598] VGAM1354 RNA, herein schematically represented by VGAM1 binds complimentarily to a host target binding site located in an untranslated region of VGAM1354 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1354 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA into VGAM1354 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN, both of Fig. 1.

[41599] VGAM1355 RNA, herein schematically represented by VGAM2 binds complimentarily to a host target binding site located in an untranslated region of VGAM1355 host target RNA, herein schematically represented by VGAM2 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1355 host target RNA, herein

schematically represented by VGAM2 HOST TARGET RNA into VGAM1355 host target protein, herein schematically represented by VGAM2 HOST TARGET PROTEIN, both of Fig. 1.

[41600] VGAM1356 RNA, herein schematically represented by VGAM3 binds complimentarily to a host target binding site located in an untranslated region of VGAM1356 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1356 host target RNA, herein schematically represented by VGAM3 HOST TARGET RNA into VGAM1356 host target protein, herein schematically represented by VGAM3 HOST TARGET PROTEIN, both of Fig. 1.

[41601] VGAM1357 RNA, herein schematically represented by VGAM4 binds complimentarily to a host target binding site located in an untranslated region of VGAM1357 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby in-

hibiting translation of VGAM1357 host target RNA, herein schematically represented by VGAM4 HOST TARGET RNA into VGAM1357 host target protein, herein schematically represented by VGAM4 HOST TARGET PROTEIN, both of Fig. 1.

[41602] VGAM1358 RNA, herein schematically represented by VGAM5 binds complimentarily to a host target binding site located in an untranslated region of VGAM1358 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1358 host target RNA, herein schematically represented by VGAM5 HOST TARGET RNA into VGAM1358 host target protein, herein schematically represented by VGAM5 HOST TARGET PROTEIN, both of Fig. 1.

[41603] VGAM1359 RNA, herein schematically represented by VGAM6 binds complimentarily to a host target binding site located in an untranslated region of VGAM1359 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1359 host target RNA, herein schematically represented by VGAM6 HOST TARGET RNA into VGAM1359 host target protein, herein schematically represented by VGAM6 HOST TARGET PROTEIN, both of Fig. 1.

[41604] VGAM1360 RNA, herein schematically represented by VGAM7 binds complimentarily to a host target binding site located in an untranslated region of VGAM1360 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1360 host target RNA, herein schematically represented by VGAM7 HOST TARGET RNA into VGAM1360 host target protein, herein schematically represented by VGAM7 HOST TARGET PROTEIN, both of Fig. 1.

[41605] VGAM1361 RNA, herein schematically represented by VGAM8 binds complimentarily to a host target binding site located in an untranslated region of VGAM1361 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA, which host target binding site corre-

sponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1361 host target RNA, herein schematically represented by VGAM8 HOST TARGET RNA into VGAM1361 host target protein, herein schematically represented by VGAM8 HOST TARGET PROTEIN, both of Fig. 1.

[41606] It is appreciated that a function of VGR3037 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3037 gene include diagnosis, prevention and treatment of viral infection by . Specific functions, and accordingly utilities, of VGR3037 gene, herein designated VGR GENE, correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the operon-like cluster of VGR3037 gene: VGAM1354 host target protein, VGAM1355 host target protein, VGAM1356 host target protein, VGAM1357 host target protein, VGAM1358 host target protein, VGAM1359 host target protein, VGAM1360 host target protein and VGAM1361 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through

VGAM HOST TARGET PROTEIN respectively. The function of these host target genes is elaborated hereinabove with reference to VGAM1354, VGAM1355, VGAM1356, VGAM1357, VGAM1358, VGAM1359, VGAM1360 and VGAM1361

[41607] Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3038(VGR3038) viral gene, which encodes an operon-like cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[41608] VGR3038 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3038 gene was detected is described hereinabove with reference to Figs. 6-15.

[41609] VGR3038 gene encodes VGR3038 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[41610] VGR3038 precursor RNA folds spatially, forming VGR3038 folded precursor RNA, herein designated VGR FOLDED